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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Homo		Mus	Ö	AC129703 Rattus no	AX201302 Sequence	AX099802 Sequence	Ar214519 Homo sapi	AC127107 Rattus no	AX099774 Sequence	AX099800 Sequence	AX398331 Sequence	AX398333 Sequence AX398335 Seguence	AX398337 Sequence	AX398339 Sequence	G67375 A898 Human	AC127107 Rattus no	AL627254 Danio rer	AC015513 Homo sapi	AC019242 Homo sapi	AC011603 Homo sapi	ACU/36IU HOMO Sapi ACU25256 HOMO Sabi		BC000358 Homo sapi	AKU9/606 Homo sapi AX364914 Segmence	AC006966 Homo sapi	AF094763 Drosophil	ACONSAA Procophil	AC008308 Drosophil	AE003733 Drosophil	I66494 Sequence 14	AX482895 Sequence AF094764 Drosophil	38			5	IIHEAK FAI US-NUV-ZUUL			Vertebrata; Euteleostomi; Hominidae; Homo.	:	ein Kinase gamma 3 subunit
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123597 137837; contig of 14241 bp in length
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46465: gap of 100 bp
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51385: gap of 100 bp
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|5144. .17123
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Calangelo, M., Collins, S., Campopiano, A., Castle, A., Choepel, Y., Calangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dear, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Carduc, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Klein, J., Lakocque, K., Lamaczers, R., Landers, T., Lehoccky, J., Lenn, J., Lakocque, K., Landers, T., Lehoccky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McDarthy, M., McEwan, P., McGurk, J., Mnensu, E., Mihova, T., Minanda, C., Mengal, Y., Morrow, J., Wurphy, T., Waylor, J., Nihova, T., Mitanda, C., Menga, Y., Rodov, P., Rothman, D., Pisani, C., Pollara, Y., Raymond, C., Rilley, R., Rodov, P., Rothman, D., Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Young, G., Zainoun, J., Zimmer, A., Wulson, B., Wull, M., Wunker, M., Wunker, M., Vel, R., Vola, R., Velland, A., Tanders, M., Trigillo, J., Young, G., Zainoun, J., Zimmer, A., Tander, Wunker, M., Wulson, B., Wann, John, Whitch, M., Wilson, B., Well, M., Wilson, B., Well, M., Well,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (33-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 7, 2000 this sequence version replaced gi:7342115.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center project Information
Center clone name: 17458
Center clone name: 504_G_11
Center clone name: 504_G_11
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap, version 0.960731
Consensus quality: 135376 bases at least Q40
Consensus quality: 143264 bases at least Q30
Consensus quality: 145263 bases at least Q30
Insert size: 161009; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; sum-of-contigs
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648 9983: contig of 2336 bp in length
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 8, 2001 this sequence version replaced g1:13431203.
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Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                          1621 CATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAA 1680
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4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                    TATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACC
                                                                                                                                                                                                                                                                                                                              2, complete sequence.
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                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                      34938 CGAATGTGGTACCCACCCCAGGATGAGAGGCTCGGCTGG 34898
                                                                                                                                                                                   1681 CGAATGTGGTACCCACCCCAGGATGAGAGGCTCGGGCTGG 1721
                                                                                                                                                                                                                                                                                                   AC009974 206854 bp DNA HOMO sapiens BAC clone RP11-459119 from AC009974
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Sulston, J.E. and Waterston, R.
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Waterston, R. H.
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4 (bases 1 to 206854)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

MAPPING INFORMATION:

Louis Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Mashington University, St. I MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

Location/Qualifiers .206854

/organism="Homo sapiens" /db_xref="taxon:9606" /clone="RP11-459119" /chromosome-"2" /map="2

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.. .37 "note="match to EST AL567345 (NID:g12920610)" /note="match to EST AW880850 misc_feature

(NID:98364652) tz39c01.y1" (NID:98042860)" /note="match to EST BE314060 (NID:99134719)" 1. .37 /note="match to EST BE047599 .37 misc_feature misc_feature

'note="match to EST BF183086 (NID:g11061273)" /note="match to EST BF304755 misc_feature misc_feature

'note="match to EST BG477625 (NID:913409904)" 'note="match to EST BI059713 (NID:g14467240)" misc_feature misc_feature

misc_feature

'note="similar to Homo sapiens EST BI114348
NID:g14565249)" misc_feature

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/note="match to EST BG470047 (NID:g13402322)" 281. .344 /note="match to EST A1670836 (NID:g4850567) wa04g10.x1" misc_feature misc_feature

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Center code: WGGSC Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu

Center project name: H_NH0459119

restriction digest.

The RPCI-11 human BAC library was made from the blood of one male SOURCE INFORMATION:

VECTOR: pBACe3.6 NEIGHBORING SEQUENCE INFORMATION:

source FEATURES

Best	Match	QY	අු	δλ	qu	QY	ф	δŏ	qq	Qy	qa	ΟΥ	<u>අ</u>	λo ·	gg (Ç.	gg (ð 1	3 8	73 H	3 8	\$ t	gg &o	ପ୍	ζŎ	qq	ζŎ	qa	QY	අධ	δŏ	q _Q	Oy.	q a	oy.
281 344	/note="match to EST AL567345 (NID:g12920610)"	/note="match to EST AW880850 (NID:98042860)"	281344 /note="match to EST BE047599 (NID:98364652) tz39c01.y1"		a)	281344 /note="match to EST BF183086 (NID:g11061273)"	281344 /note="match to EST BF304755 (NID:911251653)"	281344 /note="match to EST BG477625 (NID:g13409904)"	Z81344 Anote-match to EST BI059713 (NID:g14467240)"	.21344 /note="similar to Homo sapiens EST BI114348 (NID:314565249)"	294, .344 /note="match to EST BG470047 (NID:913402322)"	57558) to EST AA043371	588929 /note="match to EST T64073 (NID:9667938) yc05d12.r1"	Ę.	763 te="match to EST AA043371	594763 /note="match to EST A1670836 (NID:94850567) wa04910.x1"	594 / 63 /note="match to EST AW880850 (NID:98042860)"	594763 forte-"match to EST BE908408 (NID:910402954)"	(1)	594:/83 /note=.match to EST BF304755 (NID:g11251653)" 504		ote="match to EST EG477625 (NID:gl3409904)"	594 7b3 /note="similar to Homo sapiens EST BI114348 (NID:g14565249)"	594742 /note="match to EST BE047599 (NID:98364652) tz39c01.y1"	594731 /note="match to EST BE314060 (NID:99134719)"	599083 /pote="match to EST AL567345 (NID:912920610)"	01/: .1004 /note=match to EST AA481361 (NID:92210913) zv44e01.rl" 633 - 763	022/03 /note="match to EST A1860958 (NID:95514574) w156f05.x1" 627 763	022/O3 /note="similar to Mus musculus EST AI196847 (NID:93749453) ui67e01.x1"	684763 /note="match to EST BG992568 (NID:g14396638)"	9621084 /note="match to EST A1656812 (NID:94740791) tt54b06.x1"	9671091 /note="match to EST AA043371 (NID:91521226) zk53e10.rl"	ir to Homo sapien		98.5%; Score 1697; DB 9; Length 206854;
mico feature	miso foaturo	ייידאכ_דיכמייזי	misc_reature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_reature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature					misc_reacure	misc_reature	misc_teacure	misc_feature	misc_feature	misc_feature	misc_feature	miss_reature	misc_teature	mrsc_rearure	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	Query Match

166398 166338 166278 166277 ACTGTCCTGTTCCCACAGTCCCCACTGTGTCTCAGCACAAGGACACTGGCAGGGGGGGA 166218 166099 165979 165919 165800 166638 1020 5; 909 780 840 900 420 480 99 720 960 240 300 180 360 9 1166038 AGGGGAGTCCTCCTGGAGCCTGGTGCCCTAGAAGCCCACGTTTTTGTGACTTCTGGAGTC AGGGGAGTCCTCCTGGAGCCTGGTGCCCTAGAAGCCCACGTCTTTCTGACTTCTGGAGTC 781 GGGTGAGTGGGGAGAGGAACCCGGAAAGGGGCTGTTGGTGATGGTGGCCCAGGGCTTAAG 901 GGTGCCTGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGTGACCGGCTCCCC 961 TGGCCTGACTCTGGCTCTTTCTGCAGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGT 1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC 301 AIGACCAGCIGACACCITICACCICCGCIACIGCAIGCCCIGIGCCAIAGGIGCIAGGG ACTGTCCTGTTCCCACAGTCCCCACTGTGTCTCAGCACAAGGACACTGGCAGGGTGGGGGA 541 CCTCCCCTGCAGGGATGCTGACCATCACTGACTTCATCCTGGTGCTGCATCGCTACTACA CTGTCGATGTCTAGGTCCAGATCTATGAGATTGAACAACATAAGATTGAGACCTGGAG 121 GGAGATGGAGGAGGTGAGGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 241 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGGTCAATTTCCCCCATCTGTGGAGCCGCT ACCACAGGAGGTTGGCTTCAGGCCAAGCCCAGGGGCCCAGGGTGGAGGAAAGTCCATCC Gaps 3 ö Pred. No. 0;
0; Mismatches Local Similarity 99.9%; hes 1719; Conservative 661 421 601 721 181

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/product-"AMPK gamma subunit"
join(1. 154.515. 918,1809. 1890,2349. 2407,2509. 2554,
2771. 2825,3027. 3153,3286. 3451,4578. 4615,4791. 4937,
5294. 5410)
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HFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLMDSKKQSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILITALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGCTTGGCTTCAGGCCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCCGGAG 244
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC Box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 TCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCCATCTGTGGAGCCGCTATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 GGAGCAAATGGGGGGAGGCAGGAGAGAAAAAGCCCCCACTTCTCAGGCCTGGGGGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 others
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Pred. No. 1.9e-140;
0; Mismatches 484;
                                                                                                                                                                                                                                                                                                                                                                                       /product="AMPK gamma subunit"
/protein_id="AAF/3989.1"
/db_xref="GI:8215686"
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                                                                                         organism="Sus scrofa"
                                                                                                           /db_xref="taxon:9823"
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                                                  Location/Qualifiers
1. .5888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALVLSPAGIDALGA
                                                                                                                                                                                     /gene="PRKAG3"
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                                                                                                                                                /map="15g'
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Matches 1155; Conservative
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                                   165439 CACCCTCATCAAGAACCGGATCCATCGCCTGCTGTTCTTGACCCGGTGTCAGGCAACGT 165380
                                                                                                                                                                                                                                                                                                                                                          165200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAM 03-JUN-2000
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robio,A.,
Rogel-Gailland,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
                                                                                                               1141 CAGACAAGGGAGCCTTGGTGCCCTGCCCTCTTTTAGGGGCCTGGGATGGAGGTTGTCT
                                                                                                                                 CACCCTCATCAAGAACCGGATCCATCGCCTGCTGTTCTTGACCCGGTGTCAGGCAACGT
                                                                                                                                                                                                                                                                                                                                        1321 ACTCCACATCCTCACACACAAAGGCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa AMPK gamma subunit (PRKAG3) gene, complete cds.
aF214521
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Science 288 (5469), 1248-1251 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC128U7U
Rattus norvegicus clone CH230-262H11, *** SEQUENCING IN PROGRESS
***, 65 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                       1399 GGAGACCTGGGCAGGTGATCAGAGGGCCTGAGGAGTCTTCAGCCCTAGCAGTCGTGGGGA 1458
                                                                                                                                                                                                                     ----- 5585
                                                                                                                                                                                                                                                              1459 AGAGCTGGGAGCCCTCTTGAAGCTGCTGGATCCCTGATCTCCACCTGGTCCCCATCCTAA 1518
                                                                                                                                                                                                                                                                                                         -----CTAGATCAAGTGTCTTGATCTGATGAGATCACTACCATGTCCCATCTTA 5536
                                                                                                                                                                                                                                                                                                                                                   1519 CCAGGGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCAT 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                       1579 CGCCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGA 1638
                      1339 CAAACGCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGGCCCAGGTGGGAGGAGGAAGGG 1398
GATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCACACA 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata, Craniata; Vertebrata; Buteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5415 CATCTTTGTGGACCGACGTGTCTCGCACTGCCTGTGGTCAATGAATCTGGTA 5363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1639 CATCTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGGTA 1691
                                                                                                                                                                                                                  GAGAGCCACGGGAGACACT
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Rattus norvegicus
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 65 conling. The true order of the pieces

* is not known and their order in this sequence record is
Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherers, S., Scott, G., Shen, H., Shocshtari, N., Sisson, I., Scott, G., Shen, H., Shocshtari, N., Sisson, I., Sucten, E., Sonaike, T., Sarks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Verra, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williams, G., Williams, G., Wulliamson, A., Wleczyk, R., Wooden, S., Worley, K., Weinston, Wu, Y., R., Zorrilla, S., Nelson, D., Weinston, D., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0,990129 Consensus quality: 72428 bases at least Q40 Consensus quality: 76114 bases at least Q30 Consensus quality: 79522 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project Information
Center clone name: GZRR
Center clone name: CH330-267H11
Sequencing vector: Plasmid;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                        68; Gaps
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Pred. No. 8.3e-38;
0; Mismatches 123; Indels 68; 0
J. 2428 bt.
Jf unknown len,
Jf unknown len,
Jenig of 3438 bp in
A gap of unknown length
JO2186: gap of unknown length
J6593: contig of 2407 bp in len,
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Tening of 4259 bp in length
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AC129703
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Marany, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Allen, H., Absbrooks, S., Adin, A., Angulaho, D., Allan, H., Absprooks, S., Adin, A., Angulaho, D., Angulah, A., Angulaho, D., Angulah, A., Angulaho, D., Bandarnahike, D., Bander, M., Benahmed, F., Biswallo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Carter, A., Carter, A., D., Carter, A., D., Cardens, J., Chang, J., Davila, M. L., Davals, J., Dermandez, C., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Elgen, C., Evras, C., Cayle, M., Garca, M., Harney, K., Havlak, P., Hawes, A., Handiron, C., Hamilton, C., Karff, C.L., Lobow, H., Johnson, R., Johnson, R., Johnson, R., Jackson, A., Jackson, L., Liu, W., Liu, Y., Lohow, L., Liu, W., Mahindartne, M., Mahand, M., Malloy, K., Martin, K., Martin, K., Martin, K., Martin, K., Martin, M., Maylue, N., Martin, M., Maylue, N., Martin, M., Maylue, N., Martin, M., Maylue, M., Martin, M., Mayl
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Submitted (01-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
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------- Project Information
Center project name: GDEC
center clone name: CH230-917
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Rat Genome Sequencing Consortium.
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 141109 bases at least Q40 Consensus quality: 148891 bases at least Q20 Consensus quality: 155675 bases at least Q20
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2810
4027
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7504
7604
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bp in length

PAT 02-NOV-2001

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SSERIRGKRRAKALRWIRGKSVEBGEPPGGGEGPRSRPAAESTGLEATFPKTPLAQA
DPAGVYGPPGWCLPSPACTASAAGSSTDOWELATEPPATEMECELEGLLEERPALC
LSPQAPFRLGWDDELRKPGOLYMERWGERTCYDAMATSSKLVIFDYMLBIRKAFFA
LVANGVRAAPLMDSKKGSFVGMLITTDFILVLHRYYRSPLVQIYEIEQHKIETWREIY
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GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQV
VGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIARE
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/db_xref="G1:16608834"
/translation="MePGLEHALRRTPSWSSLGGSEHQEMSFLEQENSSSWPSPAVTS
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                                                                      1603 GGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTC 1662
                                                                                                                                 Andersson, L., Luthman, H. and Marklund, S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 5 18-OCT-2001; Araxis AB (SE)
                                                                                                                    1663 TGCACTGCCTGTGGTCAACGAATGTGGTACCCACCCCAGGATGAGAGGCTCGGGCTGG 1721
                                                                                                                                                                                                                                                                           Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref~"taxon:9606"
20. .1489
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Sequence 5 from Patent WO0177305.
AX281582
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LMDSKKQSFVGMLTTDFILVLHRYKSEPLVQIPELGGKFETVS
ISPNDSLEEAVYLIKRIHELPVLDPVSGNYLHILTHKRILKFLHFGSLLFRFSFLVS
ISPNDSLEEAVYLIKRIHELPVLDPVSGNYLHILTHKRILKFLHFGSLLFRFSFLV
KRIIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVI
HLAAQOTYNHLDMSVQEALRORTLCLEGVLSCOPHESLGEVIDRIARROVHRLVLVDE
TQHLLGVVSLSDILLQALVLSPAGIDALGA"

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2115)
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., 1e Roy, P. and
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2109)
Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., lannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.
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                                                                                                                                                                                                                                                           same, and uses thereof
parent: Wo 0120003-A 3 22-MAR-2001;
INSTITUT MATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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Pred. No. 1e-30;
0; Mismatches 8; Indels 0;
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Sequence 29 from Patent W00120003.
AX099802
                              AX099776 2109 bp
Sequence 3 from Patent W00120003.
AX099776 11:13538810
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/organism="Homo sapiens"
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/db_xref="G1:13538811"
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Location/Qualifiers
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                                                                                                                 human.
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Best Local S.
Matches 173
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                                               DEFINITION
ACCESSION
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AX099802
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VERSION
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                                                                                                                                ORGANISM
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KEYWORDS
SOURCE
                                                                                                                                                                              REFERENCE
                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                            JOURNAL
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RESULT 9
AX099776
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Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                 /protein_id="CAC35801.1"
/db_xref="G1:13538837"
/translation="MSFLEQENSSWPSPAYTSSSERIRGKRRAKALRWTRQKSYEEG
EPPQGGEGPRSRPAESTGLEATFPKTTPLAQADPAGYGTPPTGWDCLPSDCTASAAG
                                                                                                                                                                                                                                                                                                                                                                                                                           RFWGEHTCYDAMATSSKLVIFDTWLEIKKAFPALVANGVRAAPLWDSKKQSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLGGCFKPLVSISPNDSLFEAVYTLI
KNRIHRLPVLDPVSGNVLHILTHKRLIKFLHIFGSLLPRPSFLYRTIGDLGIGTFRDL
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GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
                                                                                                                                                                                                                                                                                                                                                                                                       SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
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1 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
                    same, and uses thereof
Patent: WO 0120003-A 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
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gamma chain of ampk, dna sequences encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Length 2115;
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                                                                                                                                                                                                                                                     /note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471 t
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Science 288 (5469), 1248-1251 (2000)
                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                 /codon_start=1
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95.6%;
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  Variants of the
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Rattus norvegicus clone CH230-206Al3, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNBCGQV VGLYSRRDVIHLAAQOTYNHLDMSVGBALRKRTLCLEGVLGCYPESLGEVIDRIARB OVHRUNLVDSTQHLGVYSLSDTLAAVLSPAGIDPSGPEKI"

674 c 617 g 498 t
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LVANGVRAAPLWDSKKQSFVGMLFITDFILVLHRYYRSPLVQIYEIBQHKIETWREIY
LQGCFKPLVSISPNDSLFBAVYTLIKNRIHRLPVLDPVSGNVLHIITHKRLLKFLHIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MEPGLEHALRRTPSWSSIGGSEHQEMSFLEQENSSSWPSPAVTS
SSERIRGKRRAKALRWTRQKSVEEGEPPGGGEGPRSRPAAESTGLEATFPKTTPLAQA
DPGGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1071 TITGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1130
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                           /product="Ang-actived protein kinase gamma 3 subunit"
/protein_id="CAB65117.1"
/db_xref="GI:6688201"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1570 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC
2 (bases 1 to 2290)
Carling,D
Direct Submission
Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
London, W12 ON, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 /function="AMP-activated protein kinase regulatory subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.8%; Score 168.2; DB 9; Length 2290; 95.6%; Pred. No. 1e-30;
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                                                                                                                                                              1. .2290
/organism="Homo sapiens"
/db_xref="taxon:9606"
22. .1500
                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=experimental
                                                                                                                                                                                                                                       /gene="AMPK gamma 3"
22. .1500
                                                                                                                                                                                                                                                                                                   /gene="AMPK gamma 3"
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HTG; HTGS_PHASE1.
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AC127107/c
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       REFERENCE
AUTHORS
                                                TITLE
JOURNAL
                                                                                                                                                                                                                                       gene
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KEYWORDS
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                                                                                                                                           FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG
EPPGQGGGPRSRPTAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAG
SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDFILVLHRYTRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFBAYTLI
KNRHHELPVLDYVSGVHJALICHRIKAEKLHFRGSLLDRFSFLYRTDLOGGIGFRDL
AVVLETAPTLTALDIFVDRRVSALPVVNECGQVVGLYSREDVIHLAAQOTVHLLDMSV
GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
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Kalm.E., Le Roy.P., Chardon.P. and Andersson.L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 2290)

Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
Biochem. J. 346 pt 3, 659-669 (2000)

10698692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="AMP-activated protein kinase gamma subunit"
/protein_id="AAF73987.1"
/db_xref="GI:8215682"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                        /tissue_type="skeletal muscle"
1. .2115
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                                                                                                              Location/Qualifiers
1. 2115
Acrganism="Homo sapiens"
Ab xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                562 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALVLSPAGIDALGA"
                                                                                                                                                                                                                                                                                                   /gene="PRKAG3"
                                                                                                                                                                                                                                                                                                                                                                      /note-"AMPKG3"
                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                 /gene="PRKAG3"
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AJ249977.1 GI:6688200
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Carron T.F., Carter.M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Clean, R., Chen, E., Chowdhry, I., Christopoulos, C., Clean, C., Coyle, M.D., Dabtorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Sao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gannatate, P., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hennandez, O., Hodgeson, A., Hogues, M., Holloway, C., Hollins, B., Hennandez, O., Hodgeson, A., Hogues, M., Holloway, C., Hollins, B., Hamilton, K., Kartovic, J., Kally, S., Khan, U., King, L., Korwat, J., Kovar, C., Kartovic, J., Klark, S., Khan, U., King, L., Korwat, J., Kovar, C., Kratovic, J., Klark, S., Khan, U., King, L., Korwat, J., Kovar, C., Liu, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H., Li, J., Li, Z., Lu, X., Lucier, N., Lucier, R., Luna, R., Mar, J., Martinez, E., Martine, B., Martinez, E., Martin, R., Martinez, B., Marmer, G., Miner, Z., Martin, R., Martindale, A., Mayen, N., Maba, P., Mitchell, T., Mohabbat, K., Morgan, M., Mosa, D., Newtson, J., Rober, J., Rober, J., Rober, J., Sodergre, B., Stolake, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, M., Thomas, S., Usmani, K., Vasquez, L., Parka, Y., Villalon, D., Vinson, B., Warlington, S., Ward-Moore, S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 74 conlists. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as
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gap of unknown length
contig of 1170 bp in length
gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- Genome Center
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Unpublished
2 (bases 1 to 192968)
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REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL

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length

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Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3) mRNA, complete cds.
AF214520.
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ISPNDSLFRAVYALIKNRIHRLPVLDPVSGAVLHITHRRLLKFLHIFGTLLDRRSFL
YRTIQDIGGTGOFRDLAVVLETAPLITALDIFVDRRYSALPVVNETGQVGLYSRPDVI
HLAAQQTYNHLDMNVGEALRQPTLCIEGVLSCQPHETLGEVIDRIVREGVHRLVLVDE
TQHLLGVYSLSDIIAALUTJAALUTJAADIJAALGA
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Milan, Jeon, J. T. Looft, C., Amarger, V., Robic, A., Thelander, M.,
Rogel-Gaillard, C., Faull, S., Iannuccelli, N., Rask, L., Ronne, H.,
Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24, Sweden
                                                                                                                                                                                                                                                                                                                                                              /db_xref="G1:13538809"
/translation="MHFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Milan, Jeon, J.T., Looft, C., Amarger, V., Robic, A.,
Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
             Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
Patent: WO 0120003-A 1.2-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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Pred. No. 1e-25;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                    /note="unnamed protein product"
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Science 288 (5469), 1248-1251 (2000)
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                                                                                                                                                                                                  /organism="Sus scrofa"
/db_xref="taxon:9823"
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1. .1873
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Matches 160; Conservative
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Direct Submission
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Sus scrofa
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  Chardon, P.
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0; Mismatches 33: T-
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7: contigo of 1901 b
77: gap of unknown 1
5: contig of 3218 b
15: gap of unknown 1
77: gap of unknown 1
77: contig of 52082 b
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of 2738
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103845: contig of 2649
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82; Conservative
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8.6%; Score 148; DB 4; Length 1873;
Best Local Similarity 88.9%; Pred. No. 1e-25;
Matches 160; Conservative 0; Mismatches 20; Indels
                                      /db_xref="t-axon:8823"
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1. 1873
/gene="PRKAG3"
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/note="PRKAG3"
/organism="Sus scrofa"
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Search completed: June 14, 2003, 16:15:58 Job time : 4498 secs

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Human bone marrow Probe #1565 for g Probe #16674 used Probe #8345 used t Human genome-deriv Disease associated DNA encoding novel

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Result

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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
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/note= "3' portion of intron 4"
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                                                                                                                                               ABC98774
ABC39774
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/number= "Intron 5"
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variants of human AMP-activated protein kinase gamma3 subunit poiated with a metabolic disease e.g. diabetes or obesity and method determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAH436B1-84 represents genomic fragments encoding the human AAP-activated protein Kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PKKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A, in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a nucleotide 550; and in exon 10 variation may be a substitution of a lor of a c at nucleotide 1037, resulting in the manno acid substitution R340W. There may also be nucleotide variation in intron 6.
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                                                                                                                                                                                                                                                                            agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCIGGCCCCTCAGAICAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
                                                                                The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression nallysis is useful for assessing the toxicity of chemical
useful for measuring gene expression in sample derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.4%; Score 351; DB 22; Length 378; 99.7%; Pred. No. 9e-83;
                   breast, comprises number of single exon nucleic acid probes
                                                       Claim 1; SEQ ID NO 3401; 327pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                  from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
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                   ACTCCACATCCTCACACACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGG 1380
                                                                                                                                                                         CCCAGGTGGGAGGAAGGGGGAGACCTGGGCAGGTGATCAGAGGGCCTGAGGAGTCTTCAG 1440
 CTCCCTAGGCTGCCCCGAGGCTCACTGCTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTA
                                                                                              CCCTAGCAGTCGTGGGGAAGAGCTGGAAGCCTCTTGAAGCTGCTGGATCCCTGATCTCC
                                                                            CACCCTCATCAAGAACCGGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGT
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2000US-0608408.
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2000US-0236359.
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21-SEP-2000;
27-SEP-2000;
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120

Gaps

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180

183

243

240

123

63

SS.

27-SEP-2000; 04-OCT-2000;

Penn SG,

04-FEB-2000;

09-AUG-2001

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predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 ACCACAGGAGCTTGGCTTCAGGCCAAGCCCAGGGCCAGGGTGGAGAAAGTCCATCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCCTGATCTCTGATAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
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                                                                                                  Probe #3373 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 378;
                                                                                                                                       Human, gene expression, heart, microarray, vascular system,
cardiovascular disease, hypertension, cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.4%; Score 351; 99.7%; Pred. No. 9e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 3373; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                             congenital heart disease; ss.
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2000US-0608408.
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                                                           (first entry)
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                                                                                                                                                                                                                                                       WO200157274-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-2000;
                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
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                                                           23-JAN-2002
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGTCTGCATGGCCAGCTGGGAACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 CCTGGCCCCTCAGATCAAGAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGTGAGGAGGCTGGGGGAGGTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.4%; Score 351; DB 22; Length 378; 99.7%; Pred. No. 9e-83; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 3467; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                    DR;
                                                                                                                                                                                                                                                                                                                    Rank
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ID ABA24907 standard; DNA; 378 BP.
                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0234687.
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2000US-0608408.
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WO200157277-A2
                                                                                                                                    26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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Query Match Best Loc Matches 241

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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                   ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGGTGGAGGAAAGTCCATCC
                                                                                                                                                                                                        62 ATGACCAGCTGACACTTTCACCTCCGCTACTGCATGCCCCTGTG-CATAGGTGCTAGGG
                                   GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT
                                                                                                                                         GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGGCTCAATTTCCCCATCTGTGGAGCCGCT
                                                                                                                                                       GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT
                                                                                                                                                                                           ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG
The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                               Human bone marrow expressed single exon probe SEQ ID NO: 3431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probes useful
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ID AAK28874 standard; DNA; 378 BP.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000GB-0024263.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGGAGGCTGGGGGAGGTGAAG 120
                                               301 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG 360
GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCCAGC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
                                                              62 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTG-CATAGGTCAGGG
             Gaps
                                                                                                                                                                                                                                                                                             Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in
brains -
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                                                                                                                                                                                                                                                                      expressed single exon probe SEQ ID NO: 3414.
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; 2000US-0632366.
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99.7%;
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                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483446/52.
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                                                                                                   AGC 363
                                                                                                                   4; SEQ
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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30-JUN-2000;
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                                                                                                                                                                                                                                                                      Human brain
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Gaps 1;

Length 378; Indels

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ACCACAAGCTTGGCCTTCAGGCCCAAGCCCAGGGGCCCAGGGTGGAGGAAAGTCCATCC 240
                                                                                                                                                                                                                                                                                                                                                                       241 GGAGICIGCAIGGCCAGCIGGGAGACCCTGGGGCTCAATITCCCCATCTGTGGAGCCGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGCCCTGTGCCATAGGTGCTAGGG 360
                                                                                                                                                                                                                                                          61 CCCTCTATGGGACAGCAGAAGCAGAGCTTTGTGGGTGAGGAGGTGGGGGAGGTGAAG 120
                                                                                                                                                                                                                                                                                                        GGAGATGGAGGAGGTGAGGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                     62 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTG-CATAGGTGCTAGGG 4
The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                          1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray; human; placenta; antenatal diagnosis;
                                                                                                                                   Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                          22;
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0
                                                                                                                                                          Score 351; DB 23
Pred. No. 9e-83;
                                                                                                                                                                                   0; Mismatches
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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ID AAI34821 standard; DNA; 378
                                                                                                                                                          20.4%;
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                                                                                                                                                                    Local Similarity 99.7
mes 362; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGC 363
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| AGC 1
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                          Query Match
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Matches
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                                                                       CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC 303
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                                                                                                            GGAGATGGAGGAGGTGAGGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT
                                                                                                                                                           242 GGAGATGGAGGAGGAGAGATCTTGTACGCTTGTACTGGGGCTGATCTCTGGAGATT
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                                                 1 CCTGGCCCCTCAGATCAAGAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCAGC
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                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for gene expression analysis in human cervical cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; microarray; gene expression; cervical epithelial
                         1;
                         Indels
  Length
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 DB 22;
Score 351; DB 2;
Pred. No. 9e-83;
                        0; Mismatches
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
20.4%;
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                         362; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cervical cancer; ss.
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              Similarity
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26-MAY-2000; 2
30-JUN-2000; 2
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Query Match
Best Local
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29-JAN-2001; 2001WO-US00661
                                                                                 04-OCT-2000;
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Best Local Si
Matches 362;
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                                                                                                                                                                                                                                                                            362 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCAGC 303
                                                                                                                                                                                                                                                                                                 121 GGAGATGGAGGAGGTGAGGGGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT 180
                                                                                                                                                                                                                                                                                                                                                  241 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGACCAGCTGACCTTTCACCTCCGCTACTGCATGCCCTGTGCCATAGGTGCTAGGG 360
                                                                                                                                The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                Match 20.4%; Score 351; DB 22; Length 378; Local Similarity 99.7%; Pred. No. 9e-83; es 362; Conservative 0; Mismatches 0; Indels 1
                                                                                                                                                                                             Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                               Claim 25; SEQ ID No 3507; 654pp; English.
                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 378 BP.
                     (MOLE-) MOLECULAR DYNAMICS INC
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-2001 (first entry)
                                        Hanzel DK,
                                                            WPI; 2001-488897/53
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                                         Penn SG,
                                                                                                                                                                                                                 Query Match
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, discretes of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                               Novel single exon nucleic acid probe used to measuring gene expression in a human breast \mbox{\, --}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGATGGAGGAGGTGAGGGGGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID No 3335; 322pp; English.
                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS03407 standard; DNA; 378 BP.
                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0633366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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362; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-476286/51
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ABS03407/c
ID ABS0340
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DK,
                                                                                 WPI; 2002-114183/15.
                                                                            Hanzel
                                         WO200186003-A2.
                                                         26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                     Homo sapiens.
                                                               21-SEP-2000;
27-SEP-2000;
                                                                    04-OCT-2000;
                                                      34-FEB-2000;
      19-AUG-2002
                                              15-NOV-2001.
 ABS03407;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12614 nucleic acid Sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung can a collection of detectably labeled nucleic acids derived from human lung can a lagorithmically predicting at least one exon from genomic sequences of the enkaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from enkaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon comprising (a) identifying exons from genomic sequence by the method comprising (b) detectably assigning exons to a single exon comprising the expression of each of the exons in several crissues and/or cell types using hybridisation to a single exon expression of the exons in the tissues and/or cell types using hybridisation to a single exon expression of the exons the exons that the expression of the exons in the tissues and/or cell types using hybridisation to a single exon expression of the exons that the expression of the exons that the expression of the exons that the expression of expression of the exons in the tissues and/or cell types with the expression of the exons the expression of the exons the expression of the exons that the expression of the exons the expression expression of the exons the exons the expression expression expression expression expression ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the exons should be assigned to a single gene; a peptide comprising one of 1201 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPP), interstitial lung disease (LLD), familial idiopathic pulmonary
                                                                                                                                                                                                                            Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; chanilial idopathic pulmonary fibrosis; neurofibromatosis; tubercus sclerosis; daisease; wiemann-pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicocytosis; lymphangioleiomyomicosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                         Human genome-derived single exon probe from lung SEQ ID No 3398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 3398; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00665
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2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0632366.
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                                                                                                       (first entry)
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181 ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGTGAGGAGGCTGGGGGAGGTGAAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GGAGATGGAGGTGAGGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGTCTGCATGGCCAGCTGGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGCCCTGTGCCATAGGTGCTAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ATGACCAGCTGACACTTTCACCTCCGCTACTGCATGGCCCTGTG-CATAGGTGCTAGGG 4
                                                                      haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue regeneration; wound healing; infection; immune disorder; each culture; drug screening; gene therapy; antiinfimmatory; antiasthmatic; antiarthritis; hemostatic; antiarthricisclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 GGAGATGGAGGAGGTGAGGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCCTCAATTTCCCCATCTGTGGAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proliferation; metastasis; cancer; tumour; haematopolétic disorder; myeloid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial isohaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.4%; Score 351; DB 24;
99.7%; Pred. No. 9e-83;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA08485 standard; cDNA; 547 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.7
Matches 362; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA08485;
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1630 TGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGG 1689
                                                    New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution PJIA; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the full length cDNA encoding the human
                                                                                                                      1690 TACCCACCCCAGGATGAGAGGCTCGGGCTGG 1721
                                                                                                                                                                      483
                                                                                                                                                    452 TACCCACCCCAAGATGAGAGGCTCGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Silent variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= d
/label= "C1037T"
/note= "Causes R340W"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Causes P71A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
20..1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product "PRKAG3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 5; 25pp; English.
                                                                                                                                                                                                                                                                                            AAH43685 standard; cDNA; 1647 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ° "T559C"
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/label= "C230G"
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                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; QQB47679.
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                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRKAG3 CDNA.
                                                                                                                                                                                                                                                                                                                                            AAH43685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variation
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                                                                                                                                                                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences ABA0822-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nuclectide of the invention, methods of producing the novel polypeptides, cantibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention navel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; seem cell growth activity; immunomodulatory activity; lissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; hand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1570 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue repeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          illness,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that can be used to augment or replace cells damaged by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 429; 1963pp; English.
                                                                                                                                                                                                                                                                   Tang YT, Liu C, Drmanac RT;
                                                                                               05-FEB-2001; 2001WO-US03800.
                                                                                                                                             2000US-0496914.
2000US-0560875.
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WO200157188-A2.
                                                                                                                                             03-FEB-2000;
27-APR-2000;
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Query Match Sest Local tches

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Homo sapiens
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                                                                                                                                                                    1630 TGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGG 1689
                                                                                                                                                                                                                                                                                                                                                 PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rogel-Gaillard C;
                                                                                                         1069 TITGGGCATCGCCACCATTCCGAGACTTGGCCTGTGGTGCTGGAGAGACAGCACCCATCCTGAC
                                                                                                 1570 TITGGGCATCGCCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC
                                                                                                                                                                                                                                                                                                                                      gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                 Gaps
resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
                                                             Score 168.2; DB 22; Length 1647;
Pred. No. 3.3e-34;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                       Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                  cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                              Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
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J, Le Roy P, Chardon P;
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/product= "Human Prkag3 protein"
1390..2109
/*tag= c
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(ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                0;
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                                                              9.88;
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472..1389
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                                                                      cal Similarity 95.6
173; Conservative
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Iannuccelli N,
                                                                                                                                                                                                      T 1690
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                                                                                                                                                                                                       1690
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Best Local S
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5'UTR
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The present Sequence is a constant and accompanies many properior.

The present Sequence is a constant submit muscle-specific isoform, practivated kinase (AMPK) garma subunit muscle-specific isoform, practivated metabolism, particularly in skeletal muscle-specific isoform, carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders associated with muscle metabolism cauch as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic cardiuation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3 or a heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain and present in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA,
New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders
                                                                                                                                                                                                                                                                                                                                          The present sequence is a cDNA encoding human adenosine monophosphate
                                                                                             associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.8%; Score 168.2; DB 22; Length 2109; Best Local Similarity 95.6%; Pred. No. 3.6e-34; Matches 173; Conservative 0; Mismatches 8; Indels 0;
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/product= "Human complete Prkag3 protein"
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1..1395
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AAD03295 standard; cDNA; 1867 BP.
                                 AAD03295;
AAD03295
                                  The present sequence is a cDNA encoding human adenosine monophosphate

(AMP)-activated kinase (AMEK) gamma subunit muscle-specific isoform,
complete PRKAG3. Mutation in Prkag3 results in an altered regulation of
carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
useful as therapeutic for treating carbohydrate metabolism disorders such
as diabetes, obesity, and disorders associated with muscle metabolism
such as myopathy and cardiovascular diseases, to modulate AMPK
activity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic disorder,
preferably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3 are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered allele of PRKAG3 or
transgenic animal and host cell transformed with PRKAG3 or are
neterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
encoding PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                           Rogel-Gaillard C;
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                                                                                                                                                                          Kalm E, Milan D, Robic A, J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 168.2; DB 2
Pred. No. 3.6e-34;
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                                                                                                                  INRA INST NAT RECH AGRONOMIQUE. ANDERSSON L.
                                                                                                                                                                                                                                                                                                        Claim 12; Page 65-68; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.88;
                                                        11-SEP-2000; 2000WO-EP09896.
                                                                               99EP-0402236
                                                                                         18-MAY-2000; 2000EP-0401388
                                                                                                                                                                           Looft C, Ka,
, Gellin J,
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Best Local Similarity 95.6
Matches 173; Conservative
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P-PSDB; AAE00223.
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           WO200120003-A2.
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                                                                                                                  (INRG ) INRA
(ANDE/) ANDER
                                                                              10-SEP-1999;
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                                 22-MAR-2001
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The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3: PrkAg3 gene is located in the RN locus of chromosome 15.

Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as claim of cortical carbohydrate metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic polymorphic and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a general prognosity of a sequence encoding PRKAG3, are
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                                                                                                                                                   Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease, anorectic; genetic testing; carbobydate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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J, Le Roy P, Chardon P;
                                                                     Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
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472..1389
/*tag= b
/product= "Sus scrofa PRKAG3 protein"
1390..1867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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(first entry)
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                                                                                                                                                                                                                                                                                                          chromosome 15; ss.
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13-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa.
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5'UTR
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Search completed: June 14, 2003, 16:23:08 Job time : 426 secs

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Total number

Database

Searched:

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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (Dases 1 to 572)

S Fahrenkrug; S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.

Design and use of two pooled tissue normalized cDNA libraries for BST discovery in swine

Unpublished (2000)

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

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BJ072114 BJ072114
BM488662 PGMZD.PKO
BM487789 PGMZD.PKO
BJ447789 PGMZD.PKO
BJ447789 PGMZD.PKO
BJ447782 PGMZD.PKO
BJ451523 AJ451523
AJ395118 AJ395118
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AV608257 AV608257
BF351397 CM4-HT050
BB183269 603087149
AA578815 DISCHO3.S
AA578219 DISCHO3.S
AA578219 DISCHO3.S
BE16681 CM4-HT050
BE16684 CM4-HT050
BH765123 K-EST0046
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BE821538 GO303457
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
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373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
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BE166874
BM710850
AW379936
BM765123
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BE148626
AW956906
BG740148
BG705895
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BM764743
AW411228
BM783383
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BM783383
BM78328081
BM78528081
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BM487789
BM440762
BM440762
AM395115
AM451523
AM596118
AV603335
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B1833269
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AA57821397
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AA178898 zp38d10.r
AL248229 Terracdon
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10885.491 Million cell updates/sec
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1722
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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AA178898
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EST 30-JUL-2001

132.4 116.8 88.8 84.6 82.6

Score

Ş. Result

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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNS03KJ0 1042 bp DNA linear GSS 17-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 033113 of library G from Tetraodon nigroviridis, genomic survey
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Roest-Crollius; H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Winoker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
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Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
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/note="Genoscope sequence ID : COBG033CF07LP1-end : T7"
/note="Genoscope sequence ID : COBG033CF07LP1-end : T7"
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/db_xref-"taxon:99883"
/clone="033113"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.

[ (bases 1 to 413)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Wolse,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 TTTGGGCATCGGCACATTCCGAGACTTGGCCGTGGTGCTGGAAACGGCGCCCATCCTGAC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 CGCACTGGACATCTTCGTGGACCGGCGTGTCTTCGCGCTGCCTGTGGTGGTGGTGGTGG 350
                                                                                                                                                                                                                                                    /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

190 c 151 g 124 l lothers
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258610.L.1 Stratagene musche 937209 Homo sapiens CDNA clone
IMAGE:611731 5' similar to SW.AAKG.RAT P803385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                      Score 148; DB 13; Length 572;
Pred. No. 1.1e-24;
0; Mismatches 20; Indels
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/tissue_type="muscle"
/dev_stage="adult"
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High quality sequence stop: 255.
Location/Qualifiers
                                                                                                                     /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="Markc_2PIG"
/tissue_type="pooled"
/lab_host="DHIUB"
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/db_xref="taxon:9606"
     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 119 row: I column: 11
Seq primer: ATTPAGGTCACACTATAG.
Location/Qualifiers
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AA178898.1 GI:1760259
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88.98;
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                        160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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Matches 160; Conserv
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acatinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acatinopterygii; Neopterygii; Percomorpha; Atherinomorpha; Acanthomorpha; Beloniformes; Acanthorphichyldae; Oryzinae; Oryzinae.

E 1 (bases 1 to 728)

S Kohara Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H. Medaka EST Project in Takeda's lab

L Upublished (2001)

Context: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata: Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BJ504184 728 bp mRNA linear EST 08-AUG-2002 BJ504184 MF01FSA CDNA Oryzias latipes CDNA clone MF01FSA006A14 3',
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                                                       Score 88.8; DB 13; Length 591;
Pred. No. 1.5e-10;
0; Mismatches 42; Indels 0
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1 others
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11 Similarity 77.9%; Pred. No. 1.6e-09;
102; Conservative 0; Mismatches 29;
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/sex="mixture of female and i
/tissue_type="whole embryo"
dev_stage="fry stage 40"
161 c 174 g 210 t
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0; Mismatches
133
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Location/Qualifiers
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                                                                                                                                                                                                                                                            1358 CTGCACATCTTTGTAAG------CCTGGGCCCCAGGTGGGAGGAAGGGGGAGACCTGG 1408
                                                                                                                                                                                                                                                                                                                                                                                                                            1469 GCCCTCTTGAAGCTGCTG-----GATCCCTGATCTCCACCTGGTCCCCATCCTAACC 1520
                                                                                                                                                                            Oryzias latipes
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Actinopterygi; Neopterygi; "eleoste; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.

1 (bases 1 to 591)
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                                                                                                                  556 GTACATACCGGGACATTGCTTTCATTCACCCGGACACGCCCATCATAAGGGGCTCAACA 615
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Unpublished (2001)
Contact: Tadasu Shin-i
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                                                         17; Gaps
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                DB 17; Length 1042;
                                                       Indels
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111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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/clone_lib="MF01FSA cDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="fry stage 40"
                                                       0; Mismatches 192;
              Score 116.8; DB 1
Pred. No. 3.9e-17;
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Location/Qualifiers
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              6.8%;
          Query Match
Best Local Similarity 56.3'
Matches 269; Conservative
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1599 CTGTGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTG 1658
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                                                                                                                                                                                                                                                                                                  EST 11-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage_25"
//dev_stage_25"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute).

a 162 c 148 g 179 t
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                                                                         1 (bases 1 to 633)
Kitayama,A., Terasaka,C., Mochli,M., Ueno,N., Shin-i,T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 CTCCCCAGCAGACAGCCTTTTCCAAGCTGTATTCACTCATCAAGAATAAGATCCACCG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                             BJ072114 633 bp mRNA linear EST 11-DEC-2
BJ072114 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL096jl6 5', mRNA sequence.
BJ072114
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library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Ill Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed genes in X. laevis embryo Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                    1659 TGTCTGCACTGCCTGTGGTCAACGA 1683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 ACTCAAGTTCCTTCACCTCTTG 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                  African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T. .633
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BJ072114
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BM488662
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1362 ACATCTTTGTAAG----CCTGGGCCCCAGGTGGGAGGAAGGGGGAGACCTGGGCAGGTGATC 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1419 AGAGGCCTGAGGAGTCTTCAGCCCTAGCAGTCGTGGGGAAGAGCTGGGAGCCCTCTTGA 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1479 AGCTGCTGGATCCCTGATCTCCACCTGGTCCCCATCCTAACCAGGGTTCCCTGCTGCCCC 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1539 GGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGG 1598
                                                                                       BG919314 101_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4946661 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 ACCCAGAGTCAGGCAACACCTTGTACATCCTTACTCACAAGCGGATCCTCAAGTTCCTCA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 AGAGCGGTTGGGGACAGAGGAGGGGTGTTGGTGTTGATGATTGAGCGTAGCACCTCCATG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mammary: Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 CTCT-ATCCGGAAAGCACCTGCAAGCCAATGCCCCCTTCCTCAGATCACGGAGTTCCCCA 305
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 933)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 GTCCGGTTGATGCTGTCTTCATTAATTCGAAATAAGATCCACAGGCTCCCAGTTATCG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI0895 row: d column: 22
                                                                                                                                                                                                                                                                                                                                      NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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Llarity 52.1%; Pred. No. 5.5e-09;
Conservative 0; Mismatches 209; Indels 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
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/clone="IMAGE:4946661"
/clone_lib="NCI_CGAP_Mam6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 498
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="5 months"
/lab_host="DH10B"
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                                                                                                                                                                              BG919314.1 GI:14299790
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                                                                                                                               mRNA sequence.
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Best Local Simi
Matches 232;
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ORIGIN
                                                                                                          DEFINITION
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JOURNAL
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KEYWORDS
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                                          RESULT 6
BG919314
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/dev.stage="Breast,leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,11 weeks):growth plate(ld,7d,14d post-hatch)"
/lab.host="E. coli EMDH10B"
/note="Vector: pcwvSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth flom 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1228 CTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCG 1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="pgm2n.pk005.j24"
/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgm2n)"
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate"
                                                                                                                                                                                                                                        ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNa library, USDA/IFAFS Animal Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 80.2; DB 13; Length 595;
Pred. No. 1.7e-08;
0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cogburn@udel.edu, www.chickest.udel.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1348 GCTCAAGTTCCTGCACATCTTTGTAAGCCTGGGCCCA 1384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Commercial broiler and Strains 90 & 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 t
                                                                                                                                                                                                                                                                                                                                   Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                          1 (bases 1 to 595)
Cogburn, L.A. and Monsonego-Ornan, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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EST.
                          GI:18608720
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Best Local Similarity 69.4%;
Matches 109; Conservative (
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BG713637
                                                                                                                                                                                                                                                                                                             Unpublished (2002)
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                                                                                             Gallus gallus
    BM487789
BM487789.1
                                                                           chicken.
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BG713637
    ACCESSION
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                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Breast, leg:Embryo(d19):post-hatch(ld,1,3,5,7,9,11 weeks):growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coli EmbHlost
/note="Vector: pCWVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue (embryonic
muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth
plate 33.3% of the final RNA pool). Single pass sequencing
from 5'-end"
pgm2n.pk008.g21 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk008.g21 5 similar to gb|AAC52580.1 (U42413) 5 '-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                   Cogburn, L.A. and Monsonego-Ornan, E. ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Commercial broiler and Ottawa Res. Centre
Strains 90 & 21"
/db_xref="taxon:9031"
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/clone-lb-Normalized Chicken Breast Muscle, Le and Epiphyseal Growth Plate cDNA library (pgm2n) /sex-"Male and Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
                                                                                                                                              BM488662.1 GI:18609593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth plate"
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Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                  mRNA sequence.
                                                                                                                                                                                                                  Gallus gallus
                                                                                               ], mRNA se
BM488662
                                                                                                                                                                                            chicken.
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BM487789
                                                                                                                        ACCESSION
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KEYWORDS
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Library (pg11).

Library (pg11).

Library (pg11).

//sex="Male and Female"

//tissue_type="Testis" ovary and oviduct"

/dev_stage="Various stages;embryonic, post-hatch, immature and sexually mature"

/lab host="E. coli EMOHIOB"

/note="Vector: pcMvSpORT6; Library made from three total

/note="Vector: pcMvSpORT6; Library made from three foral

/note="Vector: pcMv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AJ395115 dkfz426 Gallus gallus cDNA clone 21c2r1, mRNA sequence. AJ395115 AJ395115 AJ395115 GIIIS.1 GI:7125706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 64)
                                                                                                                                            /clone="pgrln.pk002.19"
/clone_lib="Normalized Chicken Reproductive Tract cDNA
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Heinrich-ette-Institute
Heinristr. 52, 20251 Hamburg, Germany
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Indels
                                                                                   /strain="Commercial broiler and layer" /db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1348 GCTCAAGTTCCTGCACATCTTTGTAAGCCTGGGCCCA 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Bursa of Fabricius"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
227 c 155 g 137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80.2; DB 13;
Pred. No. 1.7e-08;
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Genome Res. 10 (12), 2062-2069 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                        /organism="Gallus gallus"

    .649
    /organism="Gallus gallus"

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  Location/Qualifiers
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AJ395115
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BM440762

BM502.19 Normalized Chicken Reproductive Tract CDNA Library pgril. pk002.19 Normalized Chicken Reproductive Tract CDNA Library (pgrln) Gallus gallus CDNA clone pgrln.pk002.19 5' similar to gil4506061 ref!NP_002724.1| protein kinase, AMP-activated, gamma 1 non-catalytic, gemma-1 Homos sapiens] gil12737489 ref!XP_activated, noncatalytic, gemma-1 Homos sapiens] gil12737489 ref!XP_006778.2| protein kinase, AMP-activated, gamma 1, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 647)
Cogburn, L. A. and Nys, Y.
ESTs from Normalized Chicken Reproductive Tract cDNA library-
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archiosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 636)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80.2; DB 12; Length 636;
Pred. No. 1.7e-08;
0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Gallus gallus"
/db_xref="taxon:9011"
/clone="pg1ln.pk008.cl3"
/clone_lib="Normalized Liver Library"
/sex="Male and Female"
                                                                                                                                   Burnside, J., Morgan, R.W. and Cogburn, L.A. Chicken ESTs from a normalized liver library upublished (2001)
Contact: Joan Burnside
Molecular Endocrinology
                                                                                                                                                                                                                                                                               University of Delaware 40 Townsend Hall, Newark, DE 19717, USA e1 302 831-1345 Fax: 302-831-3411 Email: joan@UDel: Edu, www.chickest.udel.edu.
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/lab_host="E.coli EMDH10B"
/note="Vector: pCMVSPORT 6"
215 c 167 g 119 t
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University of Delaware
Townsend Hall, Newark, DE 19717, USA
1302-831-2822
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Gallus gallus
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chicken.

Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.

I (bases I to 758)
S AbdrakhmanovII., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy
J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
L Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV603335 Sos taurus kidney fetus Bos taurus cDNA clone ElKI015F02 5/, mRNA sequence.
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Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Heinrich-Tette-Institute
Heinrich 152, 20251 Hamburg, Germany
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.ppi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks 01d"
238 c 186 g 166 t
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68.8%; Pred. No. 4.5e-08;
tive 0; Mismatches 49;
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Shirakawa Institute of Animal Genetics
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/organism="Gallus gallus"
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/db_xref="taxon:9031"
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/clone_lib="dkfz426"
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                                                                                                                                                                                                                                                                 Contact: Buerstedde JM
AJ396118.1 GI:7127728
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                                                                                                                              46 CTCCCCCAATGCCAGCCTTTTTGATGCCGTCTCCCTGATCCGCAATAAGATCCACCG 105
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1 (bases 1 to 687)

Buerstedde, J.M.
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Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
I.ocation/Qualifiers
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Pred. No. 1.8e-08;
0; Mismatches 48;
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/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note-"CB inbred strain"
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/db_xref="taxon:9031"
/clone="29a6r1"
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                                                                                                                                                                          June 14, 2003, 11:14:12; Search time 90 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-223-463-14
US-08-223-463-14
US-09-272-796-14
US-09-272-796-14
US-09-272-796-17
US-09-007-005-17
US-09-007-005-17
US-09-007-005-17
US-09-165-264-14
US-09-165-264-14
US-09-165-264-13
US-09-165-266-21
US-09-165-266-21
US-09-169-266-21
US-09-169-266-21
US-09-169-266-21
US-09-169-266-21
US-09-641-638-161
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                                                                                                                                                                                                                                                                                                                                                                                                                                               441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                             nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                            IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match 1
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67.6
63.8
63.8
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1240 CAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGCCTGCTTCT 1299
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Sequence 7
Sequence 7
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Patent No. 6124125
GENERAL INFORMATION:
APPLICANT: Darimouth College, St. Vincents Institute of
APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                Sequence
                                                                 Sequence
                                                                                              Sequence
                                                                                                                               Sequence
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Live 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
COMPUTER: IBM PC
                                                                                     US-09-155-768-1
US-08-455-2008-11
US-08-455-543A-8
US-08-193-078B-8
US-08-194-097D-8
US-08-445-562-8
US-08-445-562-8
US-08-450-272-8
US-09-268-163-7
US-09-268-163-7
US-09-268-163-7
US-08-713-118-1
US-08-713-118-1
US-08-455-5437-7
US-08-455-5431-7
US-08-455-5433-7
                             PCT-US93-06160-3
US-08-687-080-115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _
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APPLICATION NUMBER: US/09/101,146
FILING DATE: October 7, 1998
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: PN7450
FILING DATE: 8 JAN 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Jane Massey Licata, Esq. STERET: 66 E. Main Street CITY: Marlton STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DC-0050
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REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: DC-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
TELEFAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97; Conservative
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STRANDEDNESS: Single
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Matches 97; Conserv
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1086 CCCCTTCCCCAGTCCCACTCAGCTCTGAACTCACCTCTTCATCCTAGGCGGCACACAGAC 1145
                                                                                                                                  1146 AAGGGAGCCTTGGTGCCCTGCCTCTTTTAGGGGCCTGGGATGGAGGTTGTCTCTCCC 1205
                                                                                                                                                             1206 TAGGCTGCCCCGAGGCTCACTGCTCCCATCTCGCAGCTGTTTGAAGCTGTCTACACCC 1265
                                                                                                                                                                                                                                      1266 TCATCAAGAACCGGATCCATCGCCTGCCTGTTCTTGACCC 1305
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF-0321 US
                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 14, Application US/08878989; Patent No. 5885803; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
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; CLONE: 1452972
US-08-878-989-14
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US-08-878-989-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1026 TCTCTCCTAATGATAGGTGGTGTCTCTGCTCATTCACCTGAGCCTCCTCCTCCTCCACAGT 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1300 TGACCCGGTGTCAGGCAACGTACTCCACATCCTCACACAAAACGCCTGCTCAAGTTCCT 1359
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                                                             501 CAGCTTGTTTGATGCTGTCTCTTCATTAATTCGCAACAAGATCCACAGGCTGCCAGTTAT 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: Foley & Lardner
: 1800 Diagonal Road, Suite 500
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                  1360 GCACATCTTTGTAAGCCTGGGCCC 1383
                                                                                                                                                    621 CAAATTGTTTATCACTGAGTTCCC 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/232,463 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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us-09-826-581-3.rni

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1402 Rerrrrrrrrrrrrrrrrrrrrrrrrrrrr 1343
                                                                                      671 TCCTGGAGCCTGGTGCCCTAGAAGCCCACGTCTTTCTGACTTCTGGAGTCCTGTCGATGT 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                      APPLICANT: DORNER, F.
APPLICANT: SCHEFFLINGER, F.
APPLICANT: FAKKER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30472/114 IMMU
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STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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APPLICATION NUMBER: US/07/935,313
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                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                            1361 CACATCTTTGT 1371
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION; 435
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Best Local Similarity
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                                                                                                                                           1301 GACCCGGTGTCAGGCAACGTACTCCACATCCTCACACAAAACGCCTGCTCAAGTTCCTG 1360
                                                                       509 AGCCTCTTCGATGCTGTATACTCCTTGATCAAAAATAAAATCCACAGATTGCCCGTTATT 568
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Pred. No. 1e-07;
0; Mismatches 42; Indels 0
Score 63.8; DB 2; Length 1435;
Pred. No. 1e-07;
0; Mismatches 42; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES UNDMER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FactorsQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0321 US
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                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09272796 Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                          Bandman, Olga
Hillman, Jennifer L.
Corley, Neil C.
Guegler, Karl G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 14:
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67.98;
 Query Match 3.7%;
Best Local Similarity 67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
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LENGTH: 1435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 67.9
Matches 89; Conservative
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                                    89; Conservative
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CLONE: 1452972
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: line IMMEDIATE SOURCE:
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APPLICANT:
APPLICANT:
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STATE:
                                    Matches
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Sequence 17, Application US/09244796 Patent No. 6281344
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Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-658-136-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORM
US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
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                                                                                                                  791 GGAGAGGAACCCGGAAAGGGGCTGTTGGTGTGGTGGGGCCCAGGGCTTAAGGTGGAGGATG 850
                                                                                                                                                                                            851 GGCAGTGGGGATGTCCTGGAGTGAACAGGGGAGGGACAATAGGAGCCTCGGGTGCCTGAC 910
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                                                                                                                                                                                                                                                                                          911 GGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGTGACCGGCTCCCCTGGCCTG 967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SZOSTAK, JACK W.
APPLICANT: ROBETTS, Richard W.
APPLICANT: Liu, Rihe
IITLE OF INVENTION: ELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 RNRSRNRNRSRNRNRSRCRARGRCRURGRCRGRURARARCRUR 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 17
LENGTH: RastSEQ for Windows Version 4.0
LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(289)
CHER INFORMATION: n = A,T,C or G
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ORGANISM: Artificial Sequence
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US-09-244-796-17
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US-09-007-005-17
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Best Local S
Matches 6
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TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: PUSIONS
TITLE OF INVENTION: PUSIONS
TITLE OF INVENTION TO PUSIONS
CURRENT PAPLICATION NUMBER: US/09/244,796
CURRENT PAPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER PELING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative 107; Mismatches 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Translation template
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/08658136
; Patent No. 6071717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
GENERAL INFORMATION:
APPLICANT: SZOSTAK, JACK W.
APPLICANT: ROBERTS, Richard W.
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CITY: FRAMINGHAM
STATE: MASSACHUSETTS
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ZIP: 01701
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NAME: ILASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEPAX: 508-872-8415
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1
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                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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Matches 95
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APPLICANT: KAINGER, KATHERINE W
APPLICANT: LANDES, GREGORY W
APPLICANT: BURN, TIMOTHY C
APPLICANT: BOUN, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: GIAN, FENC
APPLICANT: GIAN, FEN
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                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
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Pred. No. 2;
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                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
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APPLICATION NUMBER: US/08/658,136
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ADDRESSEE: GENZYME CORPORATION
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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52.1%;
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LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-08-658-136-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-658-136-2
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                                             Gaps
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DB 3; Length 53577;
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                                             80; Indels
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Patent No. 6197510

GRMERAL INFORMATION:

APPLICANT: Vinayagamoorthy, Thuraiayah

TITLE OF INVENTION: Multi-Loci Genomic Analysis

FILE REFERENCE: 4447

CURRENT APPLICATION NUMBER: US/09/165,264

CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 7

LENGTH: 320
Query Match 2.3%; Score 39; DB 3
Best Local Similarity 52.1%; Pred. No. 2;
Matches 87; Conservative 0; Mismatches
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897 CICGGGIGCCIGACGGAAGGGAAGCIGCCIGGGACIGCAAGGIGAGGCAGGIGACCGGCI 956
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ORGANISM: Artificial Sequence
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Best Local Similarity 50.6%
Matches 87; Conservative
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APPLICANT: Vinayage
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                                                                CCC 959
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LENGTH: 320
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                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-14
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                                                                                                                                                                                                                                                                                                                                    2.2%; Score 38.6; DB 4; Length 320; 48.8%; Pred. No. 0.33; tive 0; Mismatches 109; Indels
                           Sequence 14, Application US/09165264

Patent No. 6197510
GENERAL INFORMATION
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 14
SEQ ID NO 14
LENGTH: 320
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GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Wulti-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           957 CCCTGGCCTGACTCTGGCTCTTTCTGCAGAGA 989
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Patent No. 6197510
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SOFTWARE: Patentin Ver. 2.1
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Matches 104; Conservative
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Matches 92; Conserv
   RESULT 11
US-09-165-264-14
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US-09-165-264-8
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SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Primer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%; Scoré 36.2; DB 4; Length 320; Best Local Similarity 50.3%; Pred. No. 1.4; Matches 89; Conservative 0; Mismatches 88; Indels
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50.6%; Pred. No. 1.6;
tive 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                          APPLICANT: Vinnayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFREENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 13
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09165264;
Patent No. 6197510;
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVERTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747;
CURRENT FILING DATE: 1998-10-01;
NUMBER OF SEQ ID NOS: 14;
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                               US-09-165-264-13; Sequence 13, Application US/09165264; Patent No. 6197510
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671 TCCTGGAGCCTGGTGCCCTAGAAGCCCCACGTCTTTCTGACTTCTGGAGTCCTGTCGATGT 730
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                                                                      897 CTCGGGTGCCTGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGT 948
                                                                                                         2.1%; Score 36; DB 1; Length 227%; 51.9%; Pred. No. 3.6; tive 0; Mismatches 75; Indels
                                                                                                                                                           RESULT 15
US-07-959-943-6/C
; Sequence 6, Application US/07959943
; Patent No. 5418162
; GENERAL INFORMATION:
    APPLICANT: Blakely, Randy D.
    APPLICANT: Fremeau Jr., Robert T.
    APPLICANT: Caron, Marc G.
    TITLE OF INVENTION: Section Transporter cDNA
    NUMBER OF SEQUENCES:
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPDEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,943
FILING DATE: 19921014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               731 CTCTAGGTCCAGATCTATGAGATTGAACAACATAAG 766
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                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Post Office Drawer 31107 CITY: Raleigh STATE: No. 5418162th Carolina COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2278 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.18
Best Local Similarity 51.99
Matches 81, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
POSITION IN GENOME:
UNITS: 2278 basepairs
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US-07-959-943-6
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Gibson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
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ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
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Db 1823 TTCAGGAGTGATACTTTAATAATGCGCTCCTTAAG 1788
Search completed: June 14, 2003, 16:24:53
Job time : 93 secs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 3, Appli	Sequence 3373, Ap	5,	Sequence 2, Appli	-	Sequence 20146, A	Sequence 29, Appl	Sequence 112, App		Sequence 346, App	Sequence 18, Appl	Sequence 346, App	Sequence 346, App	Sequence 394, App	Sequence 47, Appl	Sequence 8, Appli	Sequence 15, Appl	Sequence 9, Appli	Sequence 2, Appli
B (U)	10 US-09-826-581-3	10 US-09-864-761-3373	10 US-09-826-581-5	10 US-09-925-297-2	9 US-10-108-605-70	10 US-09-864-761-20146	10 US-09-804-682-29	9 US-10-123-155-112	9 US-10-184-644-346	9 US-10-184-634-346	9 US-09-984-271-18	9 US-10-184-644-346	9 US-10-184-634-346	9 US-10-123-155-394	9 US-10-032-393-47	9 US-10-032-393-8	10 US-09-827-998-15	10 US-09-827-998-9	10 US-09-827-998-2
Length DB	1722	378	1647	1691	11527	92	1064	910	671	671	1512	671	671	1184	12733	12739	4158	5313	5376
% Query Match	100.0	20.4	8.6	4.1	3.9	3.8	5.6	2.5	2.5	2.5	2.4	2.4	2.4	2.3	2.3	2.3	2.3	2.3	2.3
Score	1722	351	168.2	70.4	68	65	44.2	43	42.4	42.4	40.8	40.6	40.6	40.2	40	40	39.8	39.8	39.8
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Appli Appli	GAMMA 3	0; 60 60 120 120 180 240
Sequence 8, Appli Sequence 10, Appli Sequence 10, Appli Sequence 1, Appli Sequence 574, App Sequence 574, App Sequence 574, App Sequence 49, Appl Sequence 49, Appl Sequence 49, Appl Sequence 28, Appl Sequence 28, Appl Sequence 2281, Appl Sequence 2281, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 31, Appl	KINASE (Gaps GGCAGC GGCAGC GTGAAG TGATAT TGATAT CCCATCC
Sequence 8, Sequence 1, Sequence 10, Sequence 10, Sequence 11, Paguence 574, Sequence 574, Sequence 49, Sequence 22, Sequence 22, Sequence 202, Sequence 203, Sequence 203, Sequence 33, Sequence 31, Se	PROTEIN K	0; 0; TGTGCG GGGGAG GATCTC GAAAGT
		Length Indels CCAACGG CCAACGG CCAACGGCT CCAACGCT TGGGGCT TGGGGCCT
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US-09-827-998-8 US-09-827-998-1 US-10-123-155-10 US-09-820-004-3 US-09-904-968A-1 US-10-184-644-574 US-10-184-644-574 US-10-184-644-348 US-10-184-644-348 US-10-184-644-348 US-10-184-64-348 US-10-125-540-49 US-10-126-104-68-104 US-09-771-28-33 US-09-864-761-5505 US-09-864-761-5208 US-09-864-761-5208 US-09-864-761-5208 US-09-864-761-5208 US-09-171-28-3 US-09-171-28-3 US-09-171-28-3 US-09-171-28-3 US-10-184-644-312 US-10-184-644-312 US-10-117-44-3 US-10-117-44-3 US-10-117-44-312 US-10-117-14-3 US-10-117-14-312	N AMP-A	12; De 0; De
9-827- 9-827- 9-827- 9-827- 9-827- 9-828- 9-84- 9-84- 9-864- 1184- 9-864- 1184- 9-864- 1184- 11184-	IME: JMA: 58 55 55 4	Score 1722; Pred. No. 0 Mismatche MGGCTTCTTG MGCTTCTTTG MGCAGAGCTTTG MGAGAGTTTG MINININI MGAGATCTTGTA MGAGATC
US-10	ALIO US/09826581 OA1 Leif Holger Stefan RIANTS OF THE 007001 MBER: US/09/82 2001-04-05 ER: US 60/195, 0-04-07 Hindows Versio	Sec Sec Sec
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5461 6719 6719 6719 8822 8822 8822 9311 2531 777 777 777 777 551 551 155074 1659 158 802 802 802 987	ration US/0982 1142310A1 1142310A1 1150n, Leif Ran, L. Holger Nan, VARIANTS O 1145-00701 115-00701 11E: 2001-04- 1 NUMBER: US 1 NUMBER:	100 Conservative GGCCCCTAGATU
	olic 0020 0020 0020 0020 0020 0020 0020 00	imilarity 100.0%; Score 1722; DB 10; Length 1722; Conservative 0; Mismatches 0; Indels 0; Gaps correscondative 0; Mismatches 0; Indels 0; Gaps correscondardadaeGenterTragentTragentGenter
33.33 33.33 30.22	-581-3 e 3, Appl No. US20 INCORM; ANT: And ANT: And ANT: MANT: MAN OF INVENT T FILING T FILING T FILING OF SEQ OF SEQ H: 1722	stch sal s 1722 1 1 61 61 121 121 181
22222222222222222222222222222222222222	SSULT 1 Sequence 3, Sequence 3, Batent No. U GENERAL INFO. APPLICANT: APPLICANT: APPLICANT: TITLE OF IN TITLE OF IN PRIOR APPLICANT PRIOR APPLICANT PRIOR APPLICANT PRIOR APPLICANT PRIOR APPLICANT SOGTWARE: SCOTWARE: SCOTWARE: SCOTWARE: TYPE: DNO 3 LENGTH: 17 TYPE: DNO 3 LENGTH: TYPE: T	Query Matches Matches
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                                                                                                                                                                                                                                                                                                                                       Query Match 9.8%; Score 168.2; DB 10; Length 1647; Best Local Similarity 95.6%; Pred. No. 2.7e-39; Matches 173; Conservative 0; Mismatches 8; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILLE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: EC/10S0/05989
PRIOR FILLING DATE: 2000-03-08
PRIOR FILLING DATE: 2000-03-08
PRIOR FILLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Indels
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   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: n equals a,t,g, or c US-09-925-297-2
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; Patent No. US20020081659A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98; Conservative
                                                                                                                                                                                                               US-09-826-581-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 1189
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                                                                                                                                                                                                            NAME/KEY: CDS
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                                                                      LENGTH: 1647
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                                      SEQ ID NO 5
                                                                                                                                                                            FEATURE:
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APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Markind, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT APPLICATION NUMBER: US 60/195,665
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCACAAGCTTGGCTTCAGGCCAAGCCAGGGGCCAGGGTGGAGGAAAGTCCATCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCCATGGCCCTGTGCCATAGGTGCTAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CCCTCTATGGGACAGCAAGAAGCAGACCTTTGTGGGGTGAGGAGGGCTGGGGAGGTGAAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGCAGGGGCCAGGGTGGAGGAAGTCCATCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 GGAGTCTGCATGGCCAGCTGGGAGCCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.4%; Score 351; DB 10; Length 378; 99.7%; Pred. No. 4.6e-93; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          N: EXPRESED IN HELA, SIGNAL = 4

N: EXPRESED IN HELAT, SIGNAL = 4.1

N: EXPRESED IN PLACENTA, SIGNAL = 3.9

N: EXPRESED IN HALIOO, SIGNAL = 3.9

N: EXPRESED IN HALIOO, SIGNAL = 3.8

N: EXPRESED IN BOUT LIVER, SIGNAL = 3.8

N: EXPRESED IN PETAL LIVER, SIGNAL = 5.3

N: EXPRESED IN POWE MARROW, SIGNAL = 4.8

N: EXPRESED IN LUNG, SIGNAL = 4.2

N: EXPRESED IN BRAIN, SIGNAL = 4.2
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annowmax Sequence Listing Engine vers. 1.1
SEQ ID NO 3373
LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                                                                                 TO AC009974.3
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; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 362; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 MAP
                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       FRATURE: CALL OF STATE OF STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCAGC 60
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APPLICANT: APPLICANT: Corey, Michael J.
TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS
TITLE OF INVENTION: BAL-18 POLYPEPTIDES, NUCLEIC ACIDS
TITLE OF INVENTION: MODULATING THE SAME AND METHODS FOR SCREENING FOR OR
TITLE OF INVENTION: MODULATING THE SAME
FILE REPRENDE: 130001.406
CURRENT APPLICATION NUMBER: US/09/804,682
CURRENT APPLICATION NUMBER: US/09/804,682
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4

CTHER INFORMATION: EXPRESSED IN HERA, SIGNAL = 4.1

CTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1

CTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 3.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4

OTHER INFORMATION: SEXPESSED IN BRAIN, SIGNAL = 4.4

OTHER INFORMATION: SETHINGALIANTS SIGNAL = 4.2

OTHER INFORMATION: SETHINGALIANTS SIGNAL = 4.2

OTHER INFORMATION: STRINGSPROT HIT: B54619, EVALUE 3.00e-05

USE-09-864-761-20146
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100.0%; Pred. No. 2.6e-09;
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.8%
Best Local Similarity 100.0
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
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US-09-804-682-29/c
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                                                                                                                                                                                                                               APPLICANT: Broadus, Julie
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Stam, Lynn
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Randar, Kin
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANCGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
TITLE OF INVENTION: DROSE 105/10/108,605
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR RPLICATION NUMBER: US 60/761,142
PRIOR RPLICATION NUMBER: US 60/76,418
PRIOR RPLING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PARENTIN Ver. 2.1
SEQ ID NO 70
LENGTH: 11527
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APPLICANT: Penn, Sharron G.
APPLICANT: Fank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10193 CCTCTACGATGCCATCACAAAATTCTCATCCACAGCGCGCATACATCGCCTGCCCGTCATCGA 10252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1303 CCCGGTGTCAGGCAACGTACTCCACACACACACACAAACGCCTGCTCAAGTTCCTGCA 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1243 CCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGCCTGCTGTTCTTGA 1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE OF TWENTION. GENE DEFENSION AND PLEASE OF THE REPRENCE. Accorded **1.

CURRENT TAPLICATION NUMBER: US/09/864,761

CURRENT FILMED DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,366

PRIOR PLING DATE: 2000-08-03

PRIOR PLING DATE: 2000-010-04

PRIOR FILING DATE: 2000-010-04

PRIOR FILING DATE: 2000-010-07

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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Patent No. US20020048763A1
                                                                                   US-10-108-605-70; Sequence 70. Application US/10108605; Patent No. US20020160934A1; GBMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA CORGANISM: Drosophila melanogaster US-10-108-605-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10313 CCTATACGTGAG 10324
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US-09-864-761-20146/c
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us-09-826-581-3.rnpb

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Watanabe, Colin K. Wood, William I.
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Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo Sapien
                                 Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 TCCCA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     896 PLYEA 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-184-644-346
us-10-123-155-112
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

: LOCATION: 858, 878, 884, 886, 896, 897, 901, 917, 926, 932, 939, 948,

: LOCATION: 957, 961, 965, 981, 991, 993, 1001, 1002, 1005, 1011, 1018,

: LOCATION: 1043, 1047, 1049, 1051, 1054, 1056

: OTHER INFORMATION: n = A,T,C or G
                                                                                    72, 110, 209, 214, 231, 232, 256, 282, 292, 297, 306, 319, 354, 355, 363, 372, 376, 378, 457, 458, 459, 468, 470
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                                                                                                                                                                                                                                                                                                                                                                                         2.6%; Score 44.2; DB 10; Length 1064;
47.8%; Pred. No. 0.0058;
tive 0; Mismatches 93; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                        511, 524, 652, 652, 654, 725, 731, 803, 821,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
                                                                                  LOCATION: 5, 6, 16, 21, 24, 25, 33, 39, LOCATION: 235, 237, 238, 244, 245, 246, LOCATION: 323, 330, 344, 340, 349, LOCATION: 397, 405, 432, 437, 454, 455,
                                                                                                                                                                                    LOCATION: 485, 487, 488, 494, 496, 499, LOCATION: 583, 600, 611, 613, 623, 624, LOCATION: 694, 701, 713, 716, 720, 721, LOCATION: 744, 781, 782, 785, 789, 799, OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 112, Application US/10123155
Publication No. US20030068794A1
                                                                                                                                                      OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gao,Wei-Qiang
Gerritsen,Mary E.
Goddard,Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.6%
Best Local Similarity 47.8%
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumas, Daniel
                                                                   NAME/KEY: misc_feature
                                   ORGANISM: Homo sapiens
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US-10-123-155-112
 LENGTH: 1064
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APPLICANT:
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APPLICANT:
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984 CAGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTCTCCATCTCCCTAATGATAGGT 1043
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                                                                                                                                    71 GACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGGCTGGGGAGGTGAAGGGAGATGGAG 130
                                                                                                                                                                         924 CCTGGGACTGCAAGGTGAGGCAGGTGACCGGCTCCCCTGGCCTGACTCTGGCTCTTTCTG 983
                                                                                                                                                                                                                                                                 131 GAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATATACCACAAGCT 190
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P343ORIC227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                          Gaps
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ch 2.5%; Score 43; DB 9; Length 910; l Similarity 13.2%; Pred. No. 0.013; 48; Conservative 93; Mismatches 224; Indels
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; Sequence 346, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
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1164 TGCCCTCCTTTTTAGGGGCCTGGGATGGAGGTTGTCTCTCCCTAGGCTGCCCCGAGGCTC 1223

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1226 GAGGGGGAAGGGCTAGGAAACTCCAGCAGAGGGAGGGGGTTKGGACCCACTATGGACAGT 1167
                                                                                       1224 ACTGCTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCC 1283
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                         275 Y...MMSSBHSHSSSSSSSSSSTSYTKTB...MTCHSHTMSHSHSTS.TMMMMYCC..CYY 216
                                                                                                              506 CCACCCAAAGGCCCCGGGCTGACCTCCTCCCGGCCCTCCCCTGCAGGGATGCTGACCAT
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49.1%; Pred. No. 0.062;
tive 1; Mismatches 108; Indels
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Sequence 18, Application US/0984271

Sequence 18, Application WG2003004008BA1

GENERAL INFORMATION:
APPLICANT: Rosen et al.

TILLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/984,271
CURRENT FILING DATE: 2001-10-29
PRIOR PELICATION NUMBER: 09/482,273
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR PILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR PILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR FILING DATE: 1998-07-15
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-984-271-18
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OTHER INFORMATION: n equals a, L,g, or NAME/KEY: SITE
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OTHER INFORMATION: n equals a,t,g, or
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Matches 105; Conservative
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LENGTH: 15
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                                                                 1103 1044 GGGTGTCTCTGCTCATTCACCTGAGCCTCCTCCTCCACAGTCCCCTTCCCCAGTCCCAC 1103
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                                                                                                                                                                                335 ..YYYYT ..YYYT.HYYWW.S.YHB.HSHSHSSSSS..Y ..M.MYCY.M...M.T.MYC 276
                                                                                                                                                                                                                                                                              275 Y..MMBSBHSHSSSSSSSSSSSSTSTTKTB...MTCHSHTMSHSHSTS.TMMMMYCC..CYY 216
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                                                                                                395 S..CYCYCMYCYMAB..HH.Y..HCSSCCSCY.T.CYHTY.YYY.M..M..Y.YY.... 336
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455 .SYMYAY. BMB.MT..M...YBYM.M.C.MYT..ASSS..MMTSMMT.Y...T...SHSS 396
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CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 346, Application US/10184634; Publication No. US20030068684A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  1284 ATCGCCTGCCTGTTCTT 1300
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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ORGANISM: Homo Sapien
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US-10-184-634-346/c
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Length 671; Indels

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644 CAGAGGGCGGGGGGGGAGGGGAGTCCTCCTGGAGCCTGGTGCCCTAGAAGCCCACGTCT 703
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prior Application removed - See Palm or File Wrapper WIMDER OF SEQ ID NOS: 550 SEQ ID NO 394 LENGTH: 1184
                                                                                                                                                                                                                                                                       Query Match 2.4%; Score 40.6; DB 9; Best Local Similarity 7.5%; Pred. No. 0.059; Matches 25; Conservative 135; Mismatches 173;
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CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 394, Application US/10123155; Publication No. US20030068794A1; GENERAL INFORMATION:
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DeForge, Laura
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Gurney, Austin L.
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Filvaroff, Ellen
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US-10-184-634-346
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                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 194430R.1C.27 CURRENT APPLICATION NUMBER: US/10/184,644 CURRENT FILING DATE: 2002-06-28 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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                   Sequence 346, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
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Publication No. US20030068684A1
GENERAL INFORMATION:
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Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
Pan, James
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Goddard, Audrey
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US-10-184-644-346
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US-10-184-644-346
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TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-12-27
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FASTERQ for Windows Version 4.0
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                                                                           Query Match 2.3%; Score 40.2; DB 9; Length 11 Best Local Similarity 8.8%; Pred. No. 0.089; Matches 57; Conservative 175; Mismatches 412; Indels
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-394
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                                                                                                                                 Length 12733;
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Pred. No. 0.18;
0; Mismatches 105; Indels
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ne: 292 secs
                                                              ; OTHER INFORMATION: Vector pEPEF14 US-10-032-393-47
                    ORGANISM: Artificial Sequence
                                                                                                                             Query Match 2.3%;
Best Local Similarity 49.5%;
Matches 103; Conservative
TYPE: DNA
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Title: Perfect score: (Sequence:	US-09-826-581-3_COPY_612_672 61 1 gtgaggagtgggctgggaatgggggcggaggggagtcctc 61
Scoring table: 1	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
Total number of h	f hits satisfying chosen parameters: 4109280
Minimum DB seq le Maximum DB seq le	length: 0 length: 2000000000
Post-processing:	g: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database	GenEmbl:* 1: 9D_Da:* 2: 9D_hig:* 4: 9D_Di:* 4: 9D_Da:* 5: 9D_Da:* 6: 9D_Da:* 7: 9D_Da:* 10: 9D_Pa:* 11: 9D_Sy:* 11: 9D_Sy:* 11: 9D_Sy:* 12: 9D_Di:* 13: 9D_un:* 14: 9D_un:* 15: em_fun:* 16: em_fun:* 17: em_pa:* 18: em_in:* 18: em_in:* 19: em_in:* 22: em_ov:* 22: em_ov:* 23: em_in:* 24: em_in:* 25: em_fun:* 26: em_fun:* 27: em_sts:* 28: em_un:* 28: em_un:* 29: em_fig_nun:* 30: em_htg_lnv:* 31: em_htg_lnv:* 32: em_htg_lnv:* 33: em_htg_lnv:* 34: em_htg_lnv:* 35: em_htg_lnv:* 36: em_htg_lnv:* 37: em_htg_lnv:* 38: em_htg_lnv:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Courty Score Match Length DB ID 61 100.0 206654 9 AC009974 59.4 49.8 912781 2 AC118404 29.8 48.9 127781 2 AC118404 29.8 47.9 128100 10 AC121886 28.8 47.2 128000 10 AC121886 28.6 46.9 91247 2 AC126076 28.8 47.2 117082 2 AC126076 28.8 47.2 117082 2 AC128076 28.6 46.9 945 11 G74939 27.8 46.6 184454 2 AC128911 27.8 46.6 184454 2 AC12891 27.8 46.6 184454 2 AC13891 27.4 44.9 68736 2 AC11383 27.4 44.9 68736 2 AC113868 27.4 44.9 68736 2 AC103984 27.4 44.9 68736 2 AC10361 27.4 44.9 68736 2 AC10361 27.4 44.9 166007 2 AC103681 27.4 44.9 166007 2 AC103681 27.2 44.6 115333 2 AC11343 27.2 44.6 115333 2 AC11343 27.2 44.6 157437 9 AC094535 27.2 44.6 157437 9 AC09589 27.2 44.6 157437 9 AC09589 27.2 44.6 157437 9 AC010378 27.2 44.6 157437 2 AC10398 27.2 44.6 157437 2 AC103981 27.2 44.6 157437 2 AC103983 27.2 44.6 17743 3 AC09589 27.2 44.6 17743 3 AC09589 27.2 44.6 17743 3 AC09589 27.2 44.6 17743 3 AC105883 27.2 44.6 17744 2 AC117508 27.2 44.6 178000 G G C C C C C C C C C C C C C C C C	Description	AC0274 AC0274 AC0274 AC0274 AC1184 AC1184 AC1138 AC1138 AC1184 AC094 AC096 AC094 AC094 AC094 AC094 AC094 AC094 AC094 AC094 AC096 AC094 AC096 AC0	d,S. protein kinase ga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
AC009974
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                                                                                                                                     100.0%; Score 61; DB 6; Length 1722; 100.0%; Pred. No. 3.8e-09; 1ve 0; Mismatches 0; Indels (
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459119
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Contact: sapiens@watson.wustl.edu
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1 (bases 1 to 206854)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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3 (bases 1 to 206854)
Waterston, R.H.
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Waterston, R.H.
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donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanose, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Louis
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
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/note="match to EST A1670836 (NID:g4850567) wa04g10.x1"
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    .37
    /note="match to EST BF304755 (NID:g11251653)"

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/note="match to EST BE908408 (NID:910402954)"
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/note="match to EST AW880850 (NID:g8042860)"

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/db_xref="taxon:9606"
/chromosome="2"
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NEIGHBORING SEQUENCE INFORMATION:
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/clone_lib="RPCI-11"
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/note="match to EST AA043371 (NID:g1521226) zk53el0.rl"
588. .929
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fnote="match to EST AA481361 (NID:g2210913) zv44e01.rl"
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594. .763
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594. .763
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                                                     to EST BG470047 (NID:913402322)"
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281. 344
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/note="match to EST BI059713 (NID:g14467240)"
281. 344
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/note="match to EST BI059713 (NID:914467240)"
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594. .763
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'note="match to EST AL567345 (NID:912920610)"
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594. .763
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/note="match to EST BE314060 (NID:99134719)"
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                                                                                                                                                            to EST AW880850 (NID:98042860)"
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/note="similar to Homo sapiens EST BIll4348
(NID:g14565249)"
                    to EST C05773 (NID:g1502549)"
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Pirett Submission

Direct Submission
                                                                                                                                                                                                                                                                                                                ACUZ/416 152129 bp DNA linear HTG 07-JUN-2000
Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
unordered pleces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Center: Whitehead Institute/ MIT Center for Genome Research
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
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http://ftp.genome.washington.edu/RW/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
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------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                   0; Indels
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Pred. No. 2e-09;
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NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 13376 bases at least Q40 Consensus quality: 143264 bases at least Q40 Consensus quality: 145503 bases at least Q20 Insert size: 161000; agarose-fp Insert size: 161009; sum-of-contigs Quality coverage: 3.1 in Q20 bases; agarose-fp Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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f 1286 bp in length
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Rattus norvegicus clone CH230-22513, *** SEQUENCING IN PROGRESS
***, S. unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                     0; Gaps
                                                         Length 152129;
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                                                      Score 59.4; DB 2;
Pred. No. 6.7e-09;
0; Mismatches 1;
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HTG; HTGS_PHASE1.
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2 (bases 1 to 91247) Worley, K.C.

REFERENCE AUTHORS

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                           Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:18139148.
Direct Submission
Submisted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 91247)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 46677 bases at least Q40 Consensus quality: 50328 bases at least Q20 Consensus quality: 53862 bases at least Q20
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1138: gap of unknown length
2413: contig of 1175 bp in length
2413: gap of unknown length
3595: contig of 1182 bp in length
3695: gap of unknown length
4900: gap of unknown length
6142: gap of unknown length
6142: gap of unknown length
6142: gap of unknown length
7321: contig of 1179 bp in length
8609: contig of 1179 bp in length
8709: gap of unknown length
8709: gap of unknown length
9939: contig of 1180 bp in length
11449: contig of 1025 bp in length
115574: contig of 1025 bp in length
115574: gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Query Match

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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alaberoki, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alaberoki, S., Briawa, M., Brown, B., Baryant, N. Barbaria, J., Barbaria, J., Barbaria, J., Barbaria, J., Barbaria, J., Barbaria, S., Briawa, M., Brown, B., Baryant, N. B., Brown, D., Barbaria, J., Barbaria, J., Barbaria, J., Barbaria, J., Barcha, J., Barcha, J., Barcha, J., Chavez, D., Chang, C., Chen, R., Chowler, S. R., Charcko, J., Chavez, D., Chang, C., Chen, R., Chowler, J., Christopoulos, C., Cleveland, C.D., Cox. C., Coyle, M. D., Dathorne, S. R., David, R., Davis, C., Davis, C., Blad, C., Bacarich, D., Andrew, C., Barnhart, C., Edgar, D., Edgar, D., Denn, A.L., Ding, Y., Dinh, H. H., Deltaney, K. R., Delgag, D., Edgard, C., Enda, C., Borctto, M., Earngate, P., Farague, D., Elagar, M., Garcia, A., Garcer, T., Goster, P., Frantz, P., Garcia, A., Garcer, T., Goster, P., Frantz, P., Garcia, A., Garcer, T., Goster, P., Frantz, P., Gorrell, J. H., Guevara, W., Gunarathe, P., Hale, S., Hamitton, K., Harris, K., Hartis, K., Huber, J., Hulyk, S., Hame, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jollyvet, S., Joudah, S., Karlovo, C.J., Kureshi, A., Landry, N., Liu, W., Luules, J., Lia, T., Lichtarge, O., Liew, C., Liu, J., Lia, M., Marliney, B., Macchod, M., Mai, J., Martin, R., Mareris, C., Miner, Z., Miner, Z., Miner, R., Manner, S., Martchen, R., Peters, J., Tamerisa, R., Tamaris, R., Valance, R., Neal, J., Tamaris, R., Wasquez, L., Peters, J., Vara, Peters, J., Tamarisa, R., Tamarisa, R., Tang, H., Rojas, M., Rolle, R., Sodergren, E., Sodergren, E., Sodergren, E., Weal, J., Wers, M., Peters, J., Vara, V., Villalon, D., Vinson, R., Walliamson, A., Wallen, S., Walliamson, A., Wallen, S., Wallen, S., Wallen, S., Wallen, S., Wallen, S., Wallen, S., Wallen, Wallen, Wallen, Wallen, Wallen, Wallen, Wallen, Wallen, Wallen,
                                                                                                                                                                                                                                                                                            ACLIB404 127181 bp DNA linear HTG 18-JUL-2002 Rattus norvegicus clone CH230-150G18, *** SEQUENCING IN PROGRESS ***, Su nordered pleces.
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Direct Submission
Submitted (17-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 127181)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                        Gaps
                                                                         16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC118404.2 GI:21746397
HTG; HTGS_PHASE1.
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Unpublished
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20801		Query Ma Best Loc	Matche
mi	Submitted (18-JUL-2002) Human Genome Sequencing Center, of Molecular and Human Genetics, Baylor College of Medic Baylor Plaza Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced gi:201627 On Jul 14, 2002 this sequence version replaced gi:201627 Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc.helpebcm.tmc.edu/Contact: hgsc.helpebcm.twc.edu/Contact: hgsc.helpebcm.twc.edu/Contact: hgsc.helpebcm.twc.helpebcm.twc.helpebcm.twc.helpebcm.twc.helpebcm.twc.edu/Contact: hgsc.helpebcm.twc.edu/Contact: hgsc.helpebcm.twc.helpebcc.helpebcm.twc.helpebc		28397: gap of unknown 29809: contig of 1412 29909: gap of unknown 32067: contig of 2158 32167: gap of unknown 34176: contig of 2009

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Gars gene; Cdknlc gene; cyclin-dependent kinase inhibitor 1C;
cars gene; Cdknlc gene; cyclin-dependent kinase inhibitor 1C;
cysteinyl-tRNA synthetase; PL gene; trug gene; nucleosome assembly protein llike 4 protein; Obphl gene; oxysterol
binding protein; Tnfrhl gene; Tnfrh2 gene; tumor necrosis factor
binding protein; Tnfrhl gene; Tnfrh2 gene; tumor necrosis factor
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homologue 2; tumor suppressing subtransferable candidate 5.
western European house mouse.
Was musculus domesticus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                  ROD 06-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-MAR-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, GERMANY
Revised by author 22-MAY-2000
3 (bases 1 to 281000)
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Submitted (24-JAN-2001) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-NOV-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Engemann, S., Strodicke, M., Paulsen, M., Franck, O., Reinhardt, R., Lane, N., Reik, W. and Walter, J. Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin, GERMANY
On Jan 27, 2001 this sequence version replaced gi:11191799, related accession numbers AJ300452-AJ300460
has a 1000 bp overlap with AJ271885.
Location/Qualifiers
1. 281000
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Mus musculus genomic fragment, 281000 bp, chromosome
AJ276505
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Direct Submission
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S Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Botten, S., Birva, M., Brown, M., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Deladado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
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Rattus norvegicus clone CH230-143P6, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                              Submitted (21-MaY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 140819) Materston, R. H. McPherson, J. D. and Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-701-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Jul 16, 2002 this sequence version replaced gi:21040003.
                                       Mus musculus Eukargota; Mordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus I (bases 1 to 140819)
McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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McPherson, J.D. and Waterston, R.H.
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AC126076.2 GI:21699142
HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         join(67525. 67596,72244. .72334,73711. .73838,76251. .76363,77140. .77213,77826. .77868,78677. .78828)
/gene="Infirit"
                                                                                                                                                                                                                                                                                                                                                                                                             join(31277. .31342,35572. .35662,37049. .37176,46179. .46291,
47068. .47141,48531. .48627)
/gene="Tnfrhl"
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48531. 48580)
/gene-"Tnfrhl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="tumor necrosis factor receptor p60 homologue"
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/db_xref="g1:12583597"
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/translation="mPESYSFNCPDGEYQSNDVCKTCPSGTFVKAPCKIPHTQGQCE
/translation="mpEsysproteing"
/gsne="mfith1"
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140377. 140517,141097. 141184,142468. 142590,
145511. 145624,146438. 146555,146958. 147085,
147169. 147274,147010. 147707,447985. 148174,
147169. 148792,157010. 147707,447985. 148174,
155189. 155255,157406. 157466,157904. 157988,
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AC121886.2 GI:21844658
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47068. .47141
/gene="Tnfrh1"
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48531. .48580
/gene="Tnfrh1"
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/gene="Cars"
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/gene="Tnfrh1"
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/gene="Tnfrh1"
                                                          25136. .25238
/gene="Obph1"
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/gene="Obph1"
                 'gene="Obph1"
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30593. .13068
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25136. .25
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Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hamilton,K.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Jacobson,B., Jia,Y., Unbacn,J., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L., Louiseged,H.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Martin,R., Martindale,A., Martinez,E.,
Masesy,E., Mawhiney,E., McLeod,M.P., Medoor,M., Morris,S.,
Miner,G., Milcell,T., Monbabat,R., Meris,G., Merzker,M.,
Miner,G., Milcell,T., Worbabat,R., Norgan,N., Morris,S.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M. Okwuon,G.,
Oraqunyen,N., Oviedo,R., Pace,A., Patron,B., Peerry,J., Perez,L.,
Pickens,R., Pickens,R., Pirmus,B., Pu,L.L., Quiles,M., Rn,Y.,
Sodergren,E., Sootl,G., Shen,H., Shooshhari,N., Sisson,I.,
Sodergren,E., Sott,G., Shen,H., Shooshhari,N., Sisson,I.,
Sodergren,E., Sott,G., Shen,H., Shooshhari,N., Shson,I.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telficod,B., Thomas,N., Ward,Woore,S., Warren,R., Washington,C., Walliams,G., Williams,G., Williams,G., Walliams,G., Waller, Zhou,J., Zorrilla,S., Nelson,D.,
Williams,G., Williams,G., Milliams,G., Milliams,G., Milliams,G., Shou,J., Zorrilla,S., Nelson,D.,
Direct Submission
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Direct Submission

NI Submission

Center Baylor College of Medicine

Center code: BCM

Web Site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-helpebom.tmc.edu

Contact: hgsc-helpebom.tmc.edu

Contact: project Information

Center project name: GI330-1496

Center clone name: CI330-1496

Center clone name: Sinistics
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NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as rother second in this record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
Direct Submission
Submitted (03-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 117082)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 55139 bases at least Q40 Consensus quality: 64630 bases at least Q30
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1155: gap of unknown length
2165: contig of 1010 bp in length
2265: gap of unknown length
3314: contig of 1049 bp in length
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2 (bases 1 to 117082)
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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kovar, C., Kovar, C., Lebow, H., Levan, J., Lewis, L., Liu, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Marminou, M., Marlioy, K., Margum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mandum, R., Manja, E., Montemayor, J., Moore, S., Morgan, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nquyen, N., Norris, S., Morgen, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Penez, L., Penez, L., Penez, L., Penez, R., Reidh, R., Reilly, B., Reilly, M., Ren, Y., Router, M., Rose, R., Reigh, R., Reilly, B., Reilly, M., Soherer, S., Scott, G., Shatsman, S., Shatsman, S., Shetty, J., Shvatsbeyn, A., Sisson, I., Shatsman, S., Shetty, J., Shatsman, S., Sonelle, R., Soed, A., Sodergren, E., Warlen, J., Woon, L., Toon, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tringey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Warren, R., Wel, X., White, P., White, R., Smith, D., Von, V., White, R., Smith, D., Von, Vielenbusenn, A., Mang, J., Zong, R., Smith, R., Man, J., Yon, V., White, R., Smith, D., White, R., Smith, D., White, R., Smith, D., White, R., Smith, M., Shan, M., Shan, M., Shan, M., Shan, M., Shan
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NOTE: This is a 'working draft' sequence. It currently
consists of 79 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-Ang-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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On Aug 23, 2002 this sequence version replaced gi:21716685.
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: plasmid;
Assembly program: Phrap; version 0.990329
Consensus quality: 96145 bases at least Q40
Consensus quality: 105750 bases at least Q30
Consensus quality: 11678 bases at least Q30
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1171: gap of unknown length
2289: contig of 1118 bp in length
2389: gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
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------ Project Information
Center project name: GBUZ
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Rat Genome Sequencing Consortium.
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G/5185
MARC 11245-11246:999628105:1 Sheep WBC Ovis aries STS genomic, sequence tagged site.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 899)
Freking, B.A., Leymaster, K.A., Keele, J.W. and Smith, T.P.L.
Identification of a mutation apparently causing the polar
overdominance callipyge phenotype in sheep
                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                          DB 2; Length 155645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50-200 ng genomic DNA
each 20 pmoles
each 88 uM
0.25 units (Qiagen Hotstar)
                                                                                                                                                                   / bp in .
// length
// to in length
                                                                                                                                                                                                                                                                                                        Score 28.8; DB 2; Length 1:
Pred. No. 26;
0; Mismatches 17; Indels
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Commercially supplied Qiagen HotStar buffer
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bp in length
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95 degrees for 30 seconds
54 - 60 degrees for 30 seconds
68 degrees for 2 minutes
32 to 45
                                                                 bp in length
length
                                                                                                                                                                                                                            bp in length
length
                                                                                                                                                                                                                                                       contig of 1063 bp in length
gap of unknown length
             in length
                                                                                           in length
                                                                                                                       bp in length
                                                                                                                                                                                                                                                                                 contig of 1282 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
NO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
Fax: 402 762 4173
                                                                                                         length
                                                                                                                                                        gap of unknown 1. contig of 2022 bl. gap of unknown 1. contig of 1327 bg gap of unknown 16
           contig of 2195 b
gap of unknown l
contig of 1208 b
gap of unknown l
contig of 1181 b
                                                                                                                   contig of 1308 b
gap of unknown 1
contig of 1489 k
                                                                                          contig of 2099
gap of unknown
                                                                                                                                                                                                                         contig of 1277
gap of unknown
                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: freking@email.marc.usda.gov
Primer A: AGTCTCACCCCTTCCTGGAC
Primer B: TGGAGACCCACTGGAAACTT
                                                                                                                                              contig
gap of
                                                                                gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             raq Polymerase:
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G75185.1 GI:20563988
                                     59237:
59337:
60518:
60618:
62717:
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73185:
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69.68;
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67836:
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                                                                                                        62817
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Best Local Similarity 69.6
Matches 39; Conservative
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dNTPs:
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Ovis aries
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AUTHORS
TITLE
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COMMENT
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G75185/c
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KEYWORDS
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sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of or greater.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             674939 945 bp DNA linear STS 14-MAY-2002
MARC 11247-11248:1020442896:1 Sheep WBC Ovis aries STS genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Captinae; Ovis.

1 (bases 1 to 943)
Freking, B. A., Leymaster, K. A., Keele, J. W. and Smith, T. P. L. Identification of a mutation apparently causing the polar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Dorset, Romanov, and Dorset-Romanov crossbreds"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The STS is derived from PCR amplicons generated from genomic {\sf DNA}_{\scriptscriptstyle A} sequenced from each end using the amplification primers. The
The STS is derived from PCR amplicons generated from genomic DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.25 units (Qiagen HotStar)
                                                                                                                                                                                                                                                                                                                                   2 others
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95 degrees for 30 seconds
54 - 60 degrees for 30 seconds
68 degrees for 2 minutes
32 to 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
NO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
Fax: 402 762 4173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           overdominance callipyge phenotype in sheep
                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         each 20 pmoles
each 88 uM
                                                                                                                                                                                                                                                                                                                                                                                             Score 28.6; DB
Pred. No. 59;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                   195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: freking@email.marc.usda.gov
Primer A: ATCTGGCAGCTCCTCTA
Primer B: GAACTTGCCCTTGGAAGTGA
PCR Profile:
                                                                                                                                                                                                                        /db_xref~"taxon:9940"
/clone_lib="Sheep WBC"
/dev_stage="adult"
/note="Organ: blood"
                                                                                                                                                              1. 899
/organism="Ovis aries"
                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   263 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G74939.1 GI:20563742
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                                                                                                                                                                                                                                                                                                             .>899
336 c
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 67.8
Les 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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DEFINITION
                                                                                                                                                                                                                                                                                                                                 BASE COUNT
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Matches
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G74939/c
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SOURCE
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sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of
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Submitted (22-FBB-2001) Department of Genetics, B43, University of
Liege, 20, Bd de Colonster, Liege 4000, Belgium
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF354168 215046 bp DNA linear HTG 16-MAY-2001
Ovis aries chromosome 18 clone 229G11; 359E3, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human-ovine comparative sequencing of a 250-kb imprinted domain encompassing the callippyed (clpg) locus and identification of six imprinted transcripts: DLK1, DAT, GTL2, PEG11, antiPEG11, and MEG8 Genome Res. 11 (5), 850-862 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovoidea; Caprinae; Osyis.

1. (bases 1 to 215046)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Ovis aries"
/strain="Dorset. Romanov, and Dorset-Romanov crossbreds"
/db_xref="Laxon:9940"
/clone_lb="Sheep WBC"
/dev_stage="adult"
/note="Organ: blood"
a 354 c 236 g 219 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charlier, C., Segers, K., Wagenaar, D., Karlm, L., Berghmans, S., Jaillon, O., Shay, T., Weissenbach, J., Cockett, N., Gyapay, G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charlier, C., Segers, K., Wagenaar, D., Karim, L., Berghmans, S., Jaillon, O., Shay, T., Weissenbach, J., Cockett, N., Gyapay, G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 12055 27921: contig of 12054 bp in length

* 12075 27921: contig of 18847 bp in length

* 27922 27941: gap of unknown length

* 27942 29866: contig of 1905 bp in length

* 29867 33482: contig of 1905 bp in length

* 29867 33482: contig of 3616 bp in length

* 33483 33502: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE2; HTGS_DRAFT.
Ovis aries.
                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, 30 ordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 46.9%;
1 Similarity 67.8%;
40; Conservative 0
                                                                                                                                                               . 945
                                                                                                        20 or greater.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovis aries
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Butary, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Agele, M., Banks, T., Bardraid, J., Bowle, S., Blace, M., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Barken, M., Brown, E., Blankenburg, K., Bonnin, D., Bouck, J., Burke, N. B. Erown, M., Bryant, N. B., Bowle, S., Barteva, M., Brown, E., Bard, N. C., Corle, D., Chavez, D., Chen, R., Chen, R., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Carron, T. E., Davis, C., Davy-Carroll, L., Dederich, D. A., Davis, C., Davy-Carroll, L., Dederich, D. A., Davis, C., Davis, C., Davy-Carroll, L., Dederich, D. A., Davis, C., Davy-Carroll, L., Dederich, D. A., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Beschto, M., Falls, T., Ferratude, D., Flagg, N., Ford, J., Foster, P. Frantz, P., Falls, T., Ferratude, C., Edwards, C.C., Elhaj, C., Barnitto, R., Gorzell, J. Garcia, M., Gunarathe, P., Hale, S., Hamilton, K., Harnandez, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Harnandez, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Harnandez, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Martine, K., Jacokson, J., Sucodo, R., Jay, Y., Johlaw, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, D., Kovah, J., Kovar, C., Liu, J., Liu, M., Mapua, P., Martin, R., Martin, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus norvegicus clone CH230-326J5, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 136726 bases at least Q40
Consensus quality: 144728 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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Rattus norvegicus clone CH230-195D20, *** SEQUENCING IN PROGRESS
***, 79 unordered pieces.
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                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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15. MAZONYD. M., Addms. C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C., Alabrooks, S. L., Amaratunge, H.C., Are, J. R., Ayele, M., Banks, T., Barbooks, S. L., Amaratunge, H.C., Are, J. R., Ayele, M., Bonnin, D., Barbooks, S. L., Amaratunge, H.C., Are, J. R., Ayele, M., Bonnin, D., Bands, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burkett, C., Burch, E., Burkett, C., Burch, E., Burkett, C., Burch, R., David, N. C., Chen, G., C
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Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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On Jul 13, 2002 this sequence version replaced gi:19525921.
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
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Center clone name: CH230-195D20
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Direct Submission
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 79 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T., Carrer, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, G., Chen, G., Chon, C., Chowdiry, I., Christopoulos, C., Chen, G.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davis, C., Davy-Carroll, I., Dederich, D.A., Delando, N., Daper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Fergutto, D., Edwards, C.C., Elhaj, C., Escotto, M., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gortell, J., Harris, K., Harris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 94 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 7030, USA.
On Jul 13, 2002 this sequence Version replaced g1:18701729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 103990 bases at least Q40 Consensus quality: 112822 bases at least Q30 Consensus quality: 112872 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-26L15
Center clome name: CH230-26L15
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2 (bases 1 to 170476)
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Worley, K.C.
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AUTHORS
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Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
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HTG; HTGS_PHASE1.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Search completed: June 13, 2003, 04:39:36 Job time: 197.613 secs us-09-826-581-3_copy_612_672.rng

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PRKAG3 intron 4 -
Genomic sequence e
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                                                                                                                                                                                                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                  2185239 seqs, 1125999159 residues
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Listing first 45 summaries
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1374 22 AAH18673 Human cDNa sequence 5938 23 ABK42266 Genomic sequence 9305 24 ABL54634 Human p53AIPI ass	24 ABN96428 21 AAA14998	20 AAX37383 Human 24 AAX99401 DAY C	24 ABL93040 Rat	55	22 ABK26334 Pro 22 AAK04847 Hum	22 AAK30374 Human	22 AAI36331 Probe 24 ABS04972 Human	22 ABA51286 Human	7 7 7	22 AAK43391 Human	22 AA14946U Probe 24 ABS17483 Himan	24 ABK17335	1/ AAT18020 Human 21 AAA60104 Human	21 AAA60123 Human	21 AAA60124 Human	15	17 AAT16646 Hepatitis	77	231 22 ABA73753 Human	22 ABA38943 Probe	22 AAK48368 Human	22 AAI26223	ALIGNMENTS	1; DNA; 1722 BP.		st entry)	. intron 10.	ited protein kinase gamma 3 subunit; PRKAG3; variant;		Location/Qualifiers	13 ^*tag= a ^number = "Intron 4"	"3' portion	/*tag= b //unber="Exon 5" of rs	2004
444	41	41	4.4	404	4040	40	4040	40	4.4	40	4 4	40	4 4	40	40	40	40	4 4	40	40	\circ	40.0		standard;		02 (first	intron 4 -	AMP-activated ic disease; d		Н	- ` `	. \-	```	
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AAL38336 standard; DNA; 143899 BP.

AAL38336

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There may also be nucleotide variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecriting the presence of the PKRAG3 DMA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution PTIA; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number= "Intron 10"
/note= "5' portion of intron 10"
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                                                                g Intron 7"
                                                                                                                                                                                                                    'number= "Intron 8"
                                                                                                                                                                                                                                                                                                                                                  "Intron 9"
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1689..1722
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/number= "Exon 9"
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/number= "Exon 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 3; 25pp; English.
                                                                                                                         h
Exon 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid substitution R340W.
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The invention relates to a Nogo receptor homologue polypeptide, NgR2 or NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT sequence, or a 420, 461 or 392 amino acid sequence, all given in the sequence.

Sequence, or a 420, 461 or 392 amino acid sequence, all given in the sequence, or a 420, 461 or 392 amino acid sequence, all given in the sepecification. The NgR3 protein or its binding antibody is useful for cercasing inhibition of axonal growth of a central nervous system (CNS) neuron, by contacting the neuron NgR3 or its antibody, and for treating crebral injury, Spinal cord injury, stroke, demyelinating disease, or, multiple sclerosis, monophasic cemyelinating disease, e.g. multiple sclerosis, monophasic demyelination, encephalomyelitis, multifocal leukoencephalopathy, parencephalitis, Marchiafava-Bignami disease, Spongy degeneration, Alexander's disease, Canavan's disease, Spongy degeneration, Alexander's disease, Canavan's disease, manual against NgR3, as a bait protein in a two-hybrid or three-hybrid cor and as a research tool for identification, characterisation and purification of interacting, requiatory proteins. The nucleotide sequences of the invention are useful for screening for RFLP associated
                                                                                                                                                                                                      NgR2; NgR3; axonal growth; central nervous system; CNR5; cerebral injury; spinal cord injury; stroke; demyellating diseases; multiple solenosis; monophasic demyelination; encephalomyelitis; Marchidava-Bignami disease; multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; canavan's disease; metachromatic leukodystrophy; Krabbe's disease; immuce; bait protein; genetic mapping; gene therapy; transgenic animal; urregulated cellular growth; cancer; tumour; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       purifying
                                                                                                                                                                                  Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for
ing central nervous system disorder, cerebral injury, spinal cord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NgR3, for localisation and/or quantitation of NgR4, and for diagnostic and therapeutic purposes. The sequences of the invention, vectors and antibodies are useful for treating or preventing unrequiated cellular growth such as cancer and tumour growth. This polynucleotide sequence represents the genomic sequence encoding a human NgR2 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with certain disorders, for genetic mapping, and for gene therapy. T vector containing NgR3 is useful for producing non-human transgenic animals. The NgR3 binding antibody is useful for isolating and purif
                                                                                                                                 Genomic sequence encoding a human NgR2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        injury, stroke, and demyelinating diseases
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Sequence 143899 BP; 36346 A; 35277 C; 35318 G; 35657 T; 1301 other;

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                                                                                                       Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34227
                   Length 143899;
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                   DB 24;
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                Score 27.2; DB Pred. No. 25; 0; Mismatches
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Human; connective tissue related disorder; cancer; gene therapy; cytostatic; gene; ds.
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24-FEB-2000;
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07-JUL-2000;
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  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
expension by rectifying mutations or deletions in a patient's genome
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own production of (1). Additionally, (1)
polynucleotides may be used to produce the secreted (1), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (1) proteins and polynucleotides may be used to provent,
cancers and cancer melastases of haematopoietic antigen genomic
sequences from the present invention. AAK64942 to AAK64960 and AAM82169
represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic sequence #608 encoding novel human connective tissue polypeptide.
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                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                17 -NOV-2000; 2000US-0249264.

17 -NOV-2000; 2000US-0249265.

17 -NOV-2000; 2000US-0249265.

17 -NOV-2000; 2000US-0249297.

17 -NOV-2000; 2000US-0249300.

10 -DEC-2000; 2000US-0249300.

01 -DEC-2000; 2000US-0250391.

05 -DEC-2000; 2000US-0251030.

05 -DEC-2000; 2000US-0251479.

06 -DEC-2000; 2000US-0251479.

08 -DEC-2000; 2000US-0251868.

08 -DEC-2000; 2000US-0251868.
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The present invention relates to the isolation of novel human connective tissue related polypeptides (AAU66435-AAU66923) and the polynucleotide (CDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection prevention of Chrysophrys major iridovirus. The protein encoded by the DNA is useful as an antigen for preventing infection of Chrysophrys major iridovirus. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes proteins related to neutralisation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of Ehime-1 strain of Red sea bream iridoviris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 42.6%; Score 26; DB 23; Length 17761; Local Similarity 65.5%; Pred. No. 50; nes 38; Conservative 0; Mismatches 20; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17761 BP; 3197 A; 5132 C; 5595 G; 3837 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prevention of Chrysophrys major iridovirus
                                                                                                                                                                                                                    Disclosure; SEQ ID No 1596; 673pp; English.
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(KURI/) KURITA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 13-51; 65pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a protein related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL59091 standard; DNA; 112414 BP
                                                                         Ruben SM;
                                   (HUMA-) HUMAN GENOME SCI INC.
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05-JAN-2001; 2001US-0259678.
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                                                                       Rosen CA, Barash SC,
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                                                                                                          WPI; 2001-565190/63.
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2000US-0244617.
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2000US-023239
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20000S-0239937.
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           01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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-NOV-2000;
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nucleotide sequence of the Ehime-1 strain of Red sea bream iridoviris (RSIV).
                                                                                                                                                                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25277
                                                                              42.3%; Score 25.8; DB 24; Length 112414; ilarity 73.3%; Pred. No. 67; Conservative 0; Mismatches 12; Indels 0;
                                                    Sequence 112414 BP; 26205 A; 29684 C; 30351 G; 26174 T; 0 other;
                                                                                                                                                      18391 GGGGTGGCGATCTGATGGGTGACAGGGGCTGTAGCGCAGGG 18347
                                                                                                                                      AAK70465 standard; DNA; 14070 BP
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20000S-0216880.
20000S-0217487.
20000S-0218290.
20000S-0220963.
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2000US-0186350
2000US-018674
2000US-0198123
2000US-0205515
2000US-0205467
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2000US-0225267.
2000US-0225268.
2000US-0225270.
2000US-0225447.
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2000US-0224519.
2000US-0225213.
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20000S-0225759.
20000S-0226279.
2000US-0226681.
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                                                                                                                                                                                                                                                                                           (first entry)
                                                                                           Best_Local Similarity
Matches 33; Conserv
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27 MAR - 2000)
28 MAR - 2000)
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01-SEP-2000;
01-SEP-2000;
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonoclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nuclectide sequences defined in the specification, where the oligonuclectide comprises at least 15 nuclectides, or (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to a polynuclectide which comprises a 3'-end sequence complementary to a polynuclectide which comprises a 1-end sequence, where the complementary to a polynuclectide comprises a 1-end sequence of the 5'-end sequence is selected from those defined in the 5'-end sequence 15 selected from those defined in the specification. The primers sets can be used in antisense therapy and particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by convained to the ADH3633 tepresent human cDNA sequences; ABH3646 to ABH3633 represent human end of sequences; and ABH3632 to ABH3632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent oligonucleotides, all of which are used in the exemplification
                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNas defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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, Otsuki T;
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0; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID 5249; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai T, Nishikawa T, Hayashi K, S
, Sugiyama T, Wakamatsu A, Nagai K,
                                          Human cDNA clone (5'-primer) SEQ ID NO:5249.
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                                                                                                                                                                                                                                                                                                   99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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26-JUN-2001 (first entry)
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Best Local Similarity 66.7*
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ota I,
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ID AAC7794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplaement the patients own production of (I). Additionally, (I) polynuclectides may be used to produce the secreted (I), by inserting the nucleic acids into a host ceil and culturing the cell to express the protein. (I) proteins and polynuclectides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancer and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64942 to AAK64950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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0; Mismatches 19;
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ID AAH08414 standard; CDNA; 686 BP.
XX
AC AAH08414;
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                                                                           2000US-0249218.
2000US-0249244.
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2000US-0250391
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2000US-0251990
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                                                       17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
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01-DEC-2000; 2
01-DEC-2000; 3
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08-DEC-2000;
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17-NOV-2000;
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Matches
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(first entry)

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Identifying modulators of gamma aminobutyric acid(GABA)-B receptor mediated activity by monitoring the interaction between GABAB receptor and the CREB/ATF transcription factors in the presence of a test
                                                                                                                                                                                       Human; ATFx; gamma aminobutyric acid B receptor; GABA B receptor;
transcription factor; ss.
                                                                                                                                            Human ATFx coding sequence with 5' extension.
AAF77880 standard; cDNA; 1105 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White J, Wise A, Marshall F;
                                                                                                                                                                                                                                                                                                                                                                                                            31-AUG-2000; 2000WO-GB03361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JAN-2000; 2000GB-0000516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-265904/27.
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                                                                                                                                                                                                                                                                                                               WO200116596-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-AUG-1999;
                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                            30-MAY-2001
                                                                                                                                                                                                                                                                                                                                                               08-MAR-2001
                                                  AAF77880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 include: cytostatis; proliferative; vulnerary: immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiinflammatory: antiathritic; antinflammatory: antichyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; hrombolytic; coagulant; nootropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune
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                                                                                                                                    diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acids comprising sequences encoding peptides
                                                                                                                     cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 1030;
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                                                                   cancer associated gene sequence SEQ ID NO:334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for treating or diagnosing e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25.2; DE Pred. No. 72; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 886; 2352pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2000; 2000WO-US05882
                    (first entry)
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es 36; Conserv
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P-PSDB; AAB43731
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                    08-FEB-2001
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Matches
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99GB-0020569

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                                         The present invention relates to a method for identifying a modulator of gamma aninobutyric acid_B (GABA_B) receptor_mediated activity, by monitoring the interaction between a CREB/ATF transcription factor capable of binding to GABA_B receptor. The present sequence is the coding sequence for human ATFx, which was used in the method of the present invention. ATFx is a member of the CREB/ATF family of transcription factors. ATFx contains a b21P domain, by which it interacts with the colled coil domain of GABA_B receptor. Modulators of GABA_B receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                 activity are useful for treating central nervous system or peripheral nervous system disorders. The present sequence encodes an ATFx protein
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0
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                                                                                                                                                                                                                                                                               with a N-terminal extension (compared to AAB80892).
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                                                                                                                                                                                                                                                                                                                                                                         Score 25.2;
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA sequence SEQ ID NO:18921.
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Claim 17; Fig 9; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                           41.3%;
66.7%;
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ses 36; Conserv
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RESULT 9 AAF77880/c

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2000US-0189874 2000US-0190076 2000US-0205515

2000US-0198123

2000US-0180628 2000US-0184664 2000US-0186350 2000US-0215135 2000US-0216647 2000US-0216880. 2000US-0217487. 2000US-0217496. 2000US-0218290. 2000US-0220963 2000US-0220964 2000US-0224518. 20000S-0224519

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17-JAN-2001; 2001WO-US01322
                                 WO200155343-A1.
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06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
11-SEP-2000;
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01-SEP-2000;
01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
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22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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25-SEP-2000;
26-SEP-2000;
 Homo sapiens.
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18-APR-2000;
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11-JUL-2000;
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14-AUG-2000;
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                                                                      02-AUG-2001
to the present invention describes primer sets or synthesising your full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary comprises or one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the polynucleotide which comprises a 3'-end sequence, where the complementary to a polynucleotide comprises a 1'-end sequence, where the oligonucleotide comprises a 1'-end sequence oligonucleotide comprises a 1'-end sequence)' end sequence is selected from those defined in the 5'-end sequence's' end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, catterious and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH30136 to AAH18043 and AAH13033 to AAH18042 represent human cDNA sequences; AAB92446 to AAH13033 to AAH18042 represent human amino acid sequences; and AAH13059 to AAH13032 represent human amino acid sequences; and AAH13059 to AAH13053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic sequence #165 encoding novel human connective tissue polypeptide.
                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNas defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNas -
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                                                                                                                                                                                                                                                       Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes primer sets for synthesising 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; connective tissue related disorder; cancer; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25.2; DB 22; Length 1374;
Pred. No. 73;
0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                     Saito K, Ya
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                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID 18921; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                   Isogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
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                                                                                                                        27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                      28-JUL-2000; 2000EP-0116126.
                                                                                                         99JP-0248036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 66.7
les 36; Conservative
                                                                                                                                                                                                                   (HELI-) HELIX RES INST.
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 EP1074617-A2
                                                                                                           29-JUL-1999;
                                     07-FEB-2001.
                                                                                                                                                                                                                                                                    shii S,
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Matches
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NAMES OF COLOR COL

2000US-0226681. 2000US-0226868.

2000US-0227182. 2000US-0227009

2000US-0225758. 2000US-0225759.

2000US-0226279

20000S-0225268 2000US-0225447 2000US-0225757 2000US-0229344.

2000US-0229345 2000US-0229509

2000US-0229513 2000US-0230437 2000US-0230438 2000US-0231242 2000US-0231243

2000US-0229343

2000US-0229287

2000US-0231414. 2000US-0232080. 2000US-0232081.

2000US-0231413

2000US-0234997. 2000US-0234998. 2000US-0235484.

2000US-0233063. 2000US-0233064.

2000US-0233065

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2000US-0231968 2000US-0232397 2000US-0232399

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29-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236368.
29-SEP-2000; 2000US-0236368.
29-SEP-2000; 2000US-0236369.
02-OCT-2000; 2000US-0236370.
02-OCT-2000; 2000US-0237038.
02-OCT-2000; 2000US-0237039.
03-OCT-2000; 2000US-0237039.
03-OCT-2000; 2000US-0239935.
03-OCT-2000; 2000US-0239937.
03-OCT-2000; 2000US-0239937.
03-OCT-2000; 2000US-0241808.
03-OCT-2000; 2000US-0241808.
03-OCT-2000; 2000US-0241809.
03-OCT-2000; 2000US-0241809.
03-OCT-2000; 2000US-0241809.
03-OCT-2000; 2000US-0241809.
03-OCT-2000; 2000US-0241809.
03-OCT-2000; 2000US-0241826.
03-NOV-2000; 2000US-0246477.
03-NOV-2000; 2000US-0246477.
03-NOV-2000; 2000US-0246477.
03-NOV-2000; 2000US-0246527.
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17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-026160.
01-DEC-2000; 2000US-0251030.
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17-NOV-2000; 20000S-0249215.
17-NOV-2000; 20000S-0249216.
17-NOV-2000; 20000S-0249217.
17-NOV-2000; 20000S-0249218.
17-NOV-2000; 20000S-0249244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249212.
17-NOV-2000; 2000US-0249213.
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2000US-0249209.
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2000US-0235834
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17-NOV-2000; 2
17-NOV-2000; 2
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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05-DEC-2000;
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(HUMA-) HUMAN GENOME SCI INC

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ö
                                                                                                                                                                                           tissue related polypeptides (AAU86435-AAU86923) and the polypucleotide (CDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK41102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides. Whote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                               The present invention relates to the isolation of novel human connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p53-dependent apoptosis-associated protein and its encoding gene p53AIPI, used for screening apoptosis mediated remedies for cancer and as controllers of apoptosis induction
                                                                              Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human p53-dependent apoptosis-associated protein, P53AIPI comprising fully defined 806, 777, 2659 nucleotide sequences (ABL54631-ABL54633 respectively) given in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; p53; p53AIPI; p53-dependent apoptosis-associated; apoptosis;
cytostatic; cancer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 5938;
                                                                                                                                                                                                                                                                                                                                                                             Sequence 5938 BP; 1295 A; 1601 C; 1751 G; 1291 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                               Disclosure; SEQ ID No 1153; 673pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human p53AIPI associated DNA SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                             41.3%; Score 25.2; 66.7%; Pred. No. 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 92-104; 121pp; Japanese.
                 Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL54634 standard; DNA; 9305 BP
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(ONCO-) ONCOTHERAPY SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000; 2000JP-0240399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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               Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-217192/27.
                                               WPI; 2001-565190/63.
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ABL54634/c
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Homo sapiens.
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11-FEB-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA14998;
                                                                                                                                                                                                                                                                                                                           RESULT 14
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and the three respectively encoded human p53-dependent apoptoxis.associated proteins having fully defined 124, 86 and 108 amino acid sequences (ABB08837-ABB08839 respectively) given in the specification. The protein and encoded gene have cytostatic activity, are
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                         useful in screening for regulators of apoptosis for subsequent use as cancer treatments. The present sequence is that of the Human p53AIPI associated DNA, useful to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                           DB 24; Length 9305;
                                                                                                                                                                                                                                                            Sequence 9305 BP; 2133 A; 2438 C; 2570 G; 2164 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 275 BP; 49 A; 103 C; 68 G; 50 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene #2926 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                        41.3%; Score 25.2;
66.7%; Pred. No. 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2926; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-2001; 2001WO-US30589.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                          3est_Local Similarity 66.7
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENE LOGIC INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-426119/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horne D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human proliferation and apoptosis related protein polypeptides used for diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; proliferation and apoptosis related protein; PROAP; psoriasis; cell proliferative disorder; immunological disorder; hepatitis; reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphoma; acquired immune deficiency syndrome; AIDS; allergy; anaemia; asthma; diabetes mellitus; osteoarthritis; endometriosis; uterine fibroid; menstrual cycle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "proliferation and apoptosis related protein"
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                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA encoding a human proliferation and apoptosis related protein.
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       DB 24; Length 275;
                                                                   10; Indels
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                                                                                                                                                                                                         148 GGACCTCATAGGGAGCCAGGGGGGCAGGGGCCGGGGGGGT 188
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                                                                                                                                         17 GAATCTTATGGGCACCCAGAGGGGGGGGGGGGGGGGAGT
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, Shih LL;
                                   Pred. No. 75;
0; Mismatches
          Score 25;
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                                                                                                                                                                                                                                                                                                                                                                              BP.
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                                                                                                                                                                                                                                                                                                                                                                              AAA14998 standard; cDNA; 303
   41.0%;
75.6%;
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Query Match
Best Local Similarity 75.6'
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                              gene therapy, diagnosis, cancer; tumour; neurodegenerative disorder; developmental abnormality; foetal deficiency; blood disorder; lymphoma; leukemia; immune system disorder; autoimmune disease; hepatic disease; renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS; Alzheimer's disease, cognitive disorder; schizophrenia; osteoporosis; arthritis; psoriasis; digestive; endocrine; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or amount of expression of the new polypeptides in a sample or by determining the presence or absence of mutations in the new polynucleotides. Specific uses are
                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                 secreted protein; prevention; treatment; protein therapy;
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Lafleur DW;
Shi Y, Soppet DR;
                                      41.0%; Score 25; DB 21; Length 303; 64.9%; Pred. No. 75;
                                                                  20; Indels
                                                                                                                                                                                                                                                                     Human secreted protein cDNA fragment containing gene 15.
            Sequence 303 BP; 67 A; 85 C; 110 G; 41 T; 0 other;
                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim la; Page 198; 280pp; English.
                                                                                                                                                                                        AAX37383 standard; cDNA; 541 BP.
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97us-0056368.
97us-0056369.
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97us-0056726.
97us-0056728.
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                                                   64.98;
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97US-0056555.
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97US-0056628.
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                                                                 37; Conservative
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P-PSDB; AAY07758.
                                                   Local Similarity
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Young PE;
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                                       Query Match
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B1489045 603021030 B1489015 603021030 B195192 BB195192 B1430892 0050500673 B195582 HVSNEM002 ALZO0974 82_0165_A BE963498 601657281 AU256222 AU256222

Perfect score: Sequence: Scoring table:

Total number Minimum DB Maximum DB

Database

Searched:

OM nucleic -

Run on:

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Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW026388 354 bp mRNA linear EST 09-MAR-2000 wvl2f05.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529345 3' similar to contains element MSR1 repetitive element ; mRNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dasses 1 to 354)

NCI/NINDS-CGAP http://www.ncbi.nlm.nlh.gov/nciogap.

NAtional Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)

Contact: Robert Strausberg, Ph.D.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pcMV-SPORT6; Site_1: Not1;
/note="Organ: primer: Oligo dr. Average insert size 2.1 kb."

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
flound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llol.gov
Plate: LLAMI222 row: f column: 16
High quality sequence stop: 635.
I. Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                     Gaps
                                                                                                                       0; Gaps
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                                               DB 14; Length 1208;
                                                                                     Indels
                                                                                   16;
                                           49.8%; Score 30.4; DE 71.4%; Pred. No. 69; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib-"NIH_MGC_71"
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/clone="IMAGE:5534991"
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                                                               Best_Local Similarity 71.4%;
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="melanotic melanoma"
/lab_host="bH10B (phage-resistant)"
/note="organ: skin; Vector: pCMV-SPORT6; Site_1: Not!;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1208)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: ArCC/DCTU/JUTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://fmage.lill.gov
Plate: LLAM13333 row: d column: 18
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                         /clone="IMAGE:2529345"
/clone=lb="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH108"
www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 1245 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 338.
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/db_xref="taxon:9606"
/clone="IMAGE:6062177"
                                                                                                                   /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_72"
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Location/Qualifiers
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74.1%;
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Best Local Similarity
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Vactorial Course Course
                                        /lab_host="DHIOD" (phage-resistant)"
/lab_host="DHIOD" (phage-resistant)"
/note="Organ: spleen; Vector: poins"; Site_1: XhoI; Site_2:
ECRI: CDNA made by oligo-dr priming. Directionally cloned
into ECCRI/AhoI sites using the following 5' adaptor:
GGCACAGG(6). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library.

421 c 311 g 213 t
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AL530561 LTL_NFL001_NBC4 Homo sapiens cDNA clone CSODD007Y022 5
Prime, mRNA sequence.
AL530561
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genoscope - Centre Cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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14, W.B., Gruber.C., Jessee,J. and Polayes,D.

Full-length cDMa libraries and normalization

Unpublished (2001)
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/lab_host="DH10B"
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55.2%; Pred. No. 2.4e+02;
iive 10; Mismatches 16;
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Pred. No. 1.9e+02;
0; Mismatches 17
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/db_xref="taxon:9606"
/clone="CSODD007Y022"
            clone_lib="NIH_MGC_113"
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Best Local Similarity 69.6%;
Matches 39; Conservative (
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/clone=lib="LTI_NELOOG_PL2"
/clone=lib="LTI_NELOOG_PL2"
/tissue_type="placenta"
/tissue_type="plac
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Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2472 row: n column: 07
High quality sequence stop: 415.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrbini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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                                                                                                                                                                                              Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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1 (bases 1 to 688)
Liw, B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNa libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9606"
/clone="IMAGE:6280902"
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                                                                                                                                                                  Contact: Genoscope
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Best Local Similarity 55.7
Matches 34; Conservative
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/tissue_type="1,mphona, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph: Vector: poTBF; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B0521472 403 bp mRNA linear EST 10-JUN-2002 NISC_nll1c01.x1 NICHD_XGC_Emb7 Silurana tropicalis cDNA clone IMAGE:5336064 3', mRNA sequence.
                                                                                                                                                                                                          BM909483 1729 bp mRNA linear EST 12-MAR-2002 AGENCOURT_6640847 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5434071
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MIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                        27
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Plate: LLCM1910 row: i column: 16
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Best Local Similarity 68.4%; Pred, No. 2.9e+02;
Matches 39; Conservative 0; Mismatches 18;
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Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
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/clone="IMAGE:5434071"
/clone_lib="NIH_MGC_99"
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                                                                                                                                                                                                                                                                                                                                                                                         Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, Y.D., Oates, R. and Main, D.
Pevelopment of a questically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot CDNA library Unpublished (2001)
On Feb 22, 2001 this sequence version replaced gi:13109940.
Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
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this clone see http://www.genome.clemson.edu/orders Also
                        HUSMEC0002B16f Hordeum vulgare seedling shoot EST library HVCDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEC0002B16f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Hordeum vulgare seedling shoot EST library
HVcDNA0003 (Etiolated and unstressed)"
/tissue_type="Seedling shoot"
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68.4%; Pred. No. 2.7e+02;
tive 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
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/db_xref="taxon:4513"
/clone="HVSMEc0002B16f"
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Seq primer: AATTAACCCTCACTAAAGGG
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l Similarity 69.1%;
38; Conservative
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                                                                                                                                                                                     Best_Local Similarity
Matches 40; Conserv
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                                                                                                                                            Email: cgapbs-remail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NJSC)
Clone distribution NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="tailbud"
/dev_stage="embryo, stages 20-27"
/lab_host="DH10B (phage=resistant).
/note="Vector: pCMv-SPORI6.ccdb; Site_1: NotI; Site_2:
EcoRV, Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
                                                   NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml. National Institute of Child Health and Human Development, National
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Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 530)
Morgan, R.W. and Burnside, J.
Chicken lymphoid ESTS
Unpublished (2001)
On Mar 27, 2002 this sequence version replaced gi:19772396.
Contact: Joan Burnside
Molecular Endocrinology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 403;
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Local Similarity 66.7%; Pred. No. 2.9e+02;
nes 40; Conservative 0; Mismatches 20; Indels
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40 Townsend Hall, Newark, DE 19717, USA
els 1302 831-1345
Fax: 302-831-3411
Email: joan@UDel.Edu, www.chickest.udel.edu.
                                                                                                                                                                                                                                                                                                                                                                    /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="IMAGE:5336064"
                                                                                          Cancer Insitute, Xenopus Gene Collection
                                                                                                                                                                                                                                                                                       Plate: LiAM11853 row: F column: 1
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NICHD_XGC_Emb7"
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/db_xref="taxon:9031"
                                                                                                                             Contact: Robert Strausberg, Ph.D.
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                 Kenopodinae; Silurana.
                                                                                                                                                                                                                                                                           info@image.ĺlnl.gov
Plate: LLAM11853 rc
                                  (bases 1 to 403)
                                                                                                           Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                    1. .403
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Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-132E07.R.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehitro-chou, Tsurumal-ku, Yokohama, Kanaqawa 230-0045, Japan (E-mail:chimpbes@glsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: PTB-132E07.R, genomic survey sequence.
AG122806
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                               /tissue_type="thymus, bursa, spleen, PBL, bone marrow"
/lab_host="E.coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                            /clone="pgn1c.pk010.k15"
/clone_lib="normalized chicken lymphoid cDNA library"
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 653)
Fuliyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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/clone_lib="PTB Chimpanzee Male BAC Library"
258 c 82 g 173 t
                                                                                                                                                                                                                                     ch 45.9%; Score 28; DB 14; Length 530; l Similarity 66.7%; Pred. No. 2.9e+02; 40; Conservative 0; Mismatches 20; Indels
                                                                                                                                                           33 others
                                                                                                                                                                                                                                                                                        20; Indels
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Pred. No. 3.4e+02;
0; Mismatches 17;
                                                                                                                                                           126 t
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/db_xref="taxon:9598"
                                                                                                                                /note="Vector: pCMVSPORT
149 c 142 g 126
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/clone_lib**NIFE_NGC_100*
/tissue_type="hepatocellular carcinoma, cell line"
/tab_host="baplow (phage-resistant)
/note="organ: liver; Vector: pOTB7; Site_l: XhoI; Site_2:
ECORI: CDNA made by oligo-dT priming. Directionally cloned
into EcoRI;XhoI sites using the following 5: adaptor:
GCCACGAG(G). Size-selected >500pp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis Ait (Stratagene) and superscript
I.RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH756447 493 bp DNA linear GSS 01-MAR-2002 SALK_053697.52.05.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_053697.52.05.n, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thale cress.

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 493)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can j

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2444 row: j column: 15

High quality sequence stop: 438.

Location/Qualifiers
  Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1434;
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27.8; DB 14;
Pred. No. 3.7e+02;
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/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 g 273 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                   /clone="IMAGE:6270062"
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Matches 38; Conservative
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(bases 1 to 712)

(bases 1 to 712)

Totokir, watenabe, H. and Sakakir, Taylor, T.D., Yada, T.,

Totokir, v., Watenabe, H. and Sakakir, V.

Direct Submission

Submitted (02-A0(2-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKBN), Genomic Sciences Center (GSC):

1-7-22 Suchiro-chou, Tsurumirku, Yokohama, Kanagawa 230-0045, Japan

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpensee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ648687 11434 bp mRNA linear EST 15-JUL-2002 AGENCOURT_8297851 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6270062
                                                                                                                                                           troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
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                                               GSS 03-NOV-2001
                               AG090162 712 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-089K05.R, genomic survey sequence.
AG090162
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1 (bases 1 to 1434)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                           Eukaryoťa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Pred. No. 3.5e+02;
0; Mismatches 17;
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/db_xref="taxon:9598"
/clone="PTB-089K05.R"
/sex="male"
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/clone_lib="PTB Chimpanze
230 c 205 g 150
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Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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ilarity 69.1%;
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full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NHE_MGC_Library." 2 others
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/db_xref="taxon:3702"
/clone="SALK_053697.52.05.n"
/clone="Lib="Arabidopsis thaliana TDNA insertion lines*
/olove_lib="Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html*
a 160 c 112 g 106 t 12 others
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MNH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11479 row: k column: 08
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                                                                                                                                                                                                                                                                                                         Query Match 45.2%; Score 27.6; DB 17; Length 493; Best Local Similarity 67.2%; Pred. No. 3.8e+02; Matches 39; Conservative 0; Mismatches 19; Indels 0;
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/lab_host="DH108"
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/clone~"IMAGE:5191807"
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June 13, 2003, 02:39:09; Search time 4.64516 Seconds (without alignments) 4027.262 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 3, Appli	ຳຕັ	'n		139	140,	139,		17, A	2,	Sequence 1, Appli	1, 2	Sequence 2, Appli	H	136	m	26,	74,	2, A	218	30,	1, 1	1,	11,	11,	Sequence 3, Appli
SUMMARIES 1D	US-08-459-568-3	US-08-516-859A-3	US-09-586-472-3	US-09-528-706-3	US-08-290-665A-139	US-08-290-665A-140	PCT-US95-10398-139	PCT-US95-10398-140	US-08-836-075A-17	US-09-103-840A-2	US-09-103-840A-1	US-08-323-443B-1	US-08-658-136-2	US-08-658-136-1	1	38-943	US-09-188-930-26	09-336-536	US-09-336-536-2	US-09-188-930-218	US-09-188-930-30	US-09-336-536-1	US-09-140-804-1	US-08-555-669-11	US-09-073-663-11	US-09-264-737-3
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1866 1866 573 573 573 573 573 573 803 46 46		C polication US/0845956 Huang, Shi Huang, Sh	40 67 ativ
38.0 37.7 37.7 37.7 37.7 37.7 37.7 37.7 37		568-3/C 3, Application US o. 5811304 INFORMATION: CANT: HUANG, Shi OF INVENTION: Re OF INVENTION: Re OF INVENTION: Re OF INVENTION: PARTICULAR SECONDENCE ADDRESS: RESCREE: California NTRY: USA TE: California NTRY: USA NTRY: LEM PC CONTRY: UM TYPE: FLOPPY UM TYPE: READABLE FORM: UM TYPE: LOPPY UM TYP	h Similarity 35; Conserv
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Score 24.8; DB 3; Length 5868;
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APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
Zinc Finger Proteins
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STREET: 4370 La Jolla Village Drive, Suite 700
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 18 AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
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                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-MG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-586-472-3/c
; Sequence 3. Application US/09586472
; Patent No. 632335
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 67.3%;
Matches 35; Conservative
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5868 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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121..5278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-516-859A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                 US-08-399-411-3/C

Sequence 3, Application US/08399411

Sequence 3, Application US/08399411

Patent No. 5831008

GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Ainc Finger Proteins

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amphell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 5183;
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APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCES: 006
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LJ 1264
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
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67.3%; Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5183 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 67.3
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 4370 La JOI
CITY: San Diego
STATE: California
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US-08-516-859A-3/C
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US-08-399-411-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                 Query Match 40.7%; Score 24.8; DB 4; Length 5868; Best Local Similarity 67.3%; Pred. No. 13; Matches 35; Conservative 0; Mismatches 17; Indels 0
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NUCLEOTIDE AND DEDUCED
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Pred. No. 11
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                                                                                                                                                                                                                                                                              US/08/290,665A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 758-4800
TELERAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
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CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 40.29
Best Local Similarity 70.29
Watches 33; Conservative
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TITLE OF INVENTION: AMIN
TITLE OF INVENTION: AND
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQUENCES: 263
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
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ISOLATE: Z4
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                          CDS
121..5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; INDIVIDUAL ISOLATE: US-08-290-665A-139
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                           linear
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         STRANDEDNESS:
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                                                                         ; LOCATION:
US-09-528-706-3
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                         TOPOLOGY: FEATURE:
                                                          NAME/KEY:
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Pred. No. 13; 
0; Mismatches 17; Indels 0
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TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                17;
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FILING DATE: 06-WAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.815
REGISTRATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR ADPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/516,859
FTLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FTLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATON NUMBER: 31,615
                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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                                                                                                                                                                                                              LENGTH: 5868 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09528706
Patent No. 6468985
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TELECOMMUNICATION INFORMATION:
TELEPRINE: (619) 535-9001
TELEFRX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5868 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match 40.7%;
Best Local Similarity 67.3%;
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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ZIP: 92122
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                                                                                                                                                                                                                                                                                        FEATURE
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APPLICANT: BUKH, J., MILLER, A.....
APPLICANT: PURCELL, R.H.
TAYBURTON: NUCLECTIDE AND DEDUCED
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                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMUNICATION INFORMATION:
TELEPRONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDEFFECT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398 FILING DATE: 15-AUG-1995
                                                                                                                                                                           UMBER: PCT/US95/10398
15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 140, Application PC/TUS9510398 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NOMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MORGAN & FINNEGAN
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                                                                                                                                                                                                                                                                                                                                                                                                   NAME: RICHARD W. BORK REGISTRATION NUMBER: 36,459
                                                                                                                                          SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US
                                                                               MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 PARK AVENUE NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 573 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE: 24
PCT-US95-10398-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUCLTITLE OF INVENTION: AMINITILE OF INVENTION: CORETITLE OF INVENTION: AND TITLE OF INVENTION: SEQUENCES OF SEQUENCES SECURESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                         COMPUTER READABLE FORM:
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Best Local Similarity
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NEW YORK
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                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
PCT-US95-10398-140/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
CITY: NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                      NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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ANINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBR: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATPORNEY/AGENT INFORMATION:
NAME: RICHARD W BORK
RECISTRATION NUMBER: 36,459
REPERBNEK/POCKET NUMBER: 2026-4116
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 1751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: BUKEEL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEI TITLE OF INVENTION: AMINO ACID SEQUENC
                                                                                            APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 139, Application PC/TUS9510398 GENERAL INFORMATION:
                                 Sequence 140, Application US/08290665A Patent No. 5882852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) /2.
TELEX: 421792
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                         ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORGAN & FIN
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: homosapiens INDIVIDUAL ISOLATE: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CORE
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQU
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 70.2
Matches 33; Conservative
                                                                                                                                      TITLE OF INVENTION: NUCT
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: CORE
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQUENCES: 263
UNMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS: 263
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                         NEW YORK
                                                                                                                                                                                                                                                                                                                                 NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                               USA
               US-08-290-665A-140/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-10398-139/c
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                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                       STATE:
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Gaps
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                                                                                                     40.3%; Score 24.6; DB 5; Length 573; 70.2%; Pred. No. 11;
                                                                                Indels
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3958304 GAAGGGTGGACGACGAGGAGGGCGCCCAGATCGGTGCGGACGCGATGGACACCT 3958247
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER:
APPLICANT: FRASER:
Clair M.
APPLICANT: FRASER:
CLAIR M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SIQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE. Owen R.
APPLICANT: FRAEE, Owen R.
APPLICANT: FRAEE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, OWEN C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT PRILICATION NUMBER: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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0
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40.0%; Score 24.4; Di
Best Local Similarity 63.8%; Pred. No. 30;
Matches 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                              40.0%; Score 24.4; D
68.0%; Pred. No. 14;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/09103840A; Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/09103840A; Patent No. 6294328
                         17:
REFERENCE/DOCKET NUMBER: I INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS: LENGTH: 957 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 68.09
Matches 34; Conservative
                                                                                                                                     linear
                                                                                                                                                                                                ; ANTI-SENSE: NO US-08-836-075A-17
                                                                                                                                  TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4403765
                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-103-840A-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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APPLICANT: MARRIENS, GERT
APPLICANT: STUYENEL LIEVEN
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
TITLE OF INVENTION: AGENTS
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 GCCGGGGATCATTTGGCCCCCAAGACGTCGAGAGCCGCGGGGGGAC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microsoft Word 6.0 / ASCII text output CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24.6; DB; Pred. No. 11; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
FILING DATE: 21 Apr 1997
APPLICATION DATE: 23 Oct 1995
FILING DATE: 23 Oct 1995
FILING DATE: 21 Oct 1994
FILING DATE: 22 Oct 1994
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
NAMME: KAMMERER, PATELIAN
NAME: KAMMERER, PATELIAN
NAME: KAMMERER, PATELIAN
NAME: KAMMERER, 29,775
                                                                                                                                                                                              36,459
ER: 2026-4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433
CITY: HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: TEXAS
COUNTY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: USA POOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-836-075A-17/c
; Sequence 17, Application US/08836075A
; Patent No. 6180768
                                                                                                                                                                       NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                 TELEX: 421792
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.3%;
70.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: Z8
PCT-US95-10398-140
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                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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Best Local Similarity
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  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
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POLYCYSTIC KIDNEY DISEASE GENE
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PFLICATION NUMBER: US/08/658,136
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERRENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8410
ITELERAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                       APPLICANT: KINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
TITLE OF INVENTION: POLYCYSTIC KID
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                   ; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                         ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 62.3
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: FRAMINGHAM STATE: MASSACHUSE7 COUNTRY: USA ZIP: 01701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17482 C 17482
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                  61 C 61
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US-08-658-136-2
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US-08-658-136-1
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Pred. No. 30;
0; Mismatches 21; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.7%; Score 24.2; DB 1; Length 31571; 62.3%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC Compatible
OPERATING SYSTEM: DATE: COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NO BATA:
APPLICATION NUMBER: US/08/323,443B
FILING DATE: 12-OCT-1994
CLASSIFICATION: WAS
ATTORNEY AGENT INFORMATION:
NAME: Ludwig, S: Peter
REGISTRATION NUMBER: 25,351
REPECOMMUNICATION NUMBER: 25,351
FREPECOMMUNICATION NUMBER: 0372/04462
FREPECOMMUNICATION HORDRATION:
THE COMMUNICATION HORDRATION:
THE COMMUNICATION HORDRATION:
THE COMMUNICATION HORDRATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYCYSTIC KIDNEY DISEASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
        TYPE: DNA
CRGANTSM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CONNORS, TINCTHY D. APPLICANT: DACKOWSKI, WILLIAM R. APPLICANT: GERMINO, GREGORY APPLICANT: QIAN, FENG TITLE OF INVENTION: POLYCYSTIC KID NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08323443B Patent No. 5654170
                                                                                                                                                                                                                                                                                                                                                                                   KLINGER, KATHERINE W.
LANDES, GREGORY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 527-7700
TELEBRAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 31571 base pairs TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                             40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                       BURN, TIMOTHY C.
                                                                                                    Query Match
Best Local Similarity 63.8%
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CLONE: PKD1 GENOMIC
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LENGTH: 4411529
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Gaps
39.7%; Score 24.2; DB 3; Length 53526; 62.3%; Pred. No. 26;
                                      Indels
                                                                                                                                                                                                                                                                Sequence 1, Application US/08658136; Patent No. 6071717; GENERAL INFORMATION: APPLICANT: KLINGER, KATHERINE WAPPLICANT: LANDES, GREGORY MAPPLICANT: BURN, TIMOTHY C
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APPLICANT: CONNORS, TINOTHY D
APPLICANT: DAKKONSKI WILLIAM
APPLICANT: CHANKONSKI SH
CONNERSONDENCES: 58
CONNERSONDEN
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us-09-826-581-3_copy_612_672.rnpb

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Sequence 3, Appli
Sequence 1596, Ap
Sequence 1596, Ap
Sequence 314, App
Sequence 1153, Ap
Sequence 25, Appl
Sequence 25, Appl
Sequence 318, App
Sequence 318, Appl
Sequence 318, Appl
Sequence 318, Appl
Sequence 21539, A
Sequence 21539, A
Sequence 193, Appli
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4579.068 Million cell updates/sec
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                                                                                                                                                           June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds
                                                                                                                                                                                                                                                                                                                            1: /cgnn2_6/ptodata///pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata///pubpna/USO7_PUBCOMB.seq:*
4: /cgn2_6/ptodata///pubpna/USO7_NEW_PUB.seq:*
4: /cgn2_6/ptodata///pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata///pubpna/USO6_NEW_PUB.seq:*
6: /cgn2_6/ptodata///pubpna/USO8_NEW_PUB.seq:*
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10: /cgn2_6/ptodata///pubpna/USO8_PUBCOMB.seq:*
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13: /cgn2_6/ptodata///pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/ptodata///pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/ptodata///pubpna/USO0_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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10 US-09-764-847-1153

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10 US-09-764-899-30

10 US-09-64-899-30

10 US-09-64-761-4800

10 US-09-864-761-21539

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10 US-09-864-761-21538
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                                                                                                                                                                                                                                           US-09-826-581-3_COPY_612_672
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Listing first 45 summaries
                                                                                                          nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUN
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT APPLICATION NUMBER: US 60/195,665
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
                                                              sequence 33, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 10204, A
Sequence 10204, A
Sequence 1795, Ap
Sequence 1795, Ap
Sequence 213, Appl
Sequence 213, Appl
Sequence 213, Appl
Sequence 214, Appl
Sequence 1489, Appl
Sequence 1489, Appl
Sequence 1489, Appl
Sequence 1489, Appl
Sequence 26, Appl
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Sequence 218, Appl
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; Publication No. US20030054375A1
; Publication No. US20030054375A1
; APPLICANT: ROSEN et al.
; ITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                9 US-09-738-626-11

10 US-09-867-701-10278

9 US-09-822-846-553

9 US-10-171-581-213

12 US-10-044-090-210

9 US-09-822-846-158

9 US-09-764-868-1489

10 US-09-764-868-1489

10 US-09-968-373-114

9 US-10-152-661-26

9 US-10-152-661-218

9 US-10-152-661-28

9 US-10-152-661-218

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9 US-10-152-661-218
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100.0%; Pred. No. 1.8e-12;
Live 0; Mismatches 0;
US-10-223-085-33
US-10-223-084-33
US-10-223-088-33
US-10-223-090-33
US-10-201-141-1
US-09-04-968A-1
US-09-764-891-5477
US-09-764-891-10204
US-09-738-626-1796
US-09-738-626-1796
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.(
Matches 61; Conservative
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US-09-826-581-3
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LENGTH: 1722
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Sequence 24263, A Sequence 7558, Ap Sequence 17, Appl Sequence 14, Appl

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.3%; Score 25.2; DB 9; Length 5938; 66.7%; Pred. No. 4.7; tive 0; Mismatches 18; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-10-092-154-1153/c
Sequence 1153, Application US/10092154
Publication No. US20030054375A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
                                                                                                                                                                                                                   Score 25.2; DB 10; Length
Pred. No. 5.3;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25.2; DB Fred. No. 4.7; Ob Mismatches
                                                                                                                      ; NAME/KEY: misc_feature
; LOCATION: (1023)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-922-301-334
                                              or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1153, Application US/09764847
; Patent No. US20020132767A1
                                        OTHER INFORMATION: n equals a,t,g,
                                                           NAME/KEY: misc_feature
LOCATION: (1006)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                     41.3%;
66.7%;
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Best Local Similarity 66.7%;
Matches 36; Conservative
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Best Local Similarity 66,78;
...thes 36; Conservative
                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 66.73
Matches 36; Conservative
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SOFTWARE: Patentin Ver. 2.0
    NAME/KEY: misc_feature
LOCATION: (989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
COGANISM: HOMO SapienS
US-09-764-847-1153
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US-09-764-847-1153/c
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LENGTH: 5938
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                                                                                                                                                                                                                                      Score 26; DB 9; Length 17761; Pred. No. 2.3; 0; Mismatches 20; Indels
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APPLICANT Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE REFERENCE: PA106
CURRENT PELICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 334
LINGTH: 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILLE REFERENCE: PCOOP.

CURRENT APPLICATION NUMBER: US/09/764,847

CURRENT APPLICATION NUMBER: US/09/764,847

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003

SEQ ID NO 1596

LENGTH: 17761
                CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER: OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm SEQ ID NO 1596
LENGTH: 17761
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LOCATION: (59)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1596, Application US/09764847
Patent No. US20020132767A1
GENERAL INFORMATION:
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Patent No. US20020052308A1
                                                                                                                                                                                                                                      42.68;
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Matches 38; Conservative
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hes 38; Conservative
                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1596
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; ORGANISM: Homo sapiens
US-09-764-847-1596
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FILE REFERENCE: PC009C1
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APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REPERENCE: PA-0018 US
CURRENT APPLICATION UNMER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
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Fatent No. US20020174446A1
Fatent No. US20020174446A1
FATENCE TRYORATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 4-3612 A
CURRENT APPLICATION UNMER: US/09/964,899
CURRENT APPLICATION UNMER: 06/236,893
FRIOR FILING DATE: 2000-09-27
FRIOR PAPLICATION UNMER: 60/236,893
FRIOR FILING DATE: 2000-09-29
FRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 53
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                                                                       41.0%; Score 25; DB 12; Length 1847; 64.9%; Pred. No. 6;
tive 0; Mismatches 20; Indels
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                                 Indels
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OTHER INFORMATION: Incyte ID No. US20020137081A1 344297.3
                               15;
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; Pred. No. 6.2;
0; Mismatches
      69.4%; Pred. No. 6.6;
tive 0; Mismatches
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Best Local Similarity 64.9%;
Matches 37; Conservative (
Best Local Similarity 69.4 Matches 34; Conservative
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ORGANISM: Homo sapiens
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US-09-964-899-30
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US-09-864-761-4800
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US-10-044-090-338
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US-09-964-899-30
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LENGTH: 1847
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  1855 GAGGGGACAGAGCTAGGAGAAGGGAGGCCAGAAGGGCAGGGGTGCAGGGG 1802
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                                                                                                                                                                  APPLICANT: Horne, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
ITILE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR RPLICATION NUMBER: US 60/211,379
PRIOR RPLICATION NUMBER: US 60/211,379
PRIOR PRILICATION NUMBER: US 60/211,379
PRIOR PRILICATION NUMBER: US 60/211,379
PRIOR RPLICATION NUMBER: US 60/211,379
PRIOR PRILICATION NUMBER: US 60/211,379
PRIOR PRILICATION NUMBER: US 60/211,379
PRIOR PRILICATION NUMBER: US 60/211,379
PRIOR SPECIAL OARS: 3500
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 2225
LENGTH: 275
TYPE: DAA
ORGANISM: Homo Sapiens
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Pred. No. 6.9;
0; Mismatches 10; Indels
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FILE REFERENCE: P2014P1
CURRENT APPLICATION NUMBER: US/10/144,929
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US/09/251,329
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: PCT/US98/17044
PRIOR FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 257
SEQ ID NO 25
LENGTH: 541
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CTHER INFORMATION: n = a or c or g or t
US-09-880-107-2925
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COTHER INFORMATION: n equals a,t,g, or US-10-144-929-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (11)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                          Sequence 2925, Application US/09880107
Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-144-929-25/c
; Sequence 25, Application US/10144929
; Publication No. US20030069405Al
; GENERAL INFORMATION:
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illarity 75.6%;
Conservative C
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NAME/KEY: SITE
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                                                                                  US-09-880-107-2925
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Best Local S
Matches 31
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PAPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILLE REFERENCE: Acomica-X-1
CURRENT FILLY DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR PLILNG DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-06-23
PRIOR PLILNG DATE: 2000-08-03
PRIOR PLILNG DATE: 2000-08-03
PRIOR PLILNG DATE: 2000-09-07
PRIOR PLILNG DATE: 2001-01-30
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N: EXPRESED IN B9474, SIGNAL = 1.4
N: EXPRESED IN BONE MARROW, SIGNAL = 1.1
N: EXPRESED IN LUNG, SIGNAL = 2.6
N: EXPRESED IN LUNG, SIGNAL = 1.8
N: EXPRESED IN PLACENTA, SIGNAL = 0.98
N: EXPRESED IN PLACENTA, SIGNAL = 0.98
N: THIT: 9111423021, EVALUE 0.00e+00
N: SWISSPROT HIT: Q61116, EVALUE 1.00e-09
N: EST_HUMAN HIT: BE865438.1, EVALUE 0.00e+00
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PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
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PRIOR FILLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                       Sequence 21539, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: MAP TO AL031277.1
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 35; Conserv
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INFORMATION:
INFORMATION:
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; OTHER INFORMATION:
US-09-864-761-21539
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                                                                                                                                           APPLICANT: Chen, Wenshenger Title OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 7;
0; Mismatches 17; Indels 0;
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 4800
LENGTH: 1991
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-04
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN HEAR!
OTHER INFORMATION: EXPRESSED IN BT474
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Best Local Similarity 67.3%;
Matches 35; Conservative (
                                                                                                                                    Hanzel, David K.
                                                                    APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
Patent No. US20020048763A1
GENERAL INFORMATION:
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RESULT 12

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MOLECULE TYPE: C
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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US-09-878-281-193
US-09-899-046-193
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US-10-024-450-3/C
Sequence 3, Application US/10024450
Sequence 3, Application WS/10024450
Sequence 1, Application WS/10024450
Sequence 3, Application Wo. US20030032606A1
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Mctrosatellite-Instability Positive Tumors Using RIZ
FILE REPERENCE: P-15 5101
CURRENT APPLICATION NUMBER: US 60/256,582
CURRENT FILING DATE: 2000-12-17
PRIOR PILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PASLSEQ for Windows Version 4.0
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TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
UNUMBER OF SEQUENCES: 270
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) COURRNY APPLICATION DATA:
APPLICATION NUMBER: US/09/899,046
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 193, Application US/09899046
Publication No. US20030008274A1
GENERAL INFORMATION:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 193: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: mat_peptide LOCATION: 1..495
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US-10-024-450-3
                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 5868
TYPE: DNA
ORGANISM: HOMO Sapien
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US-09-899-046-193/c
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                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: New sequences of hepatitis C virus TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy. WINDER OF SEQUENCES: 270
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/878,281
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                                                                                                          Score 24.6; DB 9; Length 498;
Pred. No. 9.1;
0; Mismatches 14; Indels
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      DB 9; Length 498;
Query Match 40.3%; Score 24.6; DB 9; Length 4 Best Local Similarity 70.2%; Pred. No. 9.1; Matches 33; Conservative 0; Mismatches 14; Indels
                                                                                      Search completed: June 13, 2003, 09:00:37 Job time: 21.2903 secs
                                                                                                                                                                                                           US-09-878-281-193/c
; Sequence 193, Application US/09878281
; Publication No. US20030032005A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 193: SEQUENCE CHARACTERISTICS: LENGTH: 498 base pairs TYPE: nucleic acid STRANDEDNESS: single
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Best Local Similarity 70.2%;
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LOCATION: 1..498
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APPLICANT:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	June 13, 2003, 01:49:14; Search time 5200.55 Seconds (without alignments) 9216.782 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-826-581-5 1647 1 ttggtctggggctggccacaacaccagcctcttagtcttc 1647
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
Total number of	Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 200000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	GenEmbl:* 1: gb_ba:* 2: gb_htg:* 3: gb_in:*

4: 9D_on: *
5: 9D_on: *
6: 9D_pat: *
7: 9D_pat: *
7: 9D_pat: *
8: 9D_pat: *
10: 9D_pat: *
11: 9D_pat: *
12: 9D_pat: *
13: 9D_un: *
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15: em_bat: *
16: em_fun: *
17: em_hun: *
18: em_pat: *
22: em_ov: *
23: em_pat: *
24: em_pat: *
25: em_ov: *
26: em_fun: *
27: em_pat: *
28: em_pat: *
29: em_fun: *
21: em_fun: *
23: em_fun: *
24: em_fun: *
25: em_fun: *
26: em_fun: *
27: em_fun: *
28: em_fun: *
29: em_fun: *
20: em_fun: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence Seq	AC009974 Homo sapi 042412 Human 5'-AM BC000358 Homo sapi AX364914 Sequence AB02580 Homo sapi AR139104 Sequence AR087875 Homo sapi BC020540 Homo sapi AC01887 Homo sapi AC070541 Drosophil AX084138 Brosophil AX084138 Brosophil AX0841381 Sequence AC01841 Brosophil AC01841 BROSOPHIL AX18181 Sequence	AF214521 AF336381 AC129703 AC129703 AC127107 AC0274107 AC127107 AC128070	647 bp DNA linear PAT 02-NOV-2001 0177305. ata; Craniata; Vertebrata; Euteleostomi; tes; Catarrhini; Hominidae; Homo. and Marklund, Sactivated protein kinase gamma 3 subunit -0CT-2001;
SUMMARIES	AX281582 AX099802 AX099802 AX099804 AX099804 AX398333 AX398333 AX398333 AX398333 AX398333 AX398339 AX398339 AX398339 AX398339 AX398339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339 AX388339	0009974 HS042412 BC000358 BC000358 AB036414 AB035890 AR139104 AR01387 AR037805 AR037	AF214521 AF336381 AC128070 AC129703 AC127107 AC27416 AX281580 AC127107 AC128070	1 t WO 33 33 hord rimar amp 5 18
Length DB	1647 6 2229 6 2229 6 22115 6 22115 6 22115 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 22115 9 6 9 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	400000000	om Pate I:16600 tazoa; heria; Luthmë he humë
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Result No. Scor	1		८ 800101€4Ω	AX281582 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM THEE AUTHORS TITLE

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1200

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2290 bp mRNA linear PRI 07-APR-2000 for AMP-activated protein kinase gamma 3 subunit
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                                                                                                                                                                                                 CATGAGTGGGGAGAAGCCCTGAGGCAGAGACACTATGTCTGGAGGAGTCCTTTCCTG
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                                                                                                                                                              CITTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGG
                                                                                                                                                                                                                                                                         CCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCCAGCAACCTACACCACCTGGA
                                                                                                                                                                                                                                                                                                                    CCTCTATTCCCGCTTTGATGTGATTCACCTGCCTGCCCAGCAAACCTACAACCTGGA
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                                                    1021 TGGTTCCCTGCTGCCCCCCGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGG
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                                                                                                                                                                                                                                      GCAGAGCTTTGTGGGGGATGCTGACCATCACTGACTTCATCCTGGTGCTGCATCGCTACTA
                                           CAGGTCCCCCTGGTCCAGATCTATGAGATTGAACATAAGATTGAGACCTGGAGGGA
                                                                              GTCAGGCAACGTACTCCACATCCTCACACACAAACGCCTGCACATCTTT
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1. 1647
7. Organism="Homo sapiens"
/db_xref="taxon:9606"
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/product-=AMP-activated protein kinase gamma 3 subunit"
/product-=AMP-activated protein kinase gamma 3 subunit"
/protein_id="CaB65117.1"
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AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
Homo sapiens.
                                                              Euteleostomi,
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Submitted (12-0CT-1999) Carling D., Cellular Stress Group, M.
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
London, W12 UNIV UNITED KINGDOM
Location/Qualifiers
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                                                                             Hominidae; Homo.
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Catarrhini; Hominidae;
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99.3%; Pred. No. 0;
ive 0; Mismatches
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Mammalia; Eutheria; Primates;
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PUBMED
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95 ATGAGCTTCCTAGAGCAAGAAAACAGCTCATGGCCATCACCAGCTGTGACCAGCAGC
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             Score 1453;
Pred. No. 0;
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97.3%;
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Matches 1501; Conservative
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Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
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Milan, D., Jeon, T.T., Looft, C., Amarger, V., Robic, A.,
Milan, D., Jeon, J.T., Looft, C., Gellin, J., Lundstrom, K., Reinsch, N.,
Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden
                                                                                                                            1535 CAATGAAGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCCACCCCCATTTGCTGGTTCAG 1594
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1 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P. and Andersson,L.
GCCCTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCACCTGCACACCTGGAAGC
                                                                       1494 CTATGATTCAGGCTTCTTCAGCCTTCCAAAATTGCCTTTGCCT 1536
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match Query Match 87.9%; Score 1447; DB 6; Length 2109; Best Local Similarity 97.3%; Pred. No. 0; Matches 1495; Conservative 0; Mismatches 35; Indels 7; Gaps 2; QY 101 TrCCTAGAGCAAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGCAGCAGCAGCAGCAGCAGAACAGCAGAAAACAGAGCAGAAAACAGAGCACACACACAGCAG	03 03 03 03 03 03 03 03		641 ACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC [ANGATIONACIONAGENICATORIA CONTROLLA
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113 GAAAACAGCAGCCATCACCAGCTGTACCAGCAGCAGCTCAGAAAGAA	706 GAGACCAAGAGGCCTTCTTCCCCTGGTGCCAACGCGCCCGGGCGCCACTTGGTGGTGTGTGT
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95 ATGAGCTTCCTAGAGCAAGAAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC	215 GTGGAGGAAGGAGGACCACCAGGTCAGGGGAAGGTCCCCGGTCCAGGCCAGCTGCTGAG 2 1 1 1 1 1 1 1 1 1	- 2	241 GCCGAGGTGGACAACCCCCCCAGGGGGGGGGATCCTCCCCTGGAGGGGGCTCAGAGGGGGGGG	301 GCCTCCGACTCCAACACACATCTGGATCTGGGCATAGAGTTCTCATCTGGCGCG G 452 TGGGAGTGTGAACTAGAAGCCTGCTGGAAGAGGCCTGCCCTGTGCATCCCCGAG F	512 GCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTAC 5	572 ATGCGCTTCATGCAGGAGCACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTC 6 [632 ATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTG E	692 CGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGATGCTGACCATCACT 7 1 1 1 1 1 1 1 1 1	752 GACTICAICCIGGIGCIGCAICGCTACAGGICCCCCCGGICCAGATCTATGAGAIT E	812 GAACAACAIAAGAITGAGACCIGGAGGAGATCIACCIGCAAGGCIGCITCAAGCCICIG E	872 GTCTCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGG 9	932 ATCCATCGCCTGCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCACACAC S	992 AAACGCCTGCTCCTGCACATCTTTGGTTCCCTGCTGCCGGCCCTCCTTCCT		1112 ACAGCACCCATCCTGACTGCACTGGACATCTTGTGGACCGGCGTGTGTCTGCACTGCCT 1
60 da 60	& 9 &	d &	qa XX	qa & qa	δδ	δ Q	δλ Op	δδ Q	Qy Qp	Qy	Qy Db	Qy	Qy	QY Dp	Oy DD
	Db 1366 GTCCTTTCCTGCCAGGCCCCCCGGGGGGGGGGGGGGGGG	TCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATCGATGCCCTCGGGGCCTGA	Oy 1490 GAAGATCTGAGTCCTCAATCCCAGCCACCTGGAAGCCAATGAAGGGAACT 1548	OY 1549 GGAGAACTCAGCTTCATCTTCCCCACCCCATTGCTGGTTCAGCTATGATTCAGGTA 1608	Db 1665 GGCTCCGCCCGGGGCC 1680	RESULT 7 AX398333 LOCUS AX398333 LOCUS AX398333 DEFINITION Sequence 3 from Patent WO0220850.	,		Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plasto Novel prkag3 alleles and use of the same as geneti reproductive and meat quality traits Patent: WO 0220850-A 3 14-MAR-2002;	IOWa State University Research Foundation, Inc. (US) FEATURES Location/Qualifiers Source 11873 /organism="Sus scrofa"	CDS 11395 //Ob_arer="taxon:9823" //Octe="unnamed protein product" //codon_start=1	/protein_id="CAD23626.1" /db_xref="G1:21261109" /translation="MSPLEOGERSMPSRAVTTSSERSHGDQGTKASRWTRQEDVEEG /translation="MSPLEOGERSMPSRAVTTSSERSHGDQGTKASRWTRQEDVEEG GPPGPREGPGSRPVAESTGQEATFPRATPLAQAAPLAEVDNPPTERDILFSDCAASAS	DSNTDBLDGGIEFSASSASGDELGIVEEKPRPCESPEYLLFRIGWDDELQKPGAVYM HFWQEHTCYDAMATSSKLVIFDYMLEIKKRFALVANGVRAPLWBSKKQSFVGMLTI TDFILVLHRYYRSPLVQIYEIEBHKIETWREIYLQGCFKPLVSISPNDSLFEAYYALI KNRIHRLPVLDPVSGAVLHILTHKRLIKFLHIEGTLERPSFLYRTIQDLGIGFRDL AVVLETAPLITALDIFVDKKSALPVVNETGOVYGLYSRFDYHLAAOOTYNHLDMNV	GEALRQRILCLEGYLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ ALVLSPAGIDALGA" BASE COUNT 381 a 581 c 535 g 376 t ORIGIN	Query Match 69.3%; Score 1142; DB 6; Length 1873; Best Local Similarity 85.8%; Pred. No. 1.2e-252; Matches 1316; Conservative 0; Mismatches 210; Indels 8; Gaps 4;

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/db_xref="G181564"
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KNRTHRLPVLDPVSGAVLHITHKRLLKFHHFGTLLPRPSEFLKRIQDLGIGTPRDL
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GEALRQRTLCLEGVLSCQPHFILGEVIDNIYRRQVHRLVLMDFYQHLLGVVELSDILQ
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                    /note="AMPKG3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF214520 1873 bp mRNA linear MAM 03-JUN-2000 Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCCAATGAAGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCCACCCCCATTTGCTGGT 1590
                          1078 GIGGTCAACGAAACTGGACAGGTAGTGGGCCTCTACTCTCGCTTTGATGTGATCCACCTG 1137
                                                                                                                                                             1197
                                                                                                                                                                                                                                                 GACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTC 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                        1412 TIGGGCGTGGICTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGCTGCATC 1471
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1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paull,S., lannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
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TOPTLUJHRYYRSPLVQIYEIEBHKIEWHETYLOGGCKFRIGSISPNOSLEEAVYALI
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GEALRQRYLCLEGVLSCQPHETLGEVIDRIVNEQVHRLVLVDETQHLLGVVSLSDILQ
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reproductive and meat quality traits Patent: WO 1220850-A 5 14-MAR-2002; Dwa State University Research Foundation, Inc.
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Novel prkag3 alleles and use of the same as reproductive and meat quality traits Patent: WO 0220850-A 7 14-MAR-2002; IOWA State University Research Foundation, Location/Qualifiers
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Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G. Novel prkag3 alleles and use of the same as genetic markers reproductive and meat quality traits Patent: WO 0220850-A 9 14-MAR-2002; IOWR State University Research Foundation, Inc. (US)
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REFERENCE 1 (bases 1 to 1867) AUTHORS Andersconi.L. Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P. TITLE Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof and uses thereof same, and uses thereof same, and uses thereof same, and uses thereof Lournal Defent: WO 0120003-A 1 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR); Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE) Source //Organism=*Sins scrofa"	/db_xref="taxon:9823" CDS 4721389 /note="named protein product" /codon_start=1 /protein_id="CAC35798.1" /db_xref="d1:1358809" /translation="MHEMQENTCNAMATSKLVIEDTMLEIKKAFFALVANGVRAAP LWDSKKQSFVGMLFITDFILVLHRYYRSPLVQIYEIEBHKIETWREIYLQGCFRFLVS	ISPUNDICTERNYALINENTRICHUPUDPVSARAVIAIUTHRRILKELHIRGTLIPRES YRTIQDICGICTERDLAVULETAPILIALDIFVDRRYSALLPVYNENGGOVGUTSRED HLAAQQTYNHLDMNVGEALRQRTLCLEGVLSCQPHETLGEVIDRIVREGOVHRLVLLY TQHLLGVVELSDILQALVLSPAGIDALGA" 380 a 583 c 529 g 375 t 68.9%; Score 1134.4; DB 6; Length 1867; nilarity 85.7%; Pred. No. 6.8e-251;	0; Mismatches AGCAGCTCATGGCCA AGCCGTTCATGGCCA AGGCCAAAGCCTTG	221 GAAGGGAACCACCAGGTCAGGGGAAGGTCCCGGTCCAGGCCAGGTCGAGTCCACC 121 GAAGGGGACCACCAGGCCCAGGGAAGGTCCCCAGTCCAGGCCAGTCCAGGTCCACC 281 GAGGGGCCCTCCGGGCCCAAGGCCAAGCCTTGGCTCAAGCTGTCACC 281 GGGTGGAGGCCACATTCCCCAAGACCACACCTTGGCTCAAGTGATCCTGCCGGG 181 GGGTAGAAGTCCCCAAGGCCAACCCTTGGCTCCAAGCTGATCCTGCCGGG 181 GGGTAGAAGTTCCCCAAGGCCAACCCTTGGCTCCAAGCTGATCCTGCCGGG 181 GGGTAGAAGTTCCCCAAGGCCAACCCTTGGCTCCAAGCCGTTGGCCCAAGCCGTTGGCCCAAGCCCTTGCCCAAGCCCTTGGCCCAAGCCCTTGGCCCAAGCCCTTGCCCAAGCCCTTGCCCAAGCCCTTGCCCAAGCCCTTGCCCAAGCCCTTGCCCAAGCCCTTGCCCAAGCCCTTGCCCAAGCCCTTGCCCAAGCCCCAAGCCCAAGCCCTTGCCCAAGCCCCAAGCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCAAGCCCAA	QY 338 GTGGGCACTCCACCAACAGGGTGGGACTGCCTCTGACTGTACAGCTCAGCTGCA 397 Db 241 GTGGACAACCCCCAACAGGGGACATCCTCCCCTCTGACTGTGCACCTCAGCCTC 300 QY 398 GGCTCCAGCACAGATGATGTGGAGCTGGCACGGAGTTCCCAGCCACAGAGGCTGGGAG 457 Db 301 GACTCCAACAGATGATGTGGAGCTTGGGCATGGGAGTTCTCCAGCCACAGAGGCTTGGGAG 457 Db 301 GACTCCAACAGACCATCTGGATTGGCCATGGGCATTGGCCATCGGCGTCGGGG 360	QY 458 TGTGAGCTAGAAGGCCTGCCCTGTCCCCGAGGCCCCA 517 D	OY 578 TTCATGCAGGAGCACCTGCTACGATGGCAACTAGCTCAAGCTAGTCATCTTC 637 [
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/product="AMP-activated protein kinase gamma"
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Direct Submission
Submitted (07-FEB-1996) D. Carling, MRC Clinical Sciences Centre, Submitted (07-FEB-1996) D. Carling, MRC Clinical Sciences Centre, Department of Molecular Medicine, RPMS, Hammersmith Hospital, DuCane Road, London, W12 ONN, UK
Location/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/function="binds to alpha and beta subunits of AMPK,
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                                                                Woods,A., Cheung,P.C., Smith,F.C., Davison,M.D.,
Berl,R.K. and Carling,D.
Characterization of AMP-activated protein kinase
subunits. Assembly of the heterotrimeric complex
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Qy	992	
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Qy	1412	TTGGGGGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCA 1457
qa	961	AGGGCATTGTATCGCTGTCTGACATCTTACAGGCTCTGGTGCTCA 1006
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This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRRAG3). Detecting the presence of the PRRAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution p71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 55); and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on consition 1 of the open reading frame.
                                                                                                                                                                                                                                                                                          New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the variant -
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ογ	541	MACCEGECECCAGATCTACATGCECTTCATGCAGGAGCACACCTGCTA 60
οp	541	GAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCT
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ογ	661	CCTTCTTGCTCGCGCGAACGGTGTGCGGGCAGCCCCTCTATGGGACAGCAAA 7
q	661	GCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCTCTATGGGACAGCAAGAA 72
οy	721	AGAGCTTTGTGGGGGATGCTGACCATCACTCATCCTGGTGCTGCTCGCACTA 78
qa	721	CAGAGCTTTGTGGGGGATGCTGACCATCACTGACTTCATCATCGTGCTGCTGCTACTA
QY	781	GGTCCAGATCTATGAGATTGAACAACATAAGATTGAGACCTGGAGGGA
QQ	781	3GTCCCCCCTGGTCCCAGATCTATGAGATTGAACAACATAAGATTGAGACCTGGAGGGA
δλ	4	
තු	841	ICTACCTGCAAGGCTGCTTCAAGCCTCTGGTCTCCATCTCTCTAATGATAGCTGTT
δŽ	901	GAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGCCTGCCT
QQ	901	CTGTTCTTGACCCGGT
٥y	961	PAGGCAACGTACTCCACACACACACACACGCTGCTCAAGTTCCTGCACATCTT
qa	196	TCAGGCAACGTACTCCACATCCTCACACACAAACGCCTGCTCAAGTTCCTGCACATCT
οχ	1021	GITCCCTGCTGCCCCGCCCTTCCTTCCTACCGCACTATCCAAGATTTGGGCATCGG
QQ	1021	GGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGG
οy	1081	CATTCCGAGACTTGCTGGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACAT 1
QQ	1081	ACATTCCGAGACTTGGCTGTGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACAT 114
οy	1141	ITTGTGGACCGGCGTGTCTGCACTGCCTGTGGTCAACGAATGTGGTCAGGTCGTGG 120
qq	1141	IOTGGACCGGCGTGTGTCTGCACTGCCTGTGTGTGTGTGTGT
Qλ	1201	CICTATICCGCTITGATGTTCACCTGGCTGCCCAGCAACCTACAACCACCAGGA 1
qa	1201	CTCTATICCCGCTITGAIGTGAIICACCIGGCIGCCCAGCAACCIACAACCACCTGGA 12
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qa	1261	AGTGTGGGAGAAGCCCTGAGGCAGGACACTATGTCTGGAGGGAG
Qy	1321	SCCCCACGAGAGCTTGGGGGAAGTGATCGACAGGATTGCTCGGGAGCAGGTACACAG 13
QQ	1321	CAGCCCCACGAGAGCTTGGGGGGAAGTGATGATTGTTGTTGTTGTTTTTTTT
δλ	1381	3CTAGTGGACGAGACCCAGCATCTCTTGGGCGTGGTCCTCCCTC
qq	1381	CTGGTGCTAGTGGACGAGACCCAGCATCTCTTGGGCGTGGTCTCCCTCTCCGACATCCT 14
ΟŊ	1441	CTGGTGCTCAGCCCTGCTGGCATCGATGCCCTCGGGGCCTGAGAAG
qa	1441	CAGCCACTGGTGAGCCCTGCTGGCATCGATGCCCTCGGGGCCTGAGAAGATCTGA
Qy	1501	CCCAAGCCACCTGCACACCTGGAAGCCAATGAAG
qq	1501	CCTCAATCCCAAGCCACCTGCACACCTGGAAGCCAATGAAGGGAACTGGAGAACTCAG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                 PRKAG3; diabetes, obesity, myopathy; cardiovascular disease, anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                               Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
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                                                                                                                                                                                                                                       gamma subunit; adenosine monophosphate-activated kinase; AMPK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGTGTGAGCTAGAAGGCCTGCTGCAAGAGGCCTGCCCTGTGCCTGTCCCCGCAGGCC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATTICCCAAGCTGGGGTGACGAACTGCGGAAACCCGGCGCCCCAGATCTACAIG 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         695 GCAGCCCCTCTAIGGGACAGCAAGAAGCAGCTTIGIGGGGAIGCIGACCAICACTGAC 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGCCCCTCTATGGGACAGCAAGAAGCAGACTTTGTGGGGGATGCTGACCATCACTGAC 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTC 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCATCTCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCCATCAAGAACCGGATC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCGCCTGCTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCACACAAA 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 ITCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCATCCTGGTGCTGCATCGCTACAGGTCCCCCCTGGTCCAGATCTATGAGATTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                 155 TCAGAAAGAATCCGTGGGAAACGGAGGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGAGTTCCCAGCCACAGAGGCCTGG
                                                                                                                                                                                                                                                                                                             95 ATGAGCTTCCTAGAGCAAGAAAACAGCAGCTCATGGCCCATCACCAGCTGTGACCAGCAGC
                                                                                                                                                                                                                                                                                                                                                           1 ATGAGCTTCCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 GIGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGICCCCGGTCCAGGCCAGCTGCTGAG
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                            Length 2115;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                      Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                 Score 1453; F
                                                                                                                                                                                                                                  Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                       Query Match 88.2%;
Sest Local Similarity 97.3%;
Matches 1501; Conservative
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The present sequence is a cDNA encoding human adenosine monophosphate

(AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,

ENRAG3. Mutation in PrkR93 results in an altered regulation of

carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is

carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is

useful as therapeutic for treating carbohydrate metabolism disorders such

cas diabetes, obesity, and disorders associated with muscle metabolism

cutivity, and for restoring a normal AMPK function. PRKAG3 sequence

activity, and for restoring a normal AMPK function. PRKAG3 sequence

carbohydrate metabolism disorder. Primers that can detect

cand its functionally altered mutants are useful for the diagnostic

carbohydrate metabolism disorder. Primers that can detect

ca genetic polymorphic marker linked to a sequence encoding PRKAG3, are

carbohydrate metabolism disorder. Primers that can detect

a genetic polymorphic marker linked to a sequence encoding PRKAG3 or a

preferrably a carbohydrate metabolism disorder. Primers that can detect

ca genetic polymorphic marker linked to a sequence encoding PRKAG3 or a

preferrable animal and host cell transformed with PRKAG3 or a

conding PRKAG3 is useful for detecting mutations in a PrKAG3 gene, or

carbohydrate animal and conding the first cystathione beta synthase (CBS) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AGAATCCGTGGGAAACGGAGGCCCAAAGCCTTGAGATGGACAAAGGCAGAAGTCGGTGGAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GGGCTGGAGGCCACATTCCCCAAGACCACCATGGCTCAAGCTGATCCTGCCGGGGTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCCAGGCCAACTGCTGAGTCCACC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 GGCACTCCACCAACAGGGTGGGACTGCCTCCCCTCTGACTGTACAGCCTCAGCTGCAGGC 400
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                                                                                                                                                                                                                                                                                                                                                            New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                       Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 TTCCTAGAGCAAGAAACAGCAGCTCATGGCCCATCACCAGCTGTGACCAGCAGCTCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TICCTAGAGCAAGAAAACAGCAGCTCATGGCCATCACCAGCTGTGAAACAGCTCGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 AGAATCCGTGGGAAACGGAGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCGGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 GGCTGGAGGCCACATTCCCCAAGACCACACCTTGGCTCAAGCTGATCCTGCCGGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
                                                                                                                                                                                                                                     Looft C, Kalm E, Milan D, Robic A, Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1447; DB 22;
Pred. No. 0;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRKAG3 and is useful in gene therapy.
                                                                                                                              (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Fig 2; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.9%;
97.3%;
                      11-SEP-2000; 2000WO-EP09896
                                                                 10-SEP-1999; 99EP-0402236
18-MAY-2000; 2000EP-0401388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 1495; Conservative
                                                                                                                                                                                                                                                                                                  WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                             KALM E.
                                                                                                                                                                                                                                                         Iannuccelli N,
                                                                                                                                                                                                                                     Andersson
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                                                                                                                                                                                                                                                            GCCCAGCAAACCTACAACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGGAC 1294
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Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; preskA3; diabetes, obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                      CGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACA
                                                                                                                                                  GCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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1390..2109
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diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting
                                                                                                                                                                                                                                                                          Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; RKRA3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbolydrate netabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle specific isoform, PRKAG3 splice variant DNA. PrkaG3 gene is located in the RN locus of chromosome 15. Mutation in PrkaG3 seults in an allered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rogel-Gaillard
                                                                                                                                                                                                                                                                                                                                                                                                                  "Sus scrofa Prkag3 splice variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lm E, Milan D, Robic A,
Le Roy P, Chardon P;
                                                                                           TTCAGGCTTCTTCAGCCTTCCAAAATTGCCTTTGCCT 1530
                                                                 TTCAGGTAGGCTCTGCCCTGGGCCATGACACCAGCCT 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                 Sus scrofa PRKAG3 splice variant DNA
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                  BP,
                                                                                                                                                                AAD03321 standard; DNA; 2022
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2000EP-0401388.
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Gellin J,
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(ANDE/) ANDERSSON
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAE00224
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18-MAY-2000;
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Transpente animal and host cell transformed with PRKAG3 or a the manner and host cell transformed with PRKAG3 or a screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy. GACAGCAAGAAGCAGAGCTTTGTGGGGATGCTGACCATCACTGACTTCATCCTGGTGCTG GAGATCAAGAAGGCCTTCTTTGCCCTGGTGGCCAACGGCGTCCGAGCGGCACCTTTGTGG CATCGCTACTACAGGTCCCCCCTGGTCCAGATCTATGAGATTGAACAACATAAGATTGAG ACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTCTCCATCTCTCTAAT ACATTCCCCAAGGCCACCACCTTGGCCCAAGCCGCTCCCTTGGCCGAGGTGGACAAACCCC GATGATGTGGAGCTGGCCACGGAGTTCCCAGCCACAGAGGCCTGGGAGTGTGAGCTAGAA GCCCTGCTGGAAGAGGCCTGCCCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTG GCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAG ACCCCTTCCTGGAGCAGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCCTAGAGCAA AAACGGAGGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCA CCAGGTCAGGGGGAAGGTCCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGGCTGCAGGCC ACATTCCCCAAGACCACACCCTTGGCTCAAGCTGATCC - - - TGCCGGGGTGGGCACTCCA GGGCTGGTGGAAGAAAGACCAGCCCCGTGCCCATCCCCAGAGGTGCTGATACCCAGGCTG CCAACAGGGTGGGACTGCCTCCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACA Gaps DB 22; Length 2022; . 8 Score 1172.8; DB 22; Lengt. Pred. No. 5.2e-296;); Mismatches 217; Indels Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other; 0; 71.2%; 85.7%; Query Match 71.2' Best Local Similarity 85.7' Matches 1351; Conservative 830 349 469 526 530 290 646 920 904 710 770 826 886 169 173 229 233 583 293 350 409 410 470 586 991 109 53 113 qq 셤 Db ŏ δy a δ ò δ g qq ô 9 ŏ g QΫ Ω οχ a ò g 888888888888 ŏ a ŏ g à Dp ò õ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant DNA (PRRAG3-30).
                                                                                                                                                                                                                                                                                                         Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAGCTTCCTAGAGCAAGGAGAGAGCCGTTCATGGCCATCCCGAGCTGTAACCACCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGAAAGAATCCGTGGGAAACGGAGGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGGGGTGGGCACTCCACCAACAGGGTGGGACTGCCTCCCCTCTGACTGTACAGCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAGCTTCCTAGAGCAAGAAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                              those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to a method for screening animals to determine
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8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1142; DB 24;
Pred. No. 5.6e-288;
0; Mismatches 210;
                                                                                                                                                                                                                        Plastow
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 89-91; 109pp; English.
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85.8%;
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2001US-260239P.
2001US-299111P.
                                                                                                                                                                                       (IOWA ) UNIV IOWA STATE RES
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                                                                                 10-SEP-2001; 2001WO-US28283
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Matches 1316; Conservative
                                                                                                                                                                                                                          Ciobanu
                                                                                                                                                                                                                                                          2002-393850/42.
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                                                                                                                                                                                                                        Rothschild MF,
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08-JAN-2001;
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The present sequence is a cDNA encoding pig adenosine monophosphate (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRRAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, adisorders as such as metabolism, to reaching carbohydrate metabolism disorders such as myopathy and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK such as myopathy and cardiovascular diseases, to modulate AMPK cativity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allege of PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
                                                                                                                                                                 Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                               /product= "Sus scrofa complete Prkag3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robic A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalm E, Milan D, Robic
J, Le Roy P, Chardon P;
                                                                                                                                 Pig AMPK gamma subunit muscle-specific isoform,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                     AAD03319 standard; cDNA; 1873 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                (first entry)
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                                                                                                                                                                                                                                               chromosome 15; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                       WO200120003-A2
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                                                                                              13-JUN-2001
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                                                         AAD03319;
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AAD03319
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Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

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                                                      95 ATGAGCTTCCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC 154
                                                                                                                        241 GCCGAGGTGGACAACCCCCCAACAGGGGGACATCCTCCCCTCTGACTGTGCAGCCTCA 300
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                                                                                                            TCAGAAAGAATCCGTGGGAAACGGAGGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCG 214
                                                                                                                                                                                          121 GTAGAGGAAGGGGGGCCTCCGGGCCCCGAGGAAGGTCCCCAGTCCAGGCCAGTTGCTGAG 180
                                                                                                                                                                                                                     TCCACCGGGCTGGAGGCCACATTCCCCAAGACCACACCCTTGGCTCAAGCTGATCC---T 331
                                                                                                                                                                                                                                                                           GCCGGGGTGGGCACTCCACCAACAGGGTGGGACTGCCTCCCCTCTGACTGTACAGCCTCA 391
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                                                                        ATGAGCTTCCTAGAGCAAGGAGAGAGCCGTTCATGGCCATCCCGAGCTGTAACCACCACCACC
                                                                                                                                                                  GIGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCCAGGCCAGCTGCTGAG
                             Gaps
  Length 1873;
                             <del>.</del>
                             211; Indels
  22;
Score 1140.4; DB 2. Pred. No. 1.5e-287;
                             0; Mismatches
 69.2%;
85.7%;
               Best_Local Similarity 85.7
Matches 1315; Conservative
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                                                                                                                                                                                                                                                     1531 AAGCCAATGAAGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCCACCCCCATTTGCTGGT 1590
                                                                               GCTGCCCAGCAAACCTACAACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGG 1291
                                                                                                         ACACTATGTCTGGAGGGGGTCCTTTCCTGCCAGCCCCACGAGAGCTTGGGGGGAAGTGATC 1351
                                                                                                                  ACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCT 1171
                                  GTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTG 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymorphism (SNP)"
                                                                                                                                            GACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTC
                                                                                                                                                                               TTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATC
                                                                                                                                                                                                                                   GATGCCCTCGGGGCCTGAGAACCTTGGAACCTTTGCTCTCAGGCCACCTGGCACACCTGG
                                                                                                                                                                                                                                                              polymorphism (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Single nucleotide polymorphism (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                           AMP activated protein kinase regulatory gamma subunit; PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Pig PRKAG3 wild-type protein"
replace (89, C)
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/standard_name= "Single nucleotide
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85.7%; Pred. No. 1.5e-287;
ive 0; Mismatches 211;
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                                                2000US-231045P.
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2001US-299111P.
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10-SEP-2001; 2001WO-US28283
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Matches 1315; Conserv
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                                                                       08-JAN-2001;
18-JUN-2001;
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Matches 1314;
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                                                                                     GACTICATCITGGTGCTGCACCGCTATTACAGGTCCCCCTGGTCCAGATCTACGAGATT
                                                                                                     GAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTG
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                  ATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCCCTGGTGGCCAACGGCGTC
                                   CGGGCAGCCCCTCTATGGGACAGCAGAAGCAGAGCTTTGTGGGGGATGCTGACCATCACT
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AAD36458 standard; DNA; 1873 BP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                  polymorphic variant (PRKAG3-52)
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6
                                                                                                   AMP activated protein kinase regulatory gamma subunit; PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP; gene; variant; ds.
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                                                            PRKAG3 polymorphic variant DNA (PRKAG3-52)
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replace (154, A)
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85.7%;
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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(first entry)
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P-PSDB; AAE22986.
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polymorphic variant (PRKAG3-199)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymorphism (SNP)
                                                                                                                                                    1438 AAGCCAGTGAAGGGAGC-CGTGGACTCAGCTCTCCCCTCAGCCCCTGGTGT
GACCGGATTGTCCGGGAACAGGTGCACCGCCTGGTGCTGGATGAGACCCAGCACTT
                                          1378 GATGCCCTCGGGGCCTGAGAACCTTGGAACCTTTGCTCTCAGGCCACCTGGCACACCTGG
                            GATGCCCTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCACCT-GCACACCTGG
                                                                                                                                      1531 AAGCCAATGAAGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCACCCCCATTTGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used
                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase regulatory gamma subunit; PRKAG3 at quality; single nucleotide polymorphism; SNP;
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                                                                   GCCGAGGTGGACAACCCCCCAACAGGCGGGACATCCTCCCCTCTGACTGTGCAGCCTCA 300
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/product= "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
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                                      1198 ACACTGTGTCTGGAAGGCGTCCTTTCCTGCCAGCCCCACGAGACCTTGGGGGAAGTCATT
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                   TACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAG
                                                                                               ACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCT
                                                                                                                                                                                1172 GIGGICAACGAAIGIGGICAGGICGIGGGCCICIAIITCCCGCITIGAIGIGAITTAACCTG
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for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
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                                                                                                                                                                                                                                                   The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant DNA (PRRAG3-200).
                                                                                                                                                 Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                                                          Plastow
                                                                                                                                                                                                                             Disclosure; Page 102-104; 109pp; English
                                                                          Malek M,
                                            (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                           69.1%;
2001US-260239P.
2001US-299111P.
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                                                                       Rothschild MF, Ciobanu
                                                                                                      2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                   P-PSDB; AAE22988
                                                                                                                                                                                                  subunit gene
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preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PKKAG3. Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                  PRÄGG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heterotrimeric ANPK consisting of PRARAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, parkad3 gene is located in the kN locus of chromsome 15.

Mutation in Prag3 results in a literal regulation of carbobydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as theraqeuite for treating carbobydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robic A, Rogel-Gaillard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                   qamma subunit; adenosine monophosphate-activated kinase; AMPR;
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                                                                                                                                                                                                                                                                     protein"
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J, Le Roy P, Chardon P;
muscle-specific isoform,
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TTCCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGCTCAGAA
            AGAATCCGTGGGAAACGCAGGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCGGTGGAG
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0; Mismatches

68.9%; Score 1134.4; DB 22; Length 1867;

Pred. No. 5.4e-286;

85.78;

Best Local Similarity 85.7 Matches 1309; Conservative

Query Match

P-PSDB; ABB11241.

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                                                                          TGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCACGAGAGTTGGGGGAAGTGATCGACAGG 1357
1178 AACGAAIGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCC 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
               CAGCAAACCTACAACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGGACACTA
                                                                                                                                                                                  ATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTCTTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                            ATGATTCAGGTAGGCTCTGCCCTGGGCC 1624
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27-APR-2000; 2000US-0560875.
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0; Mismatches Score 448.8; Pred. No. 3.5

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Query Match Best Local S

Similarity

27.2%;

Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;

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121 GCTTCAAGCCTCTGGTCTCCATCTCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCC TCATCAAGAACCGGATCCATCGCCTGCTTCTTGACCCGGTGTCAGGCAACGTACTCC

GCTTCAAGCCTCTGGTCTCCATCTCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCC

1 IGCTGACCATCACTGACTTCATCCTGGTGCTGTATCGCTACTACAGGTCCCCCCTGGTCC

738 TGCTGACCATCACTGACTTCATCCTGGTGCTGCATCGCTACTACAGGTCCCCCCTGGTCC

978 ACATCCTCACACACACACAGCCTGCTCAAGTTCCTGCACATTGTTTGGTTCCCTGCTGCCCC 1037

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181

1038 GGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGG 1097

ACATCCTCACACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCC

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uncleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides.

Concleotide of the invention, methods of detecting the nucleotides, contibudes against the polypeptides, methods of detecting the nucleotides.

Cor polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities, stem cell growth factor activity; haematopoiesis regulatory activity; tissue growth activity; haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activities; the most activities; chemotactic or chemokinetic activities; haemacotactic or may be immunomodulatory activity; activities; haemacotactic or may be chromobolitic activities; receptor or ligand activities; on may be involved in oncogenesis, cancer cell proliferation or metastasis.

Computing a their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders, conditions, chromoblythy atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, coronary heart disease, retarial ischaemia, bone disorders (e.g., myeloid or lymphoid called archivity, atherosclerosis, while those which replain or nucleic acids encoding them) may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound replace the and fungal infections and ulcers), while those with the polymentials in the treatment of viral, the processing the polymentials and fungal intertions in the internal process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a CDNA encoding a
                                                                                                                                                                                                                                                              Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness,
                                                            Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel human polypeptide of the invention.
                                                                                                                                                                                                  Claim 1; Page 429; 1963pp; English.
                                                                                                                               e.g. arthritis and cancer
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Gaps

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Indels

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DB 22; Length 989; 2e-96;

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540 AGGICCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTCCCCAAGAC 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      840 GCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGC 899
                                                                                                                                                                                                                                                                                        367 CCTCCCCTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGTGGAGCTGGC 426
                                                                                                                                                                                                                                                                                                                                           CACGGAGTTCCCAGCCACACAGGCCTGGGAGTGTGAGCTAGAAGGCCTGGTGGAAGAGAG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                        547 GCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGC 606
            substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                            247 AGGTCCCCGGTCCAGGCCAGCTGAGTCCACCGGGCTGGAGGCCACATTCCCCAAGAC
                                                                                                                                                                                                                                 307 CACACCCTTGGCTCAAGCTGATCCTGCCGGGGTGGGCACTCCACCAACAGGGTGGGACTG
                                                                                                                                                                                                                                                                                                                                                                                                    GCCTGCCCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGATGACGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                  GCCTGCCCTGTGCCCGGCCGCAGCCCCATTTCCCAAGCTGGGCTGGGATGACGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATGGCAACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA differentially expressed in granulocytic cells #895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viral infection; parasitic infection; protozoal infection;
fungal infection; sterile inflammatory disease; psoriasis;
rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; granulocytic cell; DNA chip; bacterial infection;
G for a C at nucleotide 320, resulting in the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                granulocyte activation; chronic inflammation; allergy
                                                                                            Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
                                                                                                                     Score 407.2; D
Fred. No. 3.2e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK84324 standard; cDNA; 1578
                                                                                                                      24.78;
99.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                              Query Match
Best Local Similarity 99.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200228999-A2.
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                                                                 in intron 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2002
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                                                    GGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                         CTGTGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTG
                                                                                                                                                                                                                                                                                                    Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
The sequences given in AAH43681-84 represents genomic fragments encoding the human AAP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk setimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of
                                                                                                                                                                                                                                                                                                                                                                                                                               intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "5' portion of intron 4"
                                                                                              TGTCTGCACTGCCTGTGGTCAACGAATGTGGT 1189
                                                                                                            /note= "3' portion of 22..177
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r= "Intron 3"
                                                                                                                                                                                                                                                                                                                                                                                                                 "Intron 2"
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                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/number= "Exon 3"
178.541
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                                                                                                                                                                                            686
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                                                                                                                                                                                                                                                                           PRKAG3 intron 2 - intron 4.
                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                            AAH43682 standard;
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TGATCGACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGC 1406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTC 1226
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                                                                                                                                                                                                                                                                                                                                                                                                                    657 TCATGTCCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; diagnosis; identification; cytostatic; neuroprofective; noncotropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiat; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic;
                                                                                                                                       ACCGGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA
                                                                                                                                                                  CACACAAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCTGCCCGGCCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 717 GCACTACCACCCCGGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC
                       CTCTGGTCTCCATCTCCCTAATGATAGCCTGTTTGAAGCTGTCTACACCTCATCAAGA
                                                                                                                                                                                                                                                                                                       597 CCCACAAGCGCATTCTGAAGTTCCTCAAATTGTTTATCACTGAGTTCCCCAAGCCCAGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pancreatic cancer; pancreatic cancer antigen;
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                                                                                                                                                                                                                                                                                              The invention relates to detecting (MI) granulocyte (GC) activation

(GCA), by detecting the level of expression of gene(s) (GS) identified by

(GCA), by detecting the level of expression of gene(s) (GS) identified by

(DNA chip analysis as given in the specification, and comparing

(CC, where differential expression level in an unactivated

(CC, where differential expression of GS is indicative of GCA.

(Also included are modulating (M2) GA by contacting GC with an agent

(CC that alters the expression of at least one gene in GS; (2) screening (M3)

(CC that capable of modulating GCA or an inflammation (especially

(CC thronic) in a tissue, an allergic response in a subject, exposure of a

subject to a pathogen or sterile inflammatory disease using the

chronic) in a tissue, an allergic response in a subject, exposure of a

subject to a pathogen or sterile inflammatory disease, by detecting the

chronic) in a tissue, an allergic response in a subject, exposure of a

subject to a pathogen or sterile inflammatory disease, by detecting the

chronic) in a tissue, an allergic response in a subject, exposure of

(4) treating (M5) an inflammation (especially chronic) or in a tissue,

an allergic response in a subject, exposure of a subject to a pathogen

(CC thronic) in a tissue, MI is useful for modulating GCA, M2 is useful for

modulating (M3) is useful for screening an agent capable of modulating

(CC Apreferably in an inflammation in a tissue, M is useful for

detecting an inflammation in a tissue, an allergic

detecting an inflammation in a tissue, an allergic appairs of a subject and a part and a par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGC 626
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                                                                                                          differential expression
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                                                                                                       Detecting granulocyte activation by detecting differential expressic of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 24; Length 1578;
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Vockley J;
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0; Mismatches
Yamaga S,
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                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 895; 114pp; English.
Weissman SM,
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Matches 580; Conservative
                                                     WPI; 2002-435328/46.
Beazer-Barclay Y,
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WPI; 2000-579444/54.

R P-PSDB; AAB54009.

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New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition.

PT cancer, or for use in assays for diagnosing a pathological condition.

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AAC99731 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to proteins, called pancreatic cancer antigens, pave cytostatic, contraceptive, nootropic, immunomodulatory, relaxant, contraceptive, cancer in gene therapy. The polyunclectide and proteins can be used for in gene therapy. The polyunclectide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays con graventing, treating, or ameliorating a medical condition or in assays consubject. Binding partners to the proteins and the activity of the proteins can be ladentified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, sepecially cancer. Agonists and antagonists to the antigens can be used to design nucleic cancer antigens proteins can be used to design nucleic cancer antigen prolynuclectides can be used to design nucleic cancer antigen prolynuclectides can be used to design nucleic and diagnostic methods. The proteins can be used to design nucleic candid Alagnostic methods. The proteins can be used to design nucleic and langisis, tissue identification and/or typing and a variety of forensic candid Alagnostic methods. The proteins can be used to purity, detect and target the polypeptides, including contin vitro diagnostic and therapeutic methods. The proteins can be used to purity, detect and target the polypeptides, including content or proteins can be used to treat or prevent neural, immune system, muscular, contents and the exemplification of the present invention.

C proteins can be used to treat or prevent neural, incompany cardiovascular, remain or concertation or the exemplif
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Sequence 1691 BP; 458 A; 382 C; 401 G; 449 T; 1 other;
Query Match
Best Local Similarity 65.1%; Pred. No. 1.6e-92;
Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps

1047 TCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGC 1106 989 302 TCACTGACTTCATCCTGGTGCTGCATCGCTACTACAGGTCCCCCTGGTCCAGATCTATG 806 CGCTTGTCTGCATTTCTCCTAATGCCAGCTTGTTTGATGCTGTCTCTTCATTAATTCGGA 482 ACCGGATCCATCGCCTGCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA 986 ACAAGATCCACAGGCTGCCAGTTATTGACCCAGAATCAGGCAATACTTTGTACATCCTCA 542 567 TCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGC 626 123 TGTATACTTCCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 182 GTGTGCGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGATGCTGACCA 746 AGATTGAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGC 866 363 AGCTAGAAGAACACAAGATAGAAACTTGGAGAGGTGTATCTCCAGGACTCCTTTAAAC 422 CTCTGGTCTCCATCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCCCTCATCAAGA 926 627 TAGTCATCTTCGACACCATGCTGGAGATCAAGAGGCCTTCTTTGCTCTGGTGGCCAACG 183 687 243 303 423 483 747 807 927 687 867 Q ŏ g g δ a qq 8 δy a δλ Ω 엄 δ ŏ à

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1167 TGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTC 1226 1227 ACCIGGCIGCCCAGCAAACCIACAACCAGCCIGGACAIGAGIGGGGAGAAGCCCIGAGGC 1286 1287 AGAGGACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCACGAGGAGCTTGGGGGAAG 1346 1347 TGATCGACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGC 1406 723 TGCCAGTGGTGGATGAGAGGGCGTGTGGTGGACATCTACTCCAAGTTTGATGTTATCA 782 783 ATCTGGCAGCAGAAAAAACCTACAACCAAGATGTATCTGTGACTAAAGCCCTTGCAAC 842 903 TCATCAACAGGCTAGTGGAAGCAGGTTCACCGACTTGTAGTGGTGGATGAAATGATG 962 603 TCATGTCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC 662 963 TGGTCAAGGGAATTGTATCACTGTCTGACATCCTGCAGGCCCTGGTCCA 1013 1407 ATCTCTTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCA 1457 g δy 쉽 δ g δ 셤 δŽ g ò Ω

Search completed: June 13, 2003, 02:59:53 Job time: 601.355 secs

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/cgn2_6/ptodata/1/ina/PcrUS_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-757-669A-20
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Patent No. 6124125
GENERAL INFORMATION:
APPLICANT: Darfmouth College, St. Vincents Institute of APPLICANT: Medical Research, Remp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
                                                                                                                                                                                                 Sequence
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COMPUTER: IBM PC
OPERATION SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/10,146
FILING DATE: October 7, 1998
CLASSIFICATION DATA:
APPLICATION NUMBER: PN7450
FILING DATE: B JAM 1996
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 32,257
TELEPHONE: (856) 810-1515
TELEPHONE: (856) 810-1454
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARATERISTICS:
US-08-967-727-13

US-08-037-2300-13

US-09-056-105-9

US-09-110-489-1

US-09-103-84.0A-2

US-09-103-84.0A-1

US-09-103-84.0A-1

US-09-103-11-1

US-09-100-11-1

US-09-100-11-1

US-09-100-11-1

US-09-100-11-1

US-09-100-11-15

US-09-100-11-15

US-09-100-11-15

US-09-100-11-15

US-09-100-11-15

US-09-100-11-15

US-08-11-15

US-08-11-15

US-08-11-15

US-08-11-15

US-08-11-15

US-08-11-15

US-08-11-15

US-08-11-15

US-08-11-15
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66 E. Main Street
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TYPE: Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Marlton
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US-09-101-146-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
  STREET:
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567 TCTACATGCGCTTCATGCAGGAGCACCACCTGCTACGATGCCATGGCAACTAGCTCCAAGC

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Gaps

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Length 1576; Indels

23.7%; Score 390.2; DB 3; 64.9%; Pred. No. 2.1e-93; tive 0; Mismatches 313;

Query Match 23.7% Best Local Similarity 64.9° Matches 578; Conservative

Linear No

; ANTI-SENSE: US-09-101-146-63

ANTI-SENSE

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CACACAAACGCCIGCICAAGIICCIGCACAICIIIGGIICCCIGCIGCICCCGGCCCICCI 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.3%; Score 366.6; DB 2; Length 62.9%; Pred. No. 3.3e-87; Indels o; Mismatches 334; Indels
                                                                                                                                                                                    OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                           ns
                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                           PF-0321
                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 415-855-0555
                                                                                                                                                                COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS: LENGTH: 1435 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 62.93
Matches 567; Conservative
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                                                                                                                                                        Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: PENITUT01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                  Palo Alto
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                                                                                                   USA
                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                   94304
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                                                              CITY: PA
STATE: C
COUNTRY:
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TGTATACTTCCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 235
                                                    ACCEGATCCATCCCCTCCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preetl
APPLICANT: Gli, Surya K.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/08878989
Patent No. 5885803
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-08-878-989-14
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Best Local S:
Matches 567,
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                                                                                 843 ATCTIGCIGCIGAGAAAACATACAAAAAACTAGAIAICACGGIGACCCAGGCCCTICAGC
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APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purva K.
APPLICANT: Shah, Purva T.
APPLICANT: Sh
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Incyle Pharmaceuticals, STREER: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/09272796
Patent No. 6207148
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NERAL INFORMALLON.
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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CACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCCGGCCCTCCT 1046
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Pred. No. 3.3e-87;
0; Mismatches 334;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                           INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
                                                                                                                                                                                                                                                                                                                                                               22.3%;
62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                  567; Conservative
                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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CLONE: 1452972
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1104 IGCIGGAGACAGCACCCAICCTGACTGCACTGGACAICTITGTGGACCGGCGTGTGTCTG 1163
     CCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGG 1103
                                                                                         1164 CACTGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGA 1223
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APPLICANT: KIPPS, THOMAS J.
APPLICANT: WU, YUNQI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
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Pred. No. 0.3
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SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6287569
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Best Local Similarity 44.7%;
Matches 160; Conservative
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ORGANISM: HOMO sapiens
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US-08-232-463-14/c
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US-09-056-105-8
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963 TCGTGGACAGAATAGTAAGAGCTGAGGTCCATCGGCTGGTGGTGGTAAATGAAGCAGATA 1022
                                    1407 ATCTCTTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTG 1466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLEOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, SLEPHEN A.
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)863-4109
                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP 91 114 300.6
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                                                                                                                                                                                                                                   Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                         Foley & Lardner
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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ADDRESSEE: Foley & LA
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FILING DATE: 26-AUG
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Matches 10; Conserv
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ZIP: 22313-0299
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TELEFAX: (/v
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                                                                                                                                                                                                   RESULT 4
US-08-232-463-14
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; Sequence 14, Application US/08299849B; Patent No. 5612201; GENERAL INFORMATION:
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Best Local Similarity 44.4%;
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STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                           Matches 159; Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                     LENGTH: 1022
 JS-09-056-105-18
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                                                                                                                                                                                                                                                        SEQ ID NO 18
                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 AGCCTTGGGGGGTTCTGAGCATCAAGAGATGAGCTTCCTAGAGCAAGAAACAGCAGCTCA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 TGGCCATCACCAGCTGTGACCAGCAGCTCAGAAAGAATCCGTGGGAAACGGAGGGCCAAA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTTGAGATGGACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAA 247
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                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                              GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEFAX: (703)883-4109
TELEFAX: (703)683-4109
TELEX: 899140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4%; Score 40.2;
4.5%; Pred. No. 0.5
                                                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATCGCAAGCTCCCTCGACCTGCAG 1043
                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCCCCGGTCCAGGCCAGCTGCTG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP 91 114 300.6
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 14, Application US/08232463 Patent No. 5670367
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ilarity 4.5%; Pre
Conservative 150;
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                   STATE: VA
COUNTRY: USA
21P: 22313-0299
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                  ADDRESSEE:
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493 CCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAA 552 553 ACCCGCCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGC 612 613 AACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC 672 373 CTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGA 432 433 GTTCCCAGCCACAGAGGCCTGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGGCCTGC 492 419 TCATITICIGCICCGCAAGIATCGAGCCAAGGAGCIGGICACAAAGGCAGAAAIGCIGGA 478 539 CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACCTACAC 598 APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor 673 TCTGGTGGCCAACGCTGTGCGGGCAGCCCTCTATGGGACAGCAGAAGCAGAGCTTT 730 599 CCITGTCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAATCAGATCTTT 656 ó Length 1022; Sequence 18, Application US/09056105
Patent No. 6287569
Patent No. 6287569
Patent No. 6287569
Patent No. 6287569

TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
FILE REPERRNCE: 233/221
CURRENT FILING DATE: 1998-04-06
ERALIER APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
FRALIER APPLICATION NUMBER: 06/043,467
ERALIER APPLICATION NUMBER: 06/043,467
ERALIER PILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0 Indels COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage Score 39.6; DB 4; Pred. No. 0.38; 0; Mismatches 199; OPERATING SYSTEM; PC-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:

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978 TCATITICIGCICCGCAAGIATCGAGCCAAGGAGCIGGICACAAAGGCAGAAAIGCIGGA 1037
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   APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia TILLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor TITLE OF INVENTION: Rejection Antigens and Uses Thereof NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.4%; Score 39.6; DB 2; Length 2531; Best Local Similarity 44.4%; Pred. No. 0.54; Matches 159; Conservative 0; Mismatches 199; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: LUD 5253.4-US TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200 TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 057-041-500 FILING DATE: 057-041-500 FILING DATE: 057-041-1994
CLASSIETCATION: 435
PRIOR APPLICATION DATA: 07-04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION NUMBER: 07/607,043
FILING DATE: 12-DECEMBER: 1991
PRIOR APPLICATION DATA: 4PPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA: 4PPLICATION DATA: 4PPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 525729man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                             E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS
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LENGTH: 2531 base pairs
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                                                                                                                                                                                              NUMBER OF SEQUENCES: 2/
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                    CITY: New York City
STATE: New York
ZIP: 10022
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                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 CTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGTGGAGGTGGCCACGGA 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       918 CTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGC 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  493 CCTGTGCCTGTCCCCGCAGGCCCCCATTCCCCAAGCTGGGGTGGGGATGACGGAACTGCGGAA 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              673 TCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTT 730
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                                                                                                                                                                                                                                                                                                                                                                    PALICATION NUMBER: 07/807,043
PRICK APPLICATION NUMBER: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
RIOR APPLICATION DATA:
APPLICATION NUMBER: 9-JULY-1991
RAPPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: HARNON, NO. 5612201man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 10D 5355
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/US92/04354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08142368A Patent No. 5925729 GENERAL INFORMATION:
                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2531 base pairs
                                                                                                                                                                                                                                                                                                             FILING DATE: 22-MAY-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MAGE-41 gene
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                                       FILING DATE: 1-SEPT: CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-299-849B-14
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Sequence 14, Application US/08037230D
Patent No. 6235525
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
                                                                                                                                                                                                                                              978 TCATTITCIGCICCGCAAGTATCGAGCCAAGGACTGGTCACAAAGGCAGAAATGCTGGA 1037
                                                                                                                                                                                                                                                                                                                                                  1098 CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACTACAC 1157
                                 433 GTICCCAGCCACAGAGGCCTGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGAGGGCCTGC 492
                                                                                                                                                        918 CTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCCAGTAACAAGGTGGATGAGTTGGC 977
                                                                                                                                                                                                                                                                                                                   553 ACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGC 612
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673 TCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTT 730
                                                                                                                                                                                                          193 CCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAA
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APPLICATION NUMBER: US/08/037,230D
FILING DATE: 26-WARCH-1993
CLASSIFFICATION NUMBER: US/08/037,230D
FILING DATE: 26-WARCH-1993
CLASSIFFICATION WIBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
FRINK APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
FRINK APPLICATION NUMBER: 07/807,043
FILING DATE: 23-SEPTEMBER-1991
FRINK APPLICATION NUMBER: 23-SEPTEMBER-1991
FRINK APPLICATION DATA: 23-SEPTEMBER-1991
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TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hanson, No. 6235525man D. REGISTRATION NUMBER: 30,946
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
APPLICANT: Nan der Bruggen, Pierre; Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
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                                               1098 ccrgaagargarcrirgecarrgacgrgaaggaagrggaccccaccaggaacarcraca 1157
613 AACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC 672
                                                                                                                                  673 TCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGGACAGAAGAAGCAGAGCTTT 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATE: 07/807,043
FILING DATE: 12-DECEMBER-1991
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/728,838

FILING DATE: 9-JULY-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/706

APPLICATION NUMBER: 07/706

APPLICATION NUMBER: 07/706

APPLICATION NUMBER: 07/706

APPLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hanson, No. 6025474man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/967,727
                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08967727 Patent No. 6025474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-MAY-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2531 base pairs
IYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York City
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
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978 TCATITICIGCICCGCAAGTAICGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGA 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         553 ACCCGGCCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 GTTCCCAGCCACAGAGGCCTGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGGCCTGC 492
                                                                                                                                                                                                                                                                                                         373 CICTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGA 432
                                                                                                                                                                                                                                                                                                                                         858 CACTIGCIGGAGCAACCCAAIGAGGIICCAGCAGCCAAGAAGAAGGAGGGGCCAAGCAC 917
                                                                                                                                                                                                                                                                                                                                                                                        493 CCTGTGCCTGTCCCCGCAGGCCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAA 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 CTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    673 TCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTT 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                              Length 2531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR TITLE OF INVENTION: PROCESSING FILE REPERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39.6; DB 4; I
Pred. No. 0.69;
0; Mismatches 199;
                                                                                                                                                                                                                          Query Match 2.4%; Score 39.6; DB 4; 1
Best Local Similarity 44.4%; Pred. No. 0.54;
Matches 159; Conservative 0; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09056105
Patent No. 6287569
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.4%;
Best Local Similarity 44.4%;
Matches 159; Conservative
              SEQUENCE CHARACTERISTICS:
LENGTH: 2531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                   MOLECULE TYPE: genomic DNA
                                                                                                                                                                NAME/KEY: MAGE-41 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KIPPS, THOMAS J. APPLICANT: WU, YUNQI
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                      linear
                                                                                                                                                                       ; NAME/ASI:
US-08-037-230D-14
                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-056-105-10
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                                                                                                                                                        613 AACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC 672
                                                                            553 ACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGC 612
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493 CCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAA 552
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/09007005B
Patent No. 625858
GENERAL INFORMATION:
APPLICANT: SZOSTAK, Jack W.
APPLICANT: SZOSTAK, Jack W.
APPLICANT: LIU, Rihe
TITLE OF INVENTION: ELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: EVISIONS
FILE REFRENCE: 00786/150003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/055,963
EARLIER PILING DATE: 1997-01-27
EARLIER PILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASISEQ for Windows Version 4.0
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US-09-244-796-17/c
; Sequence 17, Application US/09244796
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LENGIH: 289
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US-09-404-650-1

| Sequence 1, Application US/09404650
| Patent No. 630968
| Patent No. 630968
| GENERAL INFORMATION:
| APPLICANT: Dietrich, Paul S.
| APPLICANT: Dietrich, Paul S.
| TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
| TITLE OF INVENTION: AND USES
| FILE REPERENCE: R00438-R6S sequence listing
| CURRENT APPLICATION NUMBER: US/09/404,650
| CURRENT FILING DATE: 1999-09-23
| NUMBER OF SEQ ID NOS: 12
| SEQ ID NO 10 NOS: 12
| SEQ ID NO 10 NOS: 12
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                GENERAL INFORMATION:
APPLICANT: SCOSTAK, Jack W.
APPLICANT: ROBERTS, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: RASLSEQ for Windows Version 4.0
SSPOID NO 17
LENGTH: 289
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; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
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ORGANISM: Artificial Sequence
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; LOCATION: (192)..(6716)
US-09-404-650-1
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ORGANISM: Homo sapiens
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Patent No.
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                                      Gaps
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Query Match 2.4%; Score 38.8; DB 4; Length 6816; Best Local Similarity 47.5%; Pred. No. 1.3; Matches 115; Conservative 0; Mismatches 127; Indels 0
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Sequence 3, Appliagements 3, Appliagements 59, Appliagements 59, Appliagements 3373, Appliagements 11098, A Sequence 2282, Appliagements 2472, App
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1 ttggtctggggctggccaca......acaccagcctcttagtcttc 1647
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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GenCore version 5.1.6
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0 US-09-8645-20146
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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181 GCCCAAAGCCTTGAGATGGACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCACCAGGTCA 240

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APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANG
TITLE OF INVENTION: VARIANG
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT APPLICATION NUMBER: US/09/826,581
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-07
                                           Sequence 14, Appl Sequence 20, Appl Sequence 20, Appl Sequence 14, Appl Sequence 2, Appl Sequence 395, App Sequence 402, App Sequence 346, App Sequence 346, App Sequence 14, Appl Sequence 11, Appl Sequence 41, Appl
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 5, Application US/09826581; Patent No. US20020142310A1; GENERAL INFORMATION:
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; LOCATION: (20)...(1486)
US-09-826-581-5
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ORGANISM: Homo sapiens
          1647
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          SEQ ID NO 5
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APPLICANT: Andersson, Leif
APPLICANT: Andersson, Leif
APPLICANT: Andersson, Leif
APPLICANT: Buthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VAISATS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 & FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT PILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1014
                                                                                     TGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTAATTCCCGCTTTGATGTGATTT 1226
                                                                                                                                              ACCTGGCTGCCCAGCAAACCTACAACCAGCTGGACATGTGGGAGAAGCCCTGAGGC 1286
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                                              TCATGTCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC 662
                                                                                                       1358 ATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTTGGGC
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Pred. No. 1.1e-72;
0; Mismatches 7;
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ilarity 97.6%;
Conservative
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                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and FILE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PAJO5
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SEQ ID NO 2
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) OTHER INFORMATION: n equals a,t,g, or US-09-925-297-2
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; Patent No. US20020081659A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 580; Conserv
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9976 CATGCTAACCATCACGACTTTATCAAGATCCTGCAAATGTATTACAAATCGCCAAATGC 10035
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556 CGCCCCCAGATCTACATGCGCTTCATGCAGGAGCACCTGCTACGATGCCATGGCAAC
                                                                                616 TAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCT
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
TITLE REPERENCE: GIN 6400
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10276 ACATCCTGACACATAAACGCATACTTAGGTTCCTTTTCCTAT 10317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     978 ACATCCTCACACACACACGCCTGCTCAAGTTCCTGCACATCT 1019
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Steininger II, Robert J.
Bowman, Michael R.
Spaulding, Vikki
Wong, Gordon G.
Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 559, Application US/09822846 Publication No. US20030027139A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/195,605 PRIOR FILING DATE: 2000-04-06
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LaVallie, Edward R.
Collins-Racie, Lisa A.
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Gulukota, Kamalakar
Graham, James R.
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Merberg, David
Treacy, Maurice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 559
LENGTH: 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fechtel, Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-822-846-559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      918
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                        GENERAL INFORMATION:

APPLICANT: Anderson, Leif
APPLICANT: Luthman, L. Belger
APPLICANT: Luthman, L. Belger
APPLICANT: Luthman, L. Belger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REFERENCE: 11145-007001
CURRENT FILIG DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1129 TGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGGTCAACGAATGTGG 1188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 168.2; DB 10; Length 1722;
Pred. No. 9.3e-40;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 11527;
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56.7%; Pred. No. 2.5e-27;
tive 0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 311338
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 99/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 70, Application US/10108605; Patent No. US20020160934A1
GENERAL INFORMATION: APPLICANT: Broadus, Julie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila melanogaster
                                        Sequence 3, Application US/09826581 Patent No. US20020142310A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.2%;
95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.6%
Matches 173; Conservative
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 56.7 Matches 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-3
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LENGTH: 11527
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US-10-108-605-70
                                                                                                                                                                                                                                                                                                                                             LENGTH: 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-10-108-605-70
                   US-09-826-581-3
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APPLICANT: Haseltine, William A.
APPLICANT: Haseltine, William A.
APPLICANT: Haseltine, William A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Seeven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 1995-04-12
PRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1994-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN BE1474, SIGNAL = 3.8

OTHER INFORMATION: EXPRESSED IN BE1474, SIGNAL = 5.3

OTHER INFORMATION: EXPRESSED IN BEATA, LIVER, SIGNAL = 5.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8

US-09-864-761-3373
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ TRAKE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          711 ACAGCAAGAAGCAGAGCTTTGTGGGGATGCTGA 743
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OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11098, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
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NAME/KEY: misc feature
LOCATION: (53)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.6
Matches 88; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11098
LENGTH: 427
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc feature
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                       1130 GCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGGTCAACGAATGTGGT 1189
                                                                                                                                                                                                                                                                                                                                         1190 CAGGICGIGGCCTCTATICCCGCTITGAIGIGAITCACCIGGCIGCCCAGCAAACCIAC 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1250 AACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGGACACTATGTCTGGAGGGA 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1370 CAGGTACACAGGCTGGTGCTAGTGGACGAGCCAGCATCTCTTGGGCGTGGTCTCCTC 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1310 GTCCTTTCCTGCCAGCCCCACGAGAGCTTGGGGGAAGTGATCGACAGGATTGCTCGGGAG 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 GTTGTGAAGTGCAATAAGCTGGAAATACTGGAGACCATCGTGGGACAGAATAGTAAGAGCT 244
                                                                                                                                                                                                                                                                                                                                                                              245 GAGGICCAICGGCIGGIGGIAAATGAAGGAGAAATAGIAGGGGIAITATITCCCIG 304
                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                   0;
                                                                                                  7.5%; Score 123.6; DB 9; Length 1446; 60.4%; Pred. No. 1.6e-26;
                                                                                                                                                             0; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1430 TCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGG 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION UNMERS: US/09/864,761
CURRENT PILING DATE: 2001-05-23
PRIOR PILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3373, Application US/09864761 Patent No. US20020048763A1
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                                                                                                                           Best Local Similarity 60.4 Matches 204; Conservative
         ; ORGANISM: Homo sapiens
US-09-822-846-559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-09-864-761-3373/c
                                                                                                     Query Match
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APPLICANT: AGREEL, DATO A.

APPLICANT: CHEN, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FY
TITLE OF INVENTION: GHEN EXPRESSION AMALYSIS BY MICROARRAY
FILE OF INVENTION: GHEN EXPRESSION AMALYSIS BY MICROARRAY
FILE OF INVENTION: GHEN EXPRESSION AMALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2000-05-04
FRIOR RELING DATE: 2000-02-04
FRIOR PILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-06-26
FRIOR APPLICATION NUMBER: US 60/23,366
FRIOR FILING DATE: 2000-08-03
FRIOR PELING DATE: 2000-08-03
FRIOR PELING DATE: 2000-09-27
FRIOR FILING DATE: 2000-09-27
FRIOR PELING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: US 60/236,359
FRIOR PELING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: US 60/236,359
FRIOR APPLICATION NUMBER: PCT/US01/00666
FRIOR APPLICATION NUMBER: PCT/US01/00667
FRIOR APPLICATION NUMBER: PCT/US01/00667
FRIOR APPLICATION NUMBER: PCT/US01/00667
FRIOR APPLICATION NUMBER: PCT/US01/00667
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NN: EXPRESSED IN HELA, SIGNAL = 4

NN: EXPRESSED IN HELAN, SIGNAL = 4.1

NN: EXPRESSED IN PLACENTA, SIGNAL = 3.9

NN: EXPRESSED IN HELLON, SIGNAL = 3.9

NN: EXPRESSED IN BY474, SIGNAL = 3.8

NN: EXPRESSED IN BY474, SIGNAL = 5.3

NN: EXPRESSED IN BY474, SIGNAL = 4.8

NN: EXPRESSED IN BY474 SIGNAL = 4.8

NN: EXPRESSED IN BONE MARROW, SIGNAL = 4.2

NN: EXPRESSED IN BALL LIVER, SIGNAL = 4.2

NN: EXPRESSED IN BALL SIGNAL = 4.2

NN: EXPRESSED IN BRAIN, SIGNAL = 4.2

NN: EXPRESSED IN BRAIN SIGNAL = 4.2

NN: EXPRESSED IN BRAIN SIGNAL = 4.3

NN: EXP
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PRIOR PELING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00661
PRIOR PELICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PLICATION NUMBER: US 69/24,687
PRIOR PLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PRIOR DATE: 2000-05-30
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PRIOR APPLICATION NUMEER: PCT/US01/00665
PRIOR FILING DATE: 2001-01:30
PRIOR FILING DATE: 2001-01:30
PRIOR FILING DATE: 2001-01:30
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APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
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SOFTWARE: Annomax Sequence
SEQ ID NO 20146
LENGTH: 92
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ORGANISM: Homo sapiens
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OTHER INFORMATION: M.
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OTHER INFORMA
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Best Local Similarity
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INFORMATION: n equals a, t, g, or
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OTHER INFORMATION: n equals a,t,9, or
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Matches 124; Conservative
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LOCATION: (360)
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LOCATION: (316)
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Sequence 20146, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:

651 AGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCTC 704

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SEQ ID NO 2472
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LENGTH: 821
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US-09-826-581-1
                       LENGTH: 897
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                                                                                                                                                                                            APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: ROR IDENTIFICATION, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARR: RastSEQ for Windows Version 4.0
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APPLICANT: And, YOUTHON
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTIONS: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 0/306,220
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FASLEEQ for Windows Version 4.0
3.2%; Score 53.4; DB 9; Length 457; 53.6%; Pred. No. 7.8e-06; Live 0; Mismatches 96; Indels (
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Publication No. US20030099974A1
GENERAL INFORMATION:
                                                                                                                                Sequence 2282, Application US/10198846 Publication No. US20030099974A1
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; LOCATION: 2, 3, 4, 5

; CTHER INFORMATION: n = A,T,C or G

US-10-198-846-2282
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Matches 111; Conservative
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                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                        RESULT 11
US-10-198-846-2282/c
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APPLICANT: Andersson, Leif
APPLICANT: Andersson, Leif
APPLICANT: Letthman, L. Holger
APPLICANT: Marklund, Stefan
TTILE OF INTENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SU
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-07
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                                                                                                   73, 462, 481, 540, 559,
774, 809, 849, 870, 873,
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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100.0%; Pred. No. 2.4e-05;
tive 0; Mismatches 0;
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56.8%; Pred. No. 2.2e-05;
tive 0; Mismatches 73;
                                                                     NAME/KEY: misc_feature

: LOCATION: 2, 16, 22, 23, 27, 28, 30, 36, 39,

: LOCATION: 590, 604, 634, 636, 676, 680, 772,

: LOCATION: 816, 886, 893, 895, 896, 897

: OTHER INFORMATION: n = A,T,C or G
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030073623A1
GENERAL INFORMATION:
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Best Local Similarity 100.C
Matches 52; Conservative
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US-09-826-581-1
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.6%; Score 43.4; DB 10; Length 458; 64.4%; Pred. No. 0.0073; ive 0; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO AC006966.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.2
OTHER INFORMATION: EXPRESSED IN BMILOO, SIGNAL = 7.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN MELA, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4
US-09-864-761-693
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                                                    PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 693
      APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
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Job time: 521.839 secs
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Best Local Similarity 64.4%;
Matches 65; Conservative
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                     116 CGGCGAGGAGCAGCCCACAGCTGCTCCACCCTCCTCTGTGTGAGAGAGGCCGGC 175
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Pred. No. 0.0012;
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
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DR APPLICATION NUMBER: PCT/US01/00668

DR FILING DATE: 2001-01-30

DR APPLICATION NUMBER: PCT/US01/00663

DR FILING DATE: 2001-01-30

DR APPLICATION NUMBER: PCT/US01/00662

DR PILING DATE: 2001-01-30
NUMBER OF SEQ 1D NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
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Best Local Similarity 47.8%;
Matches 133; Conservative 0
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                                                                                                                         TYPE: DNA ORGANISM: HOMO Sapiens
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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61
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

Andersson, L., Luthman, H. and Marklund, S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 5 18-OCT-2001;

REFERENCE AUTHORS TITLE JOURNAL

human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

02-NOV-2001

PAT

linear

DNA

Sequence 5 from Patent WO0177305. AX281582 AX281582.1 GI:16608833

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 1 AX281582

SOURCE ORGANISM

ALIGNMENTS

AC104991 AC111698

AX099774 Sequence
AX294520 Sus scrof
AX398331 Sequence
AX39833 Sequence
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2115 bp mRNA linear PRI 03-JUN-2000 HOMO sapiens AMP-activated protein kinase gamma subunit (PRKAG3) AF214519
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SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQ1YM
RFWQEHTCYDAWATSSKLVIFDTWLEIKKAFFALVANGVRAAPIWDSKKQSFVGMLFI
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KNREHRELPVLDPVSGWYLHILTHRELLERFESLLERFBLLAFOSLEPROL
AVVLETARIJTHALDIFVDRRYSALPVNBCGQVGGTSREDVIHLAAQQYYRHLDMS
GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVVDETQHLLGVVSLSDILQ
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                                                                                                       106 ACAAGGCAGAAGTCGGTGAGGAAGGGAACCACCACGTCAGGGGAAGGTCCCCGGTCC 165
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ernst (DE)
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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Patent: WO 0120003-A 29 22-WAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
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Length 2109;
                                            Indels
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100.0%; Score 61; DB 6; 100.0%; Pred. No. 5.4e-08;
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    note*"unnamed protein product"

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Sequence 29 from Patent WO0120003.
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/organism-"Homo sapiens"
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LMDSKKQSPYGMLTTPDFILVLARYTSBELVQYEEGERTETARRILYGGCFKRLVS
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YRTIODLGIGTFRDLAVVLETAPILTALDIFVDRNVSALPVVNECGQVVGLYSRFDVI
HLAAQOYTNHILDMSVGBALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRIVLDDE
TOHLLGVVSLSDILQALUSPAGIDALGA"

621 c 560 g 470 t
                                                                                                                                                                 /protein_id="Cad10589.1"
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LSPQAPPRIGWOLLPSCTTASARGATGSTTATPTATTATTSTATTSTATT
LVANGVRAAPIMDSKKQSFVGMLT1TDFILVLHRYYRSPLVQIYEIEQHKIETWREIY
                                                                                                                                                                                                                                                                                                              LOGCFRELVSISPNDSLPEAVYTLIKNEIHRLPVLDPVSGNVLHITTHKRELKFELHIF
GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNBCGQV
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QVHKLVLVDPTQHLGQVSLSDILQALVLSPAGIDALGA"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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INSTITUT MAITONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
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100.0%; Pred. No. 5.6e-08;
ive 0; Mismatches 0; Indels
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                                                                                                                           /note="unnamed protein product"
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                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
20. .1489
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Sequence 3 from Patent WO0120003.
AX099776
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/db_xref="taxon:9606"
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                   Location/Qualifiers
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/evidence-experimental
/product="AMP-activated protein kinase gamma 3 subunit"
/product="AMP-activated protein kinase gamma 3 subunit"
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/db_xref="G1:668201"
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LSPQAPPFKGWDDERREGAGITWRFTEEHTCYDAMATSSKLVIFDTMLETKRAFA
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GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRYSALPVVNECGQV
VGIXSRPDVIHLAAQOTYMHLDMSVGEALRKRYLCLEGVLEGVLGEVDRIARE
QVHRLVLVDETQHLIGVVSLSDILQALVLSPAGIDPSGFEKI"
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                                         Bukaryota Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (Dases 1 to 2390)
Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
Biochem. J. 346 Pt 3, 659-669 (2000)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (12-OCT-1999) Carling D., Cellular Stress Group, M.
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
London, W12 ONN, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="AMPK gamma 3"
/function="AMP-activated protein kinase regulatory
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100.0%; Pred. No. 5.3e-08;
iive 0; Mismatches 0;
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/db_xref="taxon:9606"
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Sequence 2 from Patent WO0177305.
AX281579
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EPPPGGEORSRPYAESTGLEATFFWTPLAGADPAGVGFPTGWDCL95CTASAAG
SSTDDVELATEFPATARMECLESCLIEERPALCISPAFPAFPKLGMDELKRPAQIYM
RFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANCVRAAPLMDSKKQSFVGMLTI
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KNRHHRLPULPVLDPVSGWYBLILTHRKLLKFLHFRSLLLPRSFLKRYIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRYSALPVVNECGGVVGLYSRFDYHLAAQQYXNHLDMSV
GEALRQRTICLEGVI.SCQPHESI.GEV INN FARQVHRANLVDBTQHLLGVYSLSDILO
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AJ249977
AJ249977.1 GI:6688200
                                                                                                                                                                                                                                          A mutation in PRKAG3 associated with excess glycogen content in pig
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
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                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P. and Andersson,L.
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/protein_id="AAF73987.1"
/db_xref="GI:8215682"
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Science 288 (5469), 1248-1251 (2000)
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/db_xref="taxon:9606"
/chromosome="2"
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622 c 56
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Signation, Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhqalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodde, S., Donino, W., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Gand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J., Landers, S., Goyette, M., Gardman, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, K., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Marphy, T., Naylor, J., Minour, T., Miranda, C., Menqa, V., Morrow, J., Wurphy, T., Naylor, J., Minour, T., Miranda, C., Menqa, V., Morrow, J., Peterson, K., Pisani, C., Pollara, V., Kaymond, C., Kiley, R., Kogov, P., Rothman, D., Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N., Subramanian, A., Talamas, J., Young, G., Zathoun, J., Zimmer, A. and Zody, M.
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Homo sapiens clone RPl1-504G11, WORKING DRAFT SEQUENCE, 32
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                              Length 989;
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100.0%; Pred, No. of
100.0%; Mismatches
                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
306 c 286 q 168
Location/Qualifiers
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NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                      Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                               gap of 100 bp in length gap of 104 bp in length gap of 106 bp in length 47: cortig of 1286 bp in length gap of 2336 bp in length
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Consensus quality: 135376 bases at least Q40 Consensus quality: 143264 bases at least Q30 Consensus quality: 146503 bases at least Q20
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33968: contig of 3698 bp in length
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66595: contig of 5900 bp in length
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contig of 2473 bp in length
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contig of 1980 bp in length
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contig of 2640 bp in length
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contig of 4820 bp in length
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85022: contig of 7807 bp
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21928: contig of 2362 bp
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60595: contig of 4624 bp
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7547; contig of
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15044 15143: gap of
-714 17123: cont.
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101194 101293: gap of
101294 113090: conti
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.. gap of
101193: ~
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12556: con
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24319: cont
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34069 38179: cont
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51285: con
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6161: cor
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9983: cor
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113091 113190: gap of 100 bp

113191 123496: contig of 10306 bp in length

123497 123596: gap of 100 bp

123597 137837: contig of 14241 bp in length

137888 137937: gap of 100 bp

137938 152129: contig of 14192 bp in length.

Location/Qualifiers
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20039. _.24319

//note="assembly_fragment"

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27160. .30170
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93415, .101193
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'note="assembly_fragment"
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66696. .73218
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AC009974 206854 bp DNA linear PRI 09-JAN-2002
Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
AC009974
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Submitted (OB-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 206854)
Waterston, R. H.
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5 (bases 1 to 206854)
Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 206854)
2 (Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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  Length 152129;
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459119
Unpublished (2001)
3 (bases 1 to 206854)
Waterston,R.H.
83.6%; Score 51; DB 2; Length 152
100.0%; Pred. No. 2e-05;
ive 0; Mismatches 0; Indels
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Contact: sapiens@watson.wustl.edu
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Waterston, R.
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/note="match to EST B1059713 (NID:914467240)"
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/note="similar to Homo sapiens EST BI114348
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                                                                                                                                                                                                                                    The RCI-11 human BAC library was made from the blood of one male donor, as described by Oscogawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                           Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Mashington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NID:98364652) tz39c01.y1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to EST A1670836 (NID:94850567) wa04910.x1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="match to EST A1670836 (NID:94850567) wa04910.x1"
ρλ
from more than one subclone; and the assembly was confirmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match to EST BG477625 (NID:gl3409904)"
1. .37
/note="match to EST BI059713 (NID:gl4467240)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="match to EST AL567345 (NID:g12920610)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match to EST BF183086 (NID:g11061273)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NID:911251653)"
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note="similar to Homo sapiens EST BI114348

(NID:g14565249)"
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/db_xref="taxon:9606"
/chromosome="2"
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281. .344
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                                                                       MAPPING INFORMATION:
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                           restriction digest
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HFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKÖSFVGMLTI
TDFIIVYLHYYRSPLVQIYEIEEHKIETWREITLGGCFKFLVSISPNDSLFBAYTALI
KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGFRDL
AVVEETAPTLITALDIFVDRRVSALPVVNHTGQYVGLYSREDVIHLAAQQTYNHLDMNV
GEALRQRTLCLEGVLSCQPHETLGEVIDRIVBEQVHRLVLVDETQHLLGVVSLSDILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPPGPREGPQSRPVAESTGGEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gailland,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Ralm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 1973) Anderson, L., Loff, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
1. .1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="AMP-activated protein kinase gamma subunit"
/protein_id="AAF73988.1"
/db_xref="GI:8215684"
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                                                                                                                                                                                                                                                                                                                                      /tissue_type="skeletal muscle"
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AX099800
                                                                                                                                                                                                                                              /organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="PRKAG3"
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                                       REFERENCE
AUTHORS
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JOURNAL
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KEYWORDS
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Lwdskkospycmlitdpilvlhryrrsplvqiyeieehkietwreiylogcekplvs
Ispnoslerayyalikhelypldpysgayllithkrlikehlifgtllerspr
Yrtigdlg igterdlavvletapiltaldifvdrrysalpvvnetgovglysredyi
HladoqyynHildmygellrorilcevlscophetigevidrivbegyhrlyludg
Tqhllgvvslsdilcalvlspagidalga"
583 c 529 g 375 t
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                                                                                 PAT 02-APR-2001
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1867)
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                 INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
                                                                                                                                                                                                                                                                                                                                                     Variants of the gamma chain of ampk, dna sequences encoding the
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Pred. No. 0.021;
0; Mismatches 12;
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Patent: WO 0120003-A I 22-MAR-2001;
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Sequence 1 from Patent W00120003.
AX099774
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/db_xref="GI:13538809"
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1. .1867
/organism="Sus scrofa"
/db_xref-"taxon:9823"
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80.3%;
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DSWTDHLDIGIEGESASASGDELGLYBERPARCPSSPEVLLPRLGMDELCRPGAQVYM
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TDFILVLHRYTRSPLVQIYEIEBHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALI
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Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Pred. No. 0.021;
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Sequence 3 from Patent W00220850.
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/organism="Sus scrofa"
/db_xref="taxon:9823"
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HFWQEHTCYDAMATSSKLV I FDFMLE I KKAFFALVANGVRAAPLWDSKKQSFVGMLT I
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KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 022086-A 1 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
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AX399331
                                                                                                   /protein_id="CAC35800.1"
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1. 1395
/organism="Sus scrofa"
/db_xref="taxon:9823"
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HFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVQAAPLWDSKKÖSFVGMLTI
TDFILVVLHYYRSPLVQIYEIEEHKIETWREIYLQGCFYFDLVSISPNDSLFBAYYALI
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GEALRQRTLCLEGVISCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVYSLSDILO
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DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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Sus scrofa
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 7 14-MAR-2002;
IOWA State University Research Foundation, Inc. (US)
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 022085-A.9 14 "MAR-2002;
IOWA State University Research Foundation, Inc. (US)
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/organism="Sus scrofa"
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PRKAG3 polymor PRKAG3 gene 5' PRKAG3 gene 5' Pig PRKAG3 polymor Pig PRKAG3 gene 5' Pig PRKAG3 gene 5' DNA encoding novel T. thermophilus ga Thermus thermophil Human LOBO homolog Human retina speci Human retina speci

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Ovary cancer relat

ABV29324 ABL68109 AAQ05872

AAQ06333

ABK95404 ABK95403 ABV23466

AAX21373 AAZ23900

Calcium activated Human IKca channel Human calcium acti

novel

Human breast DNA encoding

Sequence encoding Human IL-2R beta c Human METH2 relate

CDNA encoding nove Gene #2184 used to Drosophila melanog

X16619 CDNA clone.

Murine BMP-9 cDNA. Encodes murine bon

Human cDNA sequenc cDNA sequence #179 CDNA encoding huma DNA encoding humar

AAS62392 ABL27038 ABK13766

AAQ74084 **AAH16987** AAS40665 AAL06553

AAE30037

Murine bone morpho

Human reproductive Apolipoprotein A-I

ALIGNMENTS

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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
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Pig AMPK gamma sub
Pig wild-type PRKA
Pig PRKAG3 polymor
Pig PRKAG3 polymor
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Human AMPK gamma s
PRKAG3 intron 2 -
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6198.732 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                       2185239 seqs, 1125999159 residues
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/product= "Human Prkag3 protein"

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                                                                                                                                                                   New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                              This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting a the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon a subject to the variation of a G for a C at nucleotide 13 or resulting in the amino acid substitution of a T for a C at nucleotide 50; as useful in a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                            nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
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-haq 0; Indels
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                                                                                                              Andersson L, Luthman H, Marklund S;
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                                          06-APR-2001; 2001WO-SE00765.
                                                                  07-APR-2000; 2000US-195665P
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P-PSDB; QQB47679.
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5'UTR
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CAMP)-activated kinase (AMPK) substituting the properties of the practical states of the practical practical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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(ANDE/) ANDERSSON L.
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1390..2109
/*tag= c
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Transgenic animal and host cell transformed with PRKAG3 or a heterotriment AMPK consisting of PKKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
                                                                                                                                                                                              PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robic A, Rogel-Gaillard C;
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                                                                                                                                                             Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human complete Prkag3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..1395
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18-MAY-2000; 2000EP-0401388.
    (first entry)
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
13-JUN-2001
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(LOOF/)
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New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
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                                                                                                                          Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
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                                                                                                                                                                                                                                                  'note= "3' portion of intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "5' portion of intron 4"
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/number = "Intron 2"
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r= "Intron 3"
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r= "Intron 4"
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                "Exon 4"
                                                                                                                                                                                                                                                                                              'number= "Exon 3"
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             AAH43682 standard; DNA; 989 BP.
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                                                                                                PRKAG3 intron 2 - intron 4.
                                                                    (first entry)
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                                                                                                                                                                     Homo sapiens
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; Score 61; DB 22; ; Pred. No. 6.1e-10; 0; Mismatches 0;

100.0%; 100.0%;

l Similarity 100.0 61; Conservative

Query Match Best Local S

Matches

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Length 2115; Indels 09

106 ACAAGGCAGAAGTCGGTGAGGAAGGGAACCACCAGGTCAGGGGGAAGGTCCCCGGTCC 165

1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC

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13-JUN-2001
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Best Local :
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                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                           PRKAC3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                                                    subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                           1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGT 51
                                                ;
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                                                                                                                                                                                               Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                            Length 989;
                                               Indels
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/product= "Sus scrofa PRKAG3 protein"
1390.1867
/*tag= c
        Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
                          Best Local Similarity 100.0%; Pred. No. 7.5e-07; Matches 51; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                     AAD03295 standard; cDNA; 1867 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Fig 2; 71pp; English.
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18-MAY-2000; 2000EP-0401388
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472..1389
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                                                                                                                                                                                                                                                           chromosome 15; ss
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such as myopathy and cardiovascular diseases, to modulate AMPK
activity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic disorder,
preferably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered allele of PRKAG3.
Transgenic animal and host cell transformed with PRKAG3 or a
heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.5%; Score 41.8; DB 22; Length 1867; 80.3%; Pred. No. 0.00058;
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J, Le Roy P, Chardon P;
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0; Mismatches
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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1..1395
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18-MAY-2000; 2000EP-0401388.
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/product=
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Iannuccelli N, Gellin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 80.3 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome 15; ss.
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replace (599, A)
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   variation
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                                                                                                                                                (AMP) activated Kinase (AMPK) gamma subunit muscle-specific isoform, complete PRRAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as clabeles, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3 or a grand and host cell transformed with PRRAG3 or a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCGGGTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a sequence encoding the first cystathione beta synthase (CBS) domain PRKAG3 and is useful in gene therapy.
New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                       heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
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/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                    The present sequence is a cDNA encoding pig adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.5%; Score 41.8; DB 22; Length 1873; 80.3%; Pred. No. 0.00058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Pig PRKAG3 wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.00
0; Mismatches
                                                                                               Claim 12; Page 62-64; 71pp; English.
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1..1395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pig wild-type PRKAG3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                       myopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma subunit gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig wild-type PRKAG3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for screening animals to determine
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Pred. No. 0,00058;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malek M, Plastow G;
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1..1395
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80.3%;
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                                                                                                                                                                                             10-SEP-2001; 2001WO-US28283.
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es 49; Conserva
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1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGTCC 60
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/product= "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
                                                                                                                                                                                                                                                                                                                                                                                                        Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                       /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.5%; Score 41.8; DB 24; Length 1873; 80.3%; Pred. No. 0.00058; Dred. No. 0.0058; Live 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                             Rothschild MF, Ciobanu DC, Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
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     replace (595, A)
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2001US-260239P.
2001US-299111P.
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18-JUN-2001;
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       variation
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AAD36460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant DNA (PRRAG3-30).
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                                                                                                                                                                                                                                                                                                                                                                                                      Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                       /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.5%; Score 41.8; DB 24; Length 1873; illarity 80.3%; Pred. No. 0.00058; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                         Rothschild MF, Ciobanu DC, Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
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replace (89, C)
/*tag= b
                                                                                                                                                                                          08-SEP-2000, 2000US-231045P.
08-JAN-2001, 2001US-260239P.
18-JUN-2001, 2001US-299111P.
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Les 49; Conservat
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   variation
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AAD36459
ID AAD3
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The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 gene is located in the RN locus of chromosome 15. Therapeutic for treating an altered regulation of carbohydrate metabolism alsorders such as ciabetes, obesity, and disorders associated with muscle metabolism cardivity, and for restoring a normal AMPK function. PRKAG3 sequence activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrkaG3 demain as sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                            Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
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    /product= "Sus scrofa Prkag3 splice variant"
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80.3%; Pred. No. 0.00059;
iive 0; Mismatches 17
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                                                                                                                                              11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                       10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
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ANDERSSON I
LOOFT C.
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                                                                                                                                                                                                                                                                                                                                (KALM/) KALM E.
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                                                     WO200120003-A2
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                                                                                                  22-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                  /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                            Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 102-104; 109pp; English.
                                                                                                                                                                                                                                                                                                                              (IOWA ) UNIV IOWA STATE RES FOUND INC.
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replace (599, A)
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80.3%;
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08-JAN-2001, 2001US-260239P.
18-JUN-2001, 2001US-299111P.
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Matches 49; Conservative
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       variation
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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; polymorphism; short interspersed element; pig; SINE; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32.6; DB 24; Length 1095;
Pred. No. 0.41;
2; Mismatches 11; Indels 0;
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                                                                                                                                                                                                                                                                                                                                            /rpt_type= "DIRECT"
/note= "Direct repeat present between short
interspersed element (SINE)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon, intron and short interspersed element (SINE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rothschild MF, Ciobanu DC, Malek M, Plastow G;
              Pig PRKAG3 gene 5' flanking region with SINE.
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ilarity 74.58;
Conservative
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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826..979
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es 38; Conserv
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                                                                                                                                Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-22).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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/product= "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
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/standard_name* "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                   AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rothschild MF, Ciobanu DC, Malek M, Plastow G;
                  Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
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                                                                                                                                                                         Location/Qualifiers
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78.7%;
                                                                                                                                                                                                                                                                                                                                                                                                          10-SEP-2001; 2001WO-US28283.
                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.9
Best Local Similarity 78.7
Matches 48; Conservative
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                                                                                                                                      Sus scrofa
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Gaps

RESULT 13 AAD36461

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(first entry)

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Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                   DNA encoding novel human diagnostic protein #20327.
AAS84523
ID AAS84523 standard; cDNA; 2541 BP.
                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                         HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABG20336
                                                                                                                                                                                                                                    WO200175067-A2.
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biodiversity
                                                                                  13-FEB-2002
                                                                                                                                                                                                                                                                      11-0CT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT,
                                                  AAS84523;
                   Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 gene 5' flanking region including
                                                                                                                                                                                  AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; polymorphism; pig; ds.
                                                                                                                                                  Pig PRKAG3 gene 5' flanking region including exon and intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rothschild MF, Ciobanu DC, Malek M,
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                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                AAD36462 standard; DNA; 808 BP.
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/number= 2
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                    /number= 1
539..692
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               RESULT 14
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                                  AAD36462
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Tang YT;

2001-639362/73. Liu C,

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The coordinate production of (II) the configuration of (II) and gene are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for the correct normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid sequences. AAS4197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1114 GGCAGGGCCGGTGGGGAAACTGTGGCCCGGAGGTCAGGGGTCCTGTCCACAGTC 1168
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Claim 1; SEQ ID No 20327; 103pp; English.
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Best Local Similarity 67.3%;
Matches 37; Conservative
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Gaps

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51.5%; Score 31.4; DB 24; Length 808; 74.5%; Pred. No. 0.94; Live 1; Mismatches 12; Indels 0.

Best_Local Similarity 74.5 Matches 38; Conservative

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Query Match

Sequence 808 BP; 170 A; 230 C; 199 G; 208 T; 1 other;

1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGT 51

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June 13, 2003, 02:37:44; Search time 151.839 Seconds (without alignments) 6506.409 Million cell updates/sec
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61
1 acaaggcagaagtcggtgga.....gggggaaggtccccggtcca
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                                       OM nucleic - nucleic search, using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			Description		BB628877 BB628877	BB629521 BB629521	BB630381 BB630381	AW356079 38073 MAR	AW427435 63185 MAR	BF890374 291826 MA
	æ	Result Query	O.		BB628877	BB629521	BB630381	AW356079	AW427435	BF890374
			DB	:	10	10	10	10	10	12
			Length		621	655	685	399	422	444
			Match				63,3			
			Score		38.6	38.6	38.6	37	37	34.2
			No.		Н	2	М	4	2	9

BIT75360 467815 MA AL664508 UK25b05.y AA787023 md007a1.r AW693375 NF0653110S BJ080431 BJ080431 BE306360 601101079 BM489457 pgm2n.pk0 BM489457 pgm2n.pk0 BM466469 AGENCOURT BG244994 602359260 AL173081 Tetracadon BG244994 602359260 AL157081 Tetracadon BG244994 602359260 AL157081 Tetracadon BG244994 602359260 AL157081 AGENCOURT AW259840 33 22 MARC BF373555 33889 MAR BB335678 CM0-FN004 AW35555 33889 MAR BH235910 ATZKD11R BH235910 ATZKD11R BH235910 ATZKD11R BH235871 ATZKB13FF AU257757 AU257757 BF904178 MR3-MT032 BB653848 BB65348 BB65348 BG961198 60282235 BG324609 602422586 BG324197 UI-R-CS0-BE121408 UI-R-CS0-BE121408 UI-R-CS0-BE121408 UI-R-CS0-BE121408 UI-R-CS0-BE121408 UI-R-CS0-BE121408 UI-R-CS0-BE12170014A BM702805 UI-E-CKI-BIO02805 BG05119 HS 3176_A BM702805 UI-E-CKI-BIO0853 BG65255 AGENCOURT	pp mRNA linear EST 31-AUG-2001 riched, 16 days neonate cerebellum Mus 5 5', mRNA sequence. Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae, Musinae, Mus. 4. Ito, M., Rawai, J., Konno, H., Kouda iyazaki, A., Nomura, K., Ohno, M., Sakai, C., Sakai, K., Sano, H., Sasaki, Shiraki, T., Sogabe, Y., Suzuki, H., Hara, J., Shiraki, T., Sogabe, Y., Suzuki, H., Y., Taneda, Y., Tanaka, T., Toya, T., Y. and J. 2001) Lion Research Group, RIKEN Genomic a Institute Chemical Research (RIKEN) u, Yokohama, Kanagawa 230-0045, Japan
BI775360 AA64508 AA787203 AW693375 BW693375 BW693375 BW69631 BE306360 BB236360 BB24994 BC244994 BC344994 BC344994 BC344994 BC344994 BC344994 BC344994 BC344994 BC3555 BC8644 BE35678 BC85564 BE35678 BC35676 BC339806 BC320020 BC331120	621 b nngth enr 130039122 130039122 13 15 15 15 15 15 15 16 17 16 16 16 16 16 16 16 16 16 16 16 16 16
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548 569 669 669 669 669 669 669 669	RIKEN full-le CDNA clone 96 con
$\begin{array}{c} \text{RN} \text{A} \text$	BB628877 RI BB628877 RI BB628877 BB628877 BB628877 BB528877 BB52 BB7. house mouse Mus musculu Eukaryota; Mammalia; E Mammalia; E Mammalia; E Mammalia; E Marawa,T., 'M., Koya,S Okazaki,Y.', 'D., Shibat 'D., Shibat 'D., Shibat 'D., Shibat 'D., Shibat 'Tagami,M.' Muramatsu,M RIKEN Mouse Contact: Yo Contact:
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EUKaryotca, Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 553).

S. Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Saito, R., Sakai, K., Sano, H., Sasaki, J.D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Mixamatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu.N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Haysshizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura
is., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was prined with a primer [5' GAGAGAGAGAGAGAGAGACAGAGAGACATITITITITITITIVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
         BB629521 RIKEN full-length enriched, adult male bone Mus musculus cDNA clone 9830138C07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, adult male bone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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/clone="9830138C07"
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                             BB629521.1 GI:15399646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Fukuda,S., Hara,H., Itoh,W., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Punc. Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rappid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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/lab_host*"DH10B"
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/db_xref="taxon:10090"
/clone="9630039L22"
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGARTICTGAGTIAATTAATTAATTCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
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Email: genome-res@gsc.riken.go.jp,
UNL:http://genome.gsc.riken.go.jp,
carainci.p., Shibata,Y., Hayatsu.N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu.M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiawake,S., Inouce,K., Togawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inouc,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 685)
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Pred. No. 0.17;
0; Mismatches 14;
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Contact: Yoshihide Hayashizaki
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Best Local Similarity 77.vv.,
"-hos 47; Conservative
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
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Rayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence evaluation of four pooled-tissue normalized bovine cDNA
                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="A030014A04"
/clone_lib="RIKEN full-length enriched, 6 days neonate
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USDA, ARS, US Meat Animal Research Center
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0; Mismatches
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                                                                                                                                                                                                                                                                           /tissue_type="skin"
/dev_stage="6 days neonate"
/lab_host="DH10B"
                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                               Location/Qualifiers
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AW356079.1 GI:6860085
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1 Similarity 77.0%;
47; Conservative (
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 444)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
                                                                                                                                                                                                              /note="Yector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCGGTCC 60
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                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.7%; Score 37; DB 10; Length 422; Best Local Similarity 75.4%; Pred. No. 0.46; Matches 46; Conservative 0; Mismatches 15; Indels
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NO Box 16c, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
                                                                                                                                         /clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                               /organism="Bos taurus"
/db_xref="taxon:9913"
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/tissue_type="pooled"
/lab_host="DH10B"
  Plate: 32 row: F column: 22
Seq primer: ATTTAGGTGACACTATAG.
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Plate: 57 row: H column: 11
                                                   Location/Qualifiers
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BF890374
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                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.800904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR PRimers
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1 (bases 1 to 422)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E. Wray, J.E. Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G.,
Perrea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 25-APR-2001
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Mammalia, Eutheria, Celartiodactyla, Ruminantia, Pecora, Bovoidea,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pcMv SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from testis, thymus, emitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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AW427435.1 GI:6955382
BST.
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USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                           BACKWARD: GTTTTCCCAGTCACGACG
Plate: 17 row: P column: 9
Seg primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
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In (bases 1 to 516)

Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,M., S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The Washul-NOT Mouse EST Project 1999

L. Unpublished (1999)

L. Unpublished (1999)

Advarder: Warra M/Washur-NCI Mouse EST Project 1999

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1800
                                                                                                                                             EST 10-MAY-1999
                                                                                                                                                                                                                                                                          Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAAGCCACCAGGTCAGGGGGAAGGTCCCCG 56
                                                                                                                                                           uk25b05.yl Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:1970001 5', mRNA sequence.
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Pred. No. 13;
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    .516
    /organism "Mus musculus"

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High quality sequence stop: 484.
Location/Qualifiers
                                                                                                                                         516 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1970001"
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Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                            house mouse.
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                                                                                                                                         A1664508
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                                        97 A 97
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AA787203/c
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                                                                                                  RESULT 8
AI664508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae; Bos.
1 (bases 1 to 548)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts.A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett, G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
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Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle." 139 g 67 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA
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                                                                                                                      Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                  BI775360 548 bp mRNA linear 467815 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                    DB 12;
                                                                                                                    ; Score 34.2; DB
; Pred. No. 3;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9913"
/clone_lib="MARC_2BOV"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: I column: 16
Seq primer: ATTTAGGTGACACTATAG.
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PCR PRimers
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                                                                                                                  Query Match 56.1%;
Best Local Similarity 76.4%;
Matches 42; Conservative
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Best Local Similarity 72.10,
"hes 44; Conservative
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BJ080431 669 bp mRNA linear EST 12-DEC-2001 BJ080431 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL075j16 3', mRNA sequence.
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/note="Wector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Menopodinae; Menopus.
                          Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library
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                                                                                                    Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7568111.
Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Pooled developmental"
/note="Vector: Lambda 2ap; Contains a mixture of
internodal stem segments"
107 c 137 g 200 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 10; Length 618;
Pred. No. 2e+02;
0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                        Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tell Sam Noble Parkway, Ardmore, OK 73402, USA
Tell S80 221 7302
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Developing stem"
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/db_xref="taxon:8355"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3880"
/clone="NF063H10ST"
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Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="mouorat.
/clone_lib="mouorat.
/clone_lib="mouorat.
developmental and vegetative cDNA lambda zap library"
/fissue_type="vegetative mycelia, asexual structures"
/note="vector: pBlueScript SK-; Site_l: EcoRI; Site_2:
XhoI: 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"
a 118 c 96 g 58 t
AA787203 365 bp mRNA linear EST 31-JUL-1998 m8007al.rl Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW693375 618 bp mRNA linear EST 20-DEC-2000 NF063H10ST1F1000 Developing stem Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bmail: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ACAAGGCAGAAGTCGGTGGAGGAAGGCGAGCCACCAGGTCAGGGGGGAAGGTCCCGGGTCC 60
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He.X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
.C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ACAAGGCCGGGTGTCGCGCGAAGAAGCAGCCGACCAGAGGGGAAAGAGGTAGCTGGTCC 3
                                                                                                                                                                                                                                                                                                                                                                                      Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
Prade,R. and Roe,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
                                                                                                                                                                                                                         Emericella nidulans.
Emericella nidulans
Emericella nidulans
Estaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
1 (bases 1 to 365)
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Pred. No. 95;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Emericella nidulans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      An Aspergillus nidulans EST Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="FGSC A26"
/db_xref="taxon:162425"
/clone="m8d07a1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 346.
Location/Qualifiers
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                                                                                             m8d07a1 5', mRNA sequence
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Best Local Similarity 67.2%;
Matches 41; Conservative (
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KEYWORDS
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Gaps

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/dev_stage="Breast,leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,11 weeks);growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMvSbogm6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM466469 1029 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6456404 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5579448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="pgm2n.pk010.p18"
/clone_lib="Wormalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Archosauria, Aves; Neognathae; Galliformes; Phasianidae; Phasianiae; Gallus.

1 (base; Lo 590)

Cogburn, A. and Monsonego-Ornan, E. ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate CDNA library, USDA/IFAFS Animal Genome
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1029)
clone pgm2n.pk010.p18 5' similar to ref|NP_060575.1 (NM_018105)
hypothetical protein FLJ10477 [Homo sapiens] dbj|BAA91635.1|
(Ak001339) unnamed protein product [Homo sapiens], mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Breast muscle, leg muscle and epiphyseal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Commercial broiler and Ottawa Res. Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cogburn@udel.edu, www.chickest.udel.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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69.8%; Pred. No. 3e+02;
iive 0; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                      Townsend Hall, Newark, DE 19717, USA Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strains 90 & 21"
/db_xref="taxon:9031"
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Contact: Larry A. Cogburn
University of Delaware
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BM466469
BM466469.1 GI:18515511
                                                                                     BM489457.1 GI:18610388
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                                                                                                                               chicken.
Gallus gallus
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according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute). " 1 others
                                                                                                                                                                                                            1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 808)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo d Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

243 c 241 g 161 t
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAM6540 row: n column: 19
High quality sequence stop: 652.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                      Gaps
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                                                                                                                             Length 669;
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                                                                                                                             Score 28; DB 13;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.4e+02;
0; Mismatches 17
                                                                                                                                                                    0; Mismatches
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/strain="CZECH II"
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Gaps

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ISM Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CE 1 (bases 1 to 151)
Rs NiH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Inpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMM0330 row: h column: 16
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/tissue_type="retinoblastoma"
/lab_host="NH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Perhologies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: mammary, Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM12336 row: c column: 01
High quality sequence stop: 681.

Location/Cualifiers
1. 1029
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/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                            /organism-"Homo sapiens"
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Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli

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Sequence 214, App
Sequence 39, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 4, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 20, Appl
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SEJIRO; KONO, TAKESHI; DOI, TAKESHI; MIYASAKA, MASANOKI; TSUDO,
MITSURO; KARASUYAMA, HAJIME
TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/88,592
FILING DATE: 9-JUL-1993
PRIOR APPLICATION NUMBER: 486,155
FILING DATE: 08-APPL-1992
PRILING DATE: 08-APR-1992
PRILING DATE: 08-APR-1992
PRILING DATE: 08-APR-1990
                                                                                                                                                                                                                                                                                                                   APPLICANT: TANIGUCHI, TADATSUGU;JATAKEYAMA, MASANORI;
;MINAMOTO, SELIRO;KONO, TAKESHI;DOI, TAKESHI;MIYASAKA, MASAUKI;
;TSUDO, MITSURU;KARASUTMA, HAJIME
; TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2
; NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 6; Length 4035;
Pred. No. 16;
0; Mismatches 20; Indels
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64.9%; Pred. No. 16;
tive 0; Mismatches 20; Indels
US-09-459-133-1

US-09-103-840A-2

US-09-103-840A-1

US-09-397-787-214

US-09-182-145-13

US-09-182-145-13

US-09-182-145-14

US-09-182-145-14

US-09-182-145-14

US-08-416-788-1

US-08-416-788-1

US-08-278-10

US-09-28-275-10

US-08-28-275-10

US-08-28-28-11

US-08-28-56-1

US-08-28-56-1

US-08-28-56-1

US-08-72-665A-20

US-08-75-665A-20

US-08-75-665A-20

US-08-75-665A-20

US-08-75-665A-20
                                                                                                                                                                                                                                               ALIGNMENTS
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APPLICATION NUMBER: US/07/487,059
FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.0%;
64.9%;
  1532
4403765
4413765
431 4
431 4
431 4
1293 4
1293 4
1717 1
7171 4
7171 8
3489 7
3489 7
32207 2
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Best Local Similarity 64.99
Matches 37; Conservative
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Best Local Similarity 64.93
Matches 37; Conservative
  RESULT 2
5449756-1/c
;Patent No. 5449756
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: LENGTH: 4035
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5198359-1/c
;Patent No. 5198359
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Patent No. 5449756
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             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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1 US-09-103-840A-1

US-09-104-145-1

5198359-5

5449756-9

US-09-556-870A-1

US-07-918-314-5

US-07-918-314-5

US-07-918-314-5

US-07-918-314-5

US-08-469-412A-3

US-08-469-412A-3

US-08-469-412A-1

US-08-69-412A-1

US-08-69-412A-1

US-08-69-412A-1

US-08-80-01-715-1

US-08-826-1134-3
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                     441362 seqs, 153338381 residues
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                                                                                                                             US-09-826-581-5_COPY_200_260
61
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Maximum Match 100%
Listing first 45 summaries
                                                            nucleic search, using sw model
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Maximum DB seq length: 2000000000
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40.3 2447 3
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Match Length
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,222A
FILING DATE: 04-DEC-1996
CLASSIFICATION NUMBER: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,353
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
ATREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 40.3%; Score 24.6; DE Best Local Similarity 65.5%; Pred. No. 20; Matches 36; Conservative 0; Mismatches
RESULT 4
US-08-750-222A-1
Sequence 1, Application US/08750222A
Fatent No. 6034061
GENERAL INFORMATION:
APPLICANT: ROSEN, Vicki A.
APPLICANT: ROSEN, Vicki A.
APPLICANT: ROSEN, John M.
APPLICANT: Celeste, Anthony J.
APPLICANT: Song, Jeffrey
APPLICANT: Song, Jeffrey
TITLE OF INVENTION: BMP-9 COMPOSITIONS
UMMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RILING DATE:
ATORNEY AGENT INFORMATION:
NAME: Rapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: 61 5186B
TELEPOMNUICATION INFORMATION:
TELEPOMNE: (617) 876-1170
INFORMATION FOR SEQ ID NO: 1:
SEGUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
STRAIN: C57846xCBA
TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
1564..1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            610..1896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
ORIGINAL SOURCE:
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02140
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LOCATION:
FEATURE:
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US-08-750-222A-1
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tive 0; Mismatches 19; Indels 0
                                                                                    Sequence 1, Application US/08050132A
Sequence 1, Application US/08050132A
Fatent No. 5661007
GENERAL INFORMATION:
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REGARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatchtIn Release #1.0, Version #1.25
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/08/050,132A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI 5186A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
ATORNEY AGENT INFORMATION:
NAME: RAPINOS, Bilen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPENONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDENDESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse liver CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
STRAIN: C57B46xCBA
TISSUE TYPE: liver
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 65.5'
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: mat_peptide
LOCATION: 1564..1893
FEATURE:
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610..1896
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POSITION IN GENOME:
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MOLECULE TYPE: CDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
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ZIP: 02140
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US-08-050-132A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Ploppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC COMPUTED
COMPUTER: TBM PC COMPUTED
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,353A
FILING DATE:
CLASSIFICATION NUMBER: 32,245
RECIENTATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                              APPLICANT: ROSEN, VICKI A.
APPLICANT: ROSEN, VICKI A.
APPLICANT: Geleste, Anthony J.
APPLICANT: Song, Jeffrey
APPLICANT: Thies, Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
VORRESPONDENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
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RESULT 6
US-08-254-353A-1
Sequence 1, Application US/08254353A
Patent No. 6287816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: Mouse liver cDNA CLONE: ML14A POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
STRAIN: C57846xCBA
TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: mat_peptide
LOCATION: 1564..1893
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610..1896
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1..2447
                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ns
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ZIP: 02140
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LOCATION:
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; LOCATION:
US-08-254-353A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US

ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,652B
FILING DATE:
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: GI 5186D
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                Sequence 1.1. Application US/08815652B
Patent No. 6034062
GENERAL INFORMATION:
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
APPLICANT: Thies, R. Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPENDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
CATTY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.3%;
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LIBRARY: Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
STRAIN: C57B46xCBA
TISSUE TYPE: liver
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Best Local Similarity 65.59
Matches 36; Conservative
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LOCATION: 1564..1893
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610..1896
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1..2447
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POSITION IN GENOME:
UNITS: bp
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ORIGINAL SOURCE:
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; LOCATION:
US-08-815-652B-1
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FEATURE:
                       RESULT 5
US-08-815-652B-1
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Sequence 1, Application PC/TUS9507084
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Geleste, John M.
TILLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07084
                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY CAGENY INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERRENCE/POCKET UNMER: 31,245
TELEPHONE: (617) 876-1210
TELEPHONE: (617) 876-1210
TELEPHONE: (617) 876-1210
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4, Application US/09750580; Patent No. 6455280; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
1564..1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610..1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: C57B46xCBA
TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
1..2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE: ML14A
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                rry: US
02140
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
; LOCATION:
PCT-US95-07084-1
                                                                                                                                                                                                            STATE: MA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-09-750-580-4
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Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                   ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19920625
CLASSIFICATION:
                                                                                                     APPLICANT: Worney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI 5186A
                                                                         Sequence 1, Application PC/TUS9205374A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTORNIA PAGENT ARGUMENTANDEN
NAME: REDITON INTEREST 32,245
REFERENCE/DOCKET NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: NUCLEIC ACID
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: Mouse liver cDNA CLONE: ML14A
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 40.3%;
Best Local Similarity 65.5%;
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITS: bp
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1564..1893
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mus musculus
STRAIN: C57B46xCBA
TISSUE TYPE: liver
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 610.1896
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; LOCATION: 1..2447
PCT-US92-05374A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                     ns
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                                                       PCT-US92-05374A-1
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PCT-US95-07084-1
                                       RESULT 7
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Gaps
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40.3%; Score 24.6; DB 4; Length 5381;
Best Local Similarity 70.2%; Pred. No. 22;
Matches 33; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 TCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE PATENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/451,777A FILING DATE: 26-MAY-1995 CLASSIFICATION: 436 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10825 FILING DATE: 23-SEP-1994 ATTORNEY/AGENT INFORMATION: NAME: Eagle, Alissa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Smithkline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: 709 Swedeland Road/UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stambollan, Dwight
TITLE INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
LOCATION: 320. 338
VOTHER INFORMATION: 17-42-319.mis complement
LOCATION: 3194..3212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 17-41-250.mis
NAME/KEY: PITIMEL-bind
LOCATION: 3214..3232
OTHER INFORMATION: 17-41-250.mis complement
                        NAME/KEY: primer_bind
LOCATION: 1441..12461
LOCATION: 1441..12461
NAME/KEY: primer_bind
LOCATION: 1632..12651
OTHER INFORMATION: 17.40.rp complement
NAME/KEY: primer_bind
LOCATION: 2964..13984
OTHER INFORMATION: 17.41.pu
                                                                                                                                                                                                                                                     NAME/KET: priner_bind
LOCATION: 3432..14454
OTHER INFORMATION: 17-41.rp complement
NAME/KET: priner_bind
LOCATION: 300..318
OTHER INFORMATION: 17-42-319.mis
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: 17-42-319.probe; NAME/KEY: misc_binding. LOCATION: 3201..3225; OTHER INFORMATION: 17-41-250.probe US-09-750-580-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 7, Application US/08451777A; Patent No. 5789223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pennsylvania
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US-08-451-777A-7/c
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                                                                APPLICANT: Bihalu, Bernard
APPLICANT: Bihalu, Bernard
APPLICANT: Dunds Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Balter-Cad, Lulsa
APPLICANT: Balter-Cad, Lulsa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89.U52.C1P
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: PCT/1B00/0101
PRIOR APPLICATION NUMBER: PCT/1B00/0101
PRIOR APPLICATION NUMBER: PCT/1B99/02058
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1999-10-25
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: 17-41-250 : polymorphic base C or T NAME/KEY: conflict
LOCATION: 1241
OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
NAME/KEY: conflict
LOCATION: 1447
OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: 17-42-319 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..11022

LOCATION: 1..11022

NAME/KEY: Primer_bind

LOCATION: 553..11575

COTHER INFORMATION: 17-42.rp complement

NAME/KEY: primer_bind

LOCATION: 899..11920

COTHER INFORMATION: 17-39.pu

NAME/KEY: primer_bind

LOCATION: 1246..12267
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LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
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NAME/EXE: misc_feature
LCARION: 3941..5381
OTHER INFORMATION: 3'regulatory region
Yen, Frances
Denison, Blake
Bour, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 919..930
OTHER INFORMATION: exon 1
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OTHER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-0
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 4
LENGTH: 5381
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OTHER INFORMATION: exon 3
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LOCATION: 319
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LOCATION: 3213
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                                                                                                                                                                                                                                                                                                                                                                                               3 AAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGG 57
                                                                                                                                                                                                                                                                                                           DB 1; Length 7676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.3%; Score 24.6; DB 2; Length 7676; 65.5%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,778A FILING DATE: 26-MAY-1995 CLASSFRICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       Score 24.6; DB 1; I
Pred. No. 23;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Satent No. Sococia.
GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
APPLICANT: Stambolian, Dwight
APPLICANT: Stambolian, Dwight
APPLICANT: Stambolian, Dwight
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37,126
FP: P50268-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P50268-1B
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CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-451-778A-7/c; Sequence 7, Application US/08451778A; Patent No. 5830649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Eagle, Alissa M.
RECISTRATION NUMBER: 37,126
REFERENCE/FOCKET NUMBER: PSC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
                      REFERENCE/DOCKET NUMBER: P55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
                                                                                 TELERAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHRRACTERISTICS:
LENGTH: 7676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-451-777A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       Query Match 40.3%;
Best Local Similarity 65.5%;
Matches 36; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 7676 base pairs
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EDNESS: double
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    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-451-778A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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3 AAGCCAGAAGTCGGTGGAGGAAGGGGAAGCCCACCAGGTCAGGGGGAAGGTCCCCGG 57

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6
3 AAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGG 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/998,208
                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road/UW220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: 709 Swedeland Road/UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
UNDMER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24.6; DB; Pred. No. 23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 452
PRIOR APPLICATION DATA:
APPLICATION NAMER: 08/451,777
FILING DATE: 26-MAY-1995
APPLICATION NUMBER: PCT/40594/10825
FILING DATE: 32-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAMM: Eagle Alissa M.
REGISTRATION NUMBER: 37,126
REFERRNCE/DOCKET NUMBER: 17,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-06743-7/c; Sequence 7, Application PC/TUS9506743; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                     Sequence 7, Application US/08998208
Patent No. 5880105
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-998-208-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 40.3%;
Best Local Similarity 65.5%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 610-2.7
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              STREET: 709 Swedeland
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 7676 base I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                              RESULT 12
US-08-998-208-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
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OTHER INFORMATION: 20-853-415 : polymorphic base C or T
NAME/KEY: primer_bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : polymorphic base C or
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LOCATION: 45328...45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863...45883
OTHER INFORMATION: 20-842.rp
LOCATION: 76644...76664
OTHER INFORMATION: 20-853.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KET: PITIMET_BIDG

NAME/KET: PITIMET_BIDG

LCCATION: 1357.1377

OTHER INFORMATION: 20-828.rp complement

NAME/KET: PITIMET_BIDG

LCCATION: 12029.12050

COTHER INFORMATION: 17-42.pu

NAME/KET: PITIMET_BIDG

LCCATION: 12581..12603

LCCATION: 12581..12603

COTHER INFORMATION: 17-42.rp complement

NAME/KET: PITIMET_BIDG

LCCATION: 14992..15012

COTHER INFORMATION: 17-41.pu

NAME/KET: PITIMET_BIDG

LCCATION: 15460..15482
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                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 14271...15968
OTHER INFORMATION: exon 4
NAMENT: misc_feature
LOCATION: 15969..17969
OTHER INFORMATION: 3'regulatory region
                                                                                         NAME/KEY: misc_feature
LOCATION: 10946..12946
OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTHER INFORMATION: 17-41.rp complement NAME/KEY: primer_bind LOCATION: 42070..42090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 20-841-149
NAME/KEY: allele
LOCATION: 45442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 20-828-311 NAME/KEY: allele
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NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 12347
OTHER INFORMATION: 17-42-319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DITHER INFORMATION: 17-41-250
                                                                                                                                                                                         LOCATION: 12947..12958

OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                                        OTHER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: exon 3
                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 13470..13526
                                                                                                                                                                                                                                                                                                                                    LOCATION: 13641..13752
                                               ORGANISM: Homo sapiens
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LOCATION: 42218
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APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Salter-Cid, Luisa
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89.U52.CIP
CURRENT PELICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-22
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-16-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 40.3%; Score 24.6; DB 5; Length 7676; Best Local Similarity 65.5%; Pred. No. 23; Matches 36; Conservative 0; Mismatches 19; Indels 0
                                     ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREN APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yen, Frances
Denison, Blake
Bour, Barbara
Bibain, Bernard
Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                     CLASSIFCATION:
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 3-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50.268-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09750580 Patent No. 6455280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Yen, Fra
                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-06743-7
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US-09-750-580-1
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APPLICANT:
APPLICANT:
APPLICANT:
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OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC
                              APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENEER, Claire M.
APPLICANT: VENEER, John C.
TITLE OF INVENTION: DAS REQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 4366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NOS: 2
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 2
LEMETH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 39.7%; Score 24.2; D
Best Local Similarity 62.3%; Pred. No. 40;
Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: June 13, 2003, 06:01:06
Job time : 11.6452 secs
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mycobacterium tuberculosis
        APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3821367 A 3821367
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US-09-103-840A-2
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1 Similarity 70.2%; Pred. No. 29;
33; Conservative 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 TCGCTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGTC 59
                                      O'CHER INCORMATION: 20-853.rp complement
NAME/KEY: primer_bind
LOCATION: 1220. 1238
CTHER INCORMATION: 20-828-311.mis
O'THER INCORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240..1258
O'THER INCORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 12328..12346
O'THER INCORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348..12366
O'THER INCORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 12348..12366
O'THER INCORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 1222.12210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Primer. Did of the Comptement of the Carton: 42199. 42217

OTHER INFORMATION: 20-841-149.mis complement infoRMATION: 42219. 42237

OTHER INFORMATION: 20-841-149.mis complement infoRMATION: 4223. 45441

OTHER INFORMATION: 20-842-115.mis complement infoRMATION: 4543. 45441

OTHER INFORMATION: 20-842-115.mis complement infoRMATION: 20-842-115.mis complement infoRMATION: 20-842-115.mis complement infoRMATION: 20-842-115.mis complement infoRMATION: 20-842-115.mis complement infoRMATION: 20-853-415.mis
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OCHTER INFORMATION: 20-828-311.probe NAME/KEY: misc_binding LOCATION: 1235.12359
OTHER INFORMATION: 17-42-319.probe NAME/KEY: misc_binding LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe NAME/KEY: misc_binding LOCATION: 42205..15203
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCAPION: 15242...15260
OTHER INFORMATION: 17-41-250.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 20-842-115.probe NAME/KEY: misc_binding LOCATION: 77046..77070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 20-841-149.probe NAME/KEY: misc_binding LOCATION: 45430..45454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 20-853-415.probe
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US-09-103-840A-2/C
; Sequence 2, Application US/09103840A
; Patent No. 6284328
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer_bind
LOCATION: 77059..77077
NAME/KEY: primer_bind
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Best Local Similarity
Matches 33; Conserva
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0; Gaps

23;

DB 4; Length 4403765; Indels

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Sequence 2184, App
Sequence 179, App
Sequence 817, App
Sequence 9241, App
Sequence 2241, Appli
Sequence 4, Appli
Sequence 2228, Appli
Sequence 1, Appli
Sequence 5478, Appli
Sequence 5478, Appli
Sequence 5478, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Appli
Sequence 2, Appli
Sequence 1640, Ap
Sequence 67, Appl
Sequence 32, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 69, Appl
                                                                                                                   (without alignments)
4579.068 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                 June 13, 2003, 04:39:50; Search time 19.2903 Seconds
                                                                                                                                                                                                    1 acaaggcagaagtcggtgga.....gggggaaggtcccggtcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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10 US-09-826-581-2
10 US-09-96-352-1640
9 US-10-175-523-67
9 US-09-95-793A-32
9 US-09-95-793A-30
10 US-09-95-778A-30
10 US-09-95-778A-30
10 US-09-967-768A-301
10 US-09-80-107-2184
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10 US-09-80-107-2184
10 US-09-80-107-2184
10 US-09-80-107-228
10 US-09-75-817-4
10 US-09-861-364-4
10 US-09-861-364-4
10 US-09-861-361-4
10 US-09-861-361-4
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Maximum Match 100%
Listing first 45 summaries
                                                                   OM nucleic - nucleic search, using sw model
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seq length: 2000000000
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Match Length DB
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Perfect score:
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Maximum DB :
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US-09-764-891-5478 US-09-764-891-10205

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Sequence 154, App Sequence 19511, A Sequence 19511, A Sequence 55, App Sequence 1, Appl Sequence 11, Appl Sequence 12192, A Sequence 12192, A Sequence 12192, A Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 5637, Appl Sequence 5637, Appl Sequence 5637, Appl Sequence 298, Appl Sequenc	TED PROTEIN KINASE GAMMA 3 SU	Length 1647; Indels 0; Gaps 0; AGGGGAAGGTCCCCGGTCC 60
0. US-09-962-832-154 0. US-09-864-761-19511 0. US-09-764-8918-950 0. US-09-764-891-8575 0. US-09-764-891-8575 0. US-09-764-891-8575 0. US-09-10-198-846-9038 0. US-09-884-9038 0. US-09-894-298-16 0. US-10-198-846-4363 0. US-09-904-615-16 0. US-09-904-615-16 0. US-09-904-615-16 0. US-09-906-352-9061 0. US-09-960-352-9061 0. US-09-960-352-9061 0. US-09-981-5639 0. US-09-960-352-9061 0. US-09-960-352-9061 0. US-09-981-533 0. US-09-981-533 0. US-09-981-533 0. US-09-981-533 0. US-09-981-533 0. US-09-981-533 0. US-09-981-533 0. US-09-981-2938-298 0. US-09-981-735-757 0. US-09-981-735-757 0. US-09-981-735-738 0. US-09-981-735-738	ALICHMENTS . 09-826-581-5 dequence 5. Application US/09826581 stent No. US20020142310a1 stent No. US20020142310a1 stent No. US20020142310a1 APPLICANT: Andersson, Leif APPLICANT: Andersson, Leif APPLICANT: Andersson, Leif APPLICANT: Warklund, Stefan TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE FILE REFERENCE: 11145-007001 CURRENT FILING DATE: 2000-04-07 FRICH APPLICATION NUMBER: US 60/195,665 PRIOR APPLICATION NUMBER: US 60/195,665 PRIOR APPLICATION NUMBER: US 60/195,665 PRIOR FILING DATE: 2000-04-07 SUMMER OF SEQ ID NOS: 14 SUMMER OF SEQ ID NOS: 14 SUMMER OF SEQ ID NOS: 14 SUMMER OF SEQ ID NOS: 14 CONGANISM: Homo sapiens FRATURE: NAME/KEY: CDS LOCATION: (20)(1486)	ore 61; DB 10; ed. No. 3.1e-11; Mismatches 0; AdGGGGGCACCAGGTC
302250 10 139 100 1448 9 3 14044 9 3 14044 9 6 140 10 10 10 10 10 10 10 10 10 10 10 10 10	RESULT 1 US-09-826-581-5 Sequence 5, Application US/09826581 Patent No. US20020142310A1 APPLICANT: Andersson, Leif APPLICANT: Luthman, L. Helder APPLICANT: Marklund, Stefan TITLE OF INVENTION: VARIANTS OF THE HUN TITLE OF INVENTION: VARIANTS OF THE HUN TITLE OF INVENTION: VARIANTS OF THE HUN TITLE OF INVENTION WIMBER: US/09/826, SOFTWART FILMS DATE: 2001-04-05 PRIOR PRIOR PLICATION NUMBER: US 60/195,66; PRIOR FILMS DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 14 SOFTWARE: FRASEQ for Windows Version SEQ ID NO 5 LENGTH: 1647 TYPE: DAA ORGANISM: Homo sapiens PRANTE: US LOCATION: (20)(1486) US-09-826-581-5	Query Match Best Local Similarity 100.0%; Sc Matches 61; Conservative 0; Oy 1 ACAAGGCACAAGTCGGTGGAGGA Oy CAAGGCACAAGTCGGTGGAGGA Oy 61 A 61 Db 260 A 260 Cy 61 A 61 Cy 61 Cy 61 A 61 Cy 61 A 61 Cy 61 A 61 Cy 61 A 61 Cy 61 A 61 Cy 61 A 61 Cy 61 A 61 Cy 61 A 61 Cy 61 A 61 Cy 61 A 61 Cy 61 Cy 61 A 61 C
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220 221 222 222 224 224 224 225 224 227 227 227 227 227 227 227 227 227	SULT 1 -09-826-581-5 Sequence 5, Applicatio APPLICAMT: 0. US200201423 GENERAL INFORMATION: APPLICAMT: Adersson, APPLICAMT: Marklund, TITLE OF INVENTION: V FILE REFERENCE: 11145 CURRENT APPLICATION IN FILE OF INVENTION: V CURRENT APPLICATION IN PRIOR FILING DATE: D ONRENT FILING DATE: FRICH FILING DATE: 20 NUMBER OF SEQ ID NOS: SEQ ID NO 5 LENGTH: 1647 TYPE: DNA ORGANISM: HOMO SADIE FRATURE: FRATURE: CORTION: (20)(14 -09-826-581-5	Query Match Best Local Matches 6 My 1 Db 200 Qy 61 Db 260 US-09-826-581 US-09-826-581 Sequence 2, ; Patent No. 1
0 00 00 0000	8 - SD - SD - SD - SD - SD - SD - SD - S	O O O O O O O O O O O O O O O O O O O

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Sequence 3.2 Application US/09995793A

Sequence 3.2 Application US2003005446A1

GENERAL INFORMATION:
APPLICANT: Webor, Bernard H.F.
TITLE OF INVENTION: NO. US20030054446A1e1 retina-specific human proteins C7orf9, (
FILE REFERENCE: 033488-001
CURRENT RILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 60/253,751
PRIOR PAPLICATION NUMBER: 60/253,751
PRIOR PAPLICATION NUMBER: 60/253,751
PRIOR PAPLICATION NUMBER: 60/253,751
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
SOFTWARE: So
TYPE: DNA
TYPE: DNA
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TYPE: DNA
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APPLICANT: Rajan, Prithi

TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3235/1/195-1083
CURRENT PRILING DATE: 2002-06-18
PRIOR PELICATION NUMBER: US 60/299,151
PRIOR APPLICATION NUMBER: US 60/299,151
PRIOR APPLICATION NUMBER: US 60/3917,828
PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-11-18
PRIOR FILING DATE: 2002-01-18
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tive 0; Mismatches 20; Indels
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OTHER INFORMATION: genomic DNA, Exon from 101 to 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73759 AAGGCAGAAGTTGCAGGAGGAAGGGGTTCCACCAG 73725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.3%; Score 27; DB 85.7%; Pred. No. 2.2; iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 64.99
Matches 37; Conservative
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CORGANISM: Mus musculus
US-10-175-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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US-09-995-793A-32
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                                                                           APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION. VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REPERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR PILING DATE: 2000-04-07
SOFTWARE FEASTED AND: 14
SOFTWARE FEASTED FOR Windows Version 4.0
SEQ ID NO 2
LENGTH: 989
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Patent No. US2002013713941
GENERAL INFORMATION:
Patent No. US2002013713941
GENERAL INFORMATION:
BAPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Ngqappan
APPLICANT: Mathialagan, Ngqappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
. ORGANISM: Bos taurus
: OTHER INFORMATION: Clone ID: 08-LiH188-005-Q1-E1-H7
US-09-960-352-1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.6%; Score 51, DB 10; 1
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 51; Conservative 0; Mismatches 0;
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Publication No. US20030096264A1
GENERAL INFORMATION:
APPLICANT: Brockman, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evans, David
Hook, Derek
Klimczak, Leszek
Laeng, Pascal
Palfreyman, Michael
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Matches 40; Conservative
                                                                    APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-2
                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 A 188
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US-09-960-352-1640
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APPLICANT:
APPLICANT:
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APPLICANT:
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5 GGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCCA 61
TITLE OF INVENTION: Methl and Meth2 Polynucleotides and Polypeptides CURRENT APPLICATION NUMBER: US/09/373,658
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 125
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 69
LENGTH: 8670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 CAGAAGTCGGTGGAGGGAAGGCCACCAGGTCAGGGGGAAGGTCCCCGGT 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Sequence 2184, Application US/09880107 |
| Sequence 2184, Application US/09880107 |
| Patent No. US20020142981A1 |
| GENERAL INFORMATION: |
| APPLICANT: Horne, Darci T |
| APPLICANT: Scherf, Uwe |
| APPLICANT: Gene Logic, Inc. |
| TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer |
| FILE REFERENCE: 44921-5028-W0 |
| CURRENT APPLICATION NUMBER: US 60/211,379 |
| PRIOR APPLICATION NUMBER: US 60/211,379 |
| PRIOR FILING DATE: 2000-106-14 |
| PRIOR FILING DATE: 2000-106-14 |
| PRIOR FILING DATE: 2000-106-14 |
| PRIOR FILING DATE: 2000-10-02 |
| SOFTWARE: PREACTION NUMBER: US 60/237,054 |
| PRIOR FILING DATE: 2000-10-02 |
| SOFTWARE: PREACTION NUMBER: US 60/237,054 |
| PRIOR FILING DATE: 2000-10-02 |
| SOFTWARE: PREACTION NUMBER: US 60/237,054 |
| PRIOR FILING DATE: 2000-10-02 |
| SOFTWARE: PREACTION NUMBER: US 60/237,054 |
| PRIOR FILING DATE: 2000-10-02 |
| SOFTWARE: PREACTION NUMBER: US 60/237,054 |
| PRIOR FILING DATE: 2000-10-02 |
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US-09-880-107-2184
                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 9; Length 8670;
Pred. No. 12;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Unknown Organism:Unknown US-09-373-658-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels
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40.7%; Score 24.8; Di
Best Local Similarity 67.3%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches
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; Patent No. US20020142952A1
; GENERAL INFORMATION:
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Resnick, Richard J.
Gulukota, Kamalakar
Graham, James R.
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Best Local Similarity 64.9%;
Matches 37; Conservative
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Clark, Hilary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-822-830A-179
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LENGTH: 33795
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APPLICANT:
APPLICANT:
APPLICANT:
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Fatent No. US20020150877al
GENERAL INFORMATION:
FATENCE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
FRICH APPLICATION NUMBER: US/60/236,109
FRICH APPLICATION NUMBER: US/60/236,034
FRICH ROBATE: 2000-09-28
FRICH ROBATE: 2000-09-28
FRICH ROBATE: 2000-09-28
FRICH ROBATE: 2000-09-28
FRICH FILING DATE: 2000-09-28
FRICH FILING DATE: 2000-09-28
APPLICANT: Stoehr, Heidi
TITLE OF INVENTION: No. US20030054446Alel retina-specific human proteins C7orf9, C12d
FILE REPERENCE: 033488-001
CURRENT APPLICATION NUMBER: US/09/995,793A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 60/253,751
PRIOR APPLICATION NUMBER: 00/253,751
PRIOR FILING DATE: 2000-11-29
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
LENGTH: 1188
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
; OTHER INFORMATION: artificial sequence, Translation start at 347, stop at 604
US-09-995-793A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 9; Length 1188;
Pred. No. 15;
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Publication No. US20030092900A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 325
SOFTWARE: Patenlin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.94
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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US-09-967-768A-301/c
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US-09-373-658-69/c
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APPLICATION NUMBER: 60/228,924
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 179
LENGTH: 2996
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24.6; DB 10; Length 2996;
Pred. No. 19;
0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 817, Application US/10091572
Publication No. US20030054373A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA118C1
CURRENT APPLICATION NUMBER: US/10/091,572
CURRENT FILING DATE: 2002-03-07
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PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 06/179,065
PRIOR FILING DATE: 2001-01-31
PRIOR PLING DATE: 2000-01-31
PRIOR PLING DATE: 2000-01-31
PRIOR PLING DATE: 2000-06-28
PRIOR PLING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR PLING DATE: 2000-06-14
PRIOR PLING DATE: 2000-06-14
PRIOR PLING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR PLING DATE: 2000-07-16
PRIOR PLING DATE: 2000-07-16
PRIOR PLING DATE: 2000-07-16
PRIOR PLING DATE: 2000-07-16
PRIOR PLING DATE: 2000-07-16
PRIOR PLING DATE: 2000-07-14
PRIOR PLING DATE: 2000-07-14
PRIOR PLING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,267
PRIOR APPLICATION NUMBER: 60/225,267
PRIOR APPLICATION NUMBER: 60/225,270
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-08-14
PRIOR PLING DATE: 2000-08-14
PRIOR PPLICATION NUMBER: 60/225,270
PRIOR PLING DATE: 2000-09-17
PRIOR PLING DATE: 2000-09-17
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
PRIOR PPLICATION NUMBER: 60/235,834
PRIOR PPLICATION NUMBER: 60/235,834
PRIOR PPLICATION NUMBER: 60/235,834
PRIOR PPLICATION NUMBER: 60/235,834
PRIOR PPLICATION NUMBER: 60/235,834
PRIOR PPLICATION NUMBER: 60/235,834
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APPLICATION NUMBER: 60/234,223
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 65.5%;
Matches 36; Conservative 0
                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-179
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PRIOR APPLICATION NUMBER: 60/229,343
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR PELICATION NUMBER: 60/229,345
PRIOR PELICATION NUMBER: 60/229,287
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/239,13
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-05
PRIOR PILING DATE: 2000-09-05
PRIOR PILING DATE: 2000-09-05
PRIOR PILING DATE: 2000-09-05
PRIOR PILING DATE: 2000-09-05
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PRIOR PILING DATE: 2000-09-05
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PRIOR FILING DATE: 2000-10-02
PRIOR PLING DATE: 2000-10-02
PRIOR PLING DATE: 2000-10-02
PRIOR PLING DATE: 2000-10-13
PRIOR PLING DATE: 2000-10-13
PRIOR PLING DATE: 2000-10-13
PRIOR PLING DATE: 2000-10-13
PRIOR PLING DATE: 2000-10-13
PRIOR PLING DATE: 2000-10-13
PRIOR PLING DATE: 2000-10-13
PRIOR PLING DATE: 2000-10-0-19
PRIOR PLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241, 787
                                                                                                                                                                                                                                                                                                                                                                                                                       OR APPLICATION NUMBER: 60/236, 327

OR FILING DATE: 2000-09-29

OR FILING DATE: 2000-09-29

OR FILING DATE: 2000-09-29

OR FILING DATE: 2000-10-20

OR APPLICATION NUMBER: 60/244,617

OR APPLICATION NUMBER: 60/225, 268

OR FILING DATE: 2000-10-10

OR APPLICATION NUMBER: 60/225, 268

OR FILING DATE: 2000-09-29

OR APPLICATION NUMBER: 60/251, 868

                                                                                                                                                                                                                            DR APPLICATION NUMBER: 60/220,964

DR FILING DATE: 2000-07-26

DR APPLICATION NUMBER: 60/241,809

DR FILING DATE: 2000-10-20

DR APPLICATION NUMBER: 60/249,299

DR FILING DATE: 2000-11-17
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R APPLICATION NUMBER: 60/237,037

R FILING DATE: 2000-10-02

R APPLICATION NUMBER: 60/237,040

R FILING DATE: 2000-10-02

R APPLICATION NUMBER: 60/240,960
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PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
                     APPLICATION NUMBER: 60/224,518
FILING DATE: 2000-08-14
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APPLICATION NUMBER: 60/237,038
FILING DATE: 2000-10-02
                                                    FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/236,369
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APPLICATION NUMBER: 60/234,997
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APPLICATION NUMBER: 60/229,343
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APPLICATION NUMBER: 60/249,210
                                                                                                                                                                 APPLICATION NUMBER: 60/224,519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/236,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/249,216
                                                                                                                                 FILING DATE: 2000-09-29
                                                                                                                                                                                             FILING DATE: 2000-08-14
2000-08-30
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us-09-826-581-5_copy_200_260.rnpb

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PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/226,681
PRIOR APPLICATION NUMBER: 60/225,759
PRIOR PLING DATE: 2000-08-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-16
PRIOR PELING DATE: 2000-09-16
PRIOR PELING DATE: 2000-10-17
PRIOR PELING DATE: 2000-11-17
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
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PRIOR PELING DATE: 2000
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FILING DATE: 2000-10-20
FILING DATE: 2000-10-20
PAPPLICATION NUMBER: 60/241,786
FILING DATE: 2000-10-20
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APPLICANT: DUMBAR ATHER DUMBLES, DEGLES APPLICANT: DUMBER: USUGE APPLICANT: DUMBER: USUGE APPLICANT: BOUGUELER, AYMERIC TITLE OF INVENTION: APOLIPOPROTEIN A-IV-RELATED PROTEIN: POLYPEPTIDE, POLYNOLEOT TITLE OF INVENTION: APOLIPOPROTEIN A-IV-RELATED PROTEIN: POLYPEPTIDE, POLYNOLEOT TITLE OF INVENTION: SEQUENCES AND BIALLELIC MARKERS THEREOF.

FILE REFERENCE: GENSET. 50CP2C
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR APPLICATION NUMBER: PCT/1B99/02058
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-22
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEX ING DATE: 1999-06-25
NUMBER OF SEX ING DATE: 1999-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9241, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
    APPLICANT: Rosen et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
    FILE REFERENCE: PCOOL
    CURRENT APPLICATION NUMBER: US/09/764,891
    CURRENT FILING DATE: 2001-01-17
    Prior application data removed - consult PALM or file wrapper
    NUMBER OF SEQ ID NOS: 10231
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 9241
    LENGTH: 5312
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APPLICANT: Bour, Barbara
APPLICANT: Bihain, Bernard
APPLICANT: Dimas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.3%; Score 24.6; DB Best Local Similarity 65.5%; Pred. No. 18; Matches 36; Conservative 0; Mismatches
                                                                                                                                                                                            Query Match 40.3%; Score 24.6; D. Best Local Similarity 65.5%; Pred. No. 18; Matches 36; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09842364; Publication No. US20030032783a1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yen-Potin, Frances APPLICANT: Denison, Blake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-764-891-9241
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US-09-842-364-4
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NAME/KRY: courtict

LOCATION: 1447

OTHER INFORMATION: 17-40-202; G in ref genbank AC007707

NAME/KRY: primer_bind
LOCATION: 1.11022

NAME/KRY: primer_bind
LOCATION: 53.11575

OTHER INFORMATION: 17-42.pu

NAME/KRY: primer_bind
LOCATION: 699.11120

OTHER INFORMATION: 17-42.pu

NAME/KRY: primer_bind
LOCATION: 1246.11267

OTHER INFORMATION: 17-40.pu

NAME/KRY: primer_bind
LOCATION: 1246.12267

OTHER INFORMATION: 17-40.pu

NAME/KRY: primer_bind
LOCATION: 1632.12651

OTHER INFORMATION: 17-40.pu

NAME/KRY: primer_bind
LOCATION: 1632.12651

OTHER INFORMATION: 17-40.pu

NAME/KRY: primer_bind
LOCATION: 1632.12651

OTHER INFORMATION: 17-41.pu

NAME/KRY: primer_bind
LOCATION: 300.1318

OTHER INFORMATION: 17-41.pu

NAME/KRY: primer_bind
LOCATION: 300.1318

OTHER INFORMATION: 17-41.pu

NAME/KRY: primer_bind
LOCATION: 300.1318

OTHER INFORMATION: 17-42.319.mis complement
LOCATION: 300.1318

OTHER INFORMATION: 17-42.319.mis complement
LOCATION: 301.3318

OTHER INFORMATION: 17-41.250.mis complement
LOCATION: 301.3312

OTHER INFORMATION: 17-41.250.mis complement
LOCATION: 301.3312

OTHER INFORMATION: 17-41.250.mis complement
LOCATION: 301.331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1241
OTHER INFORMATION: 17-39-343 : I in ref genbank AC007707
NAME/KEY: conflict
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 3213
OTHER INFORMATION: 17-41-250 ; polymorphic base C or
                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 2243..3940
OTHER INFORMATION: exon 4
NAME/KEY: misc_feature
LOCATION: 3941..5381
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 919..930
OTHER INFORMATION: exon 1
NAME/KEY: exon
                                                                                                                                                                                                                                                                                             LOCATION: 1442..1498
OTHER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1613.,1724
OTHER INFORMATION: exon 3
                                                                     ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon
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SEQ ID NO 4
LENGTH: 5381
                                                   TYPE: DNA
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                                                                                                 FEATURE:
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APPLICANT:
APPLICANT:
APPLICANT:
Dumas Milne Edwards, Jean-Baptiste
APPLICANT:
Bougueleret, Lydie
APPLICANT:
Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWT)
FILE REFRENCE:
BOUGUERENT APPLICATION NUMBER: US/09/751,877
CURRENT APPLICATION NUMBER: US/09/751,877
CURRENT APPLICATION NUMBER: US/09/751,877
SOFTWARE: Patent.pm
SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 4
LENGTH: 5381
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                                                                                                                                                Query Match 40.3%; Score 24.6; DB 9; Length 5381; Best Local Similarity 70.2%; Pred. No. 18; Matches 33; Conservative 0; Mismatches 14; Indels 0.
                                                                                                                                                                                                                                                                               13 TCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGGTC 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1447
OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
MANE/KEY: Primer bind
LOCATION: 1..11022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: 319
OTHER INFORMATION: 17-42-319 : polymorphic base C or
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OTHER INFORMATION: 17-41-250 : polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
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OTHER INFORMATION: exon 4
NAME/FET: misc_feature
LCCATION: 3941..5381
OTHER INFORMATION: 3'regulatory region
CTHER INFORMATION: 17-42-319.probe NAME/KEY: misc_binding LOCATION: 3201..3225 CTHER INFORMATION: 17-41-250.probe US-09-842-364-4
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09751877
Patent No. US20020142949A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KET: exon
LCARTON: 919.030
OTHER INFORMATION: exon 1
NAME/KEY: exon 1.442..1498
OTHER INFORMATION: exon 2
NAME/KEY: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bihain, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1613..1724
OTHER INFORMATION: exon 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: conflict
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US-09-751-877-4
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Gaps

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Length 8095; Indels

40.3%; Score 24.6; DB 10; 65.5%; Pred. No. 17; tive 0; Mismatches 19;

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3 AAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGG 57
                         ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L76927
US-09-880-107-2228
                                                                                                                                                                                                                                                                                                               Search completed: June 13, 2003, 09:00:39 Job time : 20.2903 secs
                                                                                    Query Match
Best Local Similarity 65.59
Watches 36; Conservative
FEATURE:
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Sequence 2228, Application US/09880107
Sequence 2228, Application US/09880107
Sequence 2228, Application
Sequence Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Uwe
TILE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REPERBUCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
SUMMER OF SEC ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.3%: Score 24.6; DB 10; Length 5381; 70.2%: Pred. No. 18;
Live 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       613 TCTCTGTTGGTGGGCCAGCCAGGTCAGTGAAAGGTC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 TCGCTCGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGGTC 59
               COCATION: 553.11575

COCATION: 553.11575

OTHER INFORMATION: 17-42.rp complement
NAME/KEY PITMEL_Dind
LOCATION: 899.11920

OTHER INFORMATION: 17-39.pu
NAME/KEY PITMEL_Dind
LOCATION: 1246.1267

OTHER INFORMATION: 17-40.pu
NAME/KEY: PITMEL_Dind
LOCATION: 1441.12461

OTHER INFORMATION: 17-40.pu
NAME/KEY: PITMEL_Dind
LOCATION: 1632.12651

OTHER INFORMATION: 17-40.pu
NAME/KEY: PITMEL_Dind
LOCATION: 2644.13984

OTHER INFORMATION: 17-41.pu
NAME/KEY: PITMEL_Dind
LOCATION: 2644.13984

OTHER INFORMATION: 17-41.pu
NAME/KEY: PITMEL_Dind
LOCATION: 342...14454

OTHER INFORMATION: 17-41.rp complement
NAME/KEY: PITMEL_Dind
LOCATION: 320...38

OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: PITMEL_Dind
LOCATION: 320...38

OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: PITMEL_Dind
COCATION: 330...38

OTHER INFORMATION: 17-41-250.mis
NAME/KEY: PITMEL_Dind
COCATION: 3314...3232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 17-42-319, probe NAME/KEY: misc_binding CATION: 3201.3225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: 17-41-250.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 70.28 Matches 33; Conservative
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  NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-880-107-2228/c
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LENGTH: 8095
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US-09-751-877-4
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June 13, 2003, 01:49:14 ; Search time 192.613 Seconds (without alignments) 9216.782 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                 US-09-826-581-5_COPY_529_589
61
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a

Andersson, L., Luthman, H. and Marklund, S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 2 18-OCT-2001;

AF214519 Homo sapia AC027416 Homo sapia AC009974 Homo sapia AC09977 Homo sapia AC09977 Homo sapia AC09977 Homo sapia AK099774 Homo sapia AK099774 Homo sapia AK099779 Substance AK39833 Sequence AK39833 Sequence AK39833 Sequence AK39833 Sequence AK39833 Sequence AK39833 Sequence AK39834 Sequence AK39834 Sequence AK39834 Sequence AK09807 Rattus no AC122703 Rattus no AC12707 Rattus no AC107063 Wacobacteria AC12865 Mus muscu AE007063 Wacobacteria AC125075 Mus muscu PAT 02-NOV-2001 AC091120 Leishmani AC121230 Leishmani Continuation (3 of AE00078 Rhizobium AC09721 Homo sapi AC107873 Homo sapi AC10429 Rattus no AC106429 Rattus no Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AX281579 Sequence AX099776 Sequence Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AL159376 STS Description linear DNA ALIGNMENTS SUMMARIES Sequence 2 from Patent W00177305. AX281579 AX398339 AX099804 AF29804 AF36804 AF36381 AC128070 AC02802 AC05802 AC05893 AC12573 AC05893 AC12573 AC05893 AC05893 AC05893 AF214519 AC027416 AC009974 HSA249977 AC091120 AC121230 AC124396_2 AC099721 AC007873 AX398335 AX398337 AF214520 AX281579.1 GI:16608830 B 100.0 100.0 100.0 100.0 100.0 100.0 1115 100.0 1115 100.0 1115 100.0 1115 100.0 1115 100.0 1117 1229 1373 1373 1373 1373 1373 1373 1373 1474 1774 1 Length Match human. DEFINITION ORGANISM ACCESSION VERSION REFERENCE AUTHORS TITLE JOURNAL KEYWORDS SOURCE RESULT 1 AX281579 Result LOCUS õ 0 0 000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSPQAPFPKLGMDDELRKPGAQIYMRFWQEHTCYDAMATSSKLYIFDTMLEIKKAFFA
LVANGVRAAPLMDSKKQSFVGMLITTUP! ILVI.HRYYRSPLVQIYEIBQHKIETWREIY
LQGCFKPI.VSISPNDSI.FEAVYTLJKNRIHKI.PVLDPVSGNVLHILTHKRLLKFILHIF
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VGLYSRDVTHLAAQOTVHLDMSVGEBLRQRTLCLEGVLSCQPHESLGEVIDRIARE
QVHRLVILVBETQHLLGVYSLSDTLGALVSPRGIDALGA"
1 502 c 462 g 337 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 3.3e-10;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 61; Conservative 0; Mismatches 0;
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Sequence 5 from Patent W00177305.
AX281582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
20. 1489
                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
306 c 286 g 168
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RESULT 3 AX099776

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ISPNDSLFERNYTLIKNR.HRLPYLDPYSGNYLAILTHKRLIKFLHIFGSLLERPSFL
YRTIGDLGIGTFRDLAAVLETAPILTALDIFUDRNYSALPVVNECGQVGLYSRFDVI
HLAAQOTYNHLDANSVGEALRQRTLCLEGVLSCQPHESLGEVJDRIAREQVHRLVLVDB
TQHLLGVVSLSDILQALVLSPAGIDALCA"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 2115)

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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Variants of the gamma chain of ampk, dna sequences encoding the
                                                                                                                                                                                                                                                                                                                                                           same, and uses thereof
Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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l Similarity 100.0%; Pred. No. 3.4e-10;
61; Conservative 0; Mismatches 0;
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AX099776 2109 bp
Sequence 3 from Patent W00120003.
AX099776
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Signature S. Linton.L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Anderson,S., Baldwin,J., Barna,N., Barstien,V., Beda,F., Boukhqaiter,B., Burwa,A., Eurkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Dolye,M., Ferreira,P., Fitzhugh,W., Gage,D., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Borton,L., Klein,J., LaRocque,K., Lamazares,R., Janders,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,R., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McCurk,A., McKernan,K., McPheters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Norman,C.H., O'Connor,T., O'Connor,T., O'Neil,D., Ollvar,T.M., Ollvar,T.M., Ollvar,T.M., Ollvar,T.M., Chiley,R., Rogov,P., Rothman,D., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talanas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Venner, R., And, Zodv, Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
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GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDFTQHLLGVVSLSDILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC027416 152129 bp DNA linear HTG 07-JUN-2000
Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
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SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152129)
/product="AMP-activated protein kinase gamma subunit"
/protein_id="AAF73987.1"
/db_xref="GI:8215682"
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AC027416.2 GI:8317289
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO Sapiens.
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PEPGGGEGRRRPTAESTGLEALFPRYTPLAQADBAGVGTPPTGMDCLESDCTBASAG
SSTDDVELATEFPAMFCELEGLLEERPALCLSPQAPFPKLGMDDELKRFGAQIYM
RENGEHTCYDAMSTSKLVJFDYMLBIKKAFFALVANGVRAAPLUMSKKQSFVGMLTI
TDFILVLHRYTRSPLVQIYELEQHKLETWREFYLQCFKPLVSISPNDSLFRWYTLI
TNRTHHLAVLDDVSGNVHLHTTWRLLKPHTFGSLLPRPSFLYFTIGLGFRDL
AVVETAPILTAALDFVDRRYSALDVVURGCQVVGIYSREDYIHLAAQQTXHHLDMSV
GEALRQRTLCLEGVLSCQPHESLGEVIDRIARREQVHRLVLVDETQHLLGVVSLSDILQ
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Milan,D. Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Tannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Galilard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
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                              /note="unnamed protein product"
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1. ,2115
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Science 288 (5469), 1248-1251 (2000)
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/protein_id="CAC35801.1"
                                                                                                        /db_xref="GI:13538837"
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AF214519
AF214519.1 GI:8215681
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66596 66695; gap of 100 bp 66696 73218; contig of 6523 bp in length 73219 77115; contig of 3797 bp in length 77215; gap of 100 bp 77319 77115; contig of 3797 bp in length 77216 7725; gap of 100 bp 77316 77215; gap of 100 bp 100 bp 85123 93314; contig of 8192 bp in length 93315 93414; gap of 100 bp 100 bp 101294 113090; contig of 1779 bp in length 101294 113090; contig of 1779 bp in length 113091 gap of 100 bp 113191; gap of 100 bp 113191; gap of 100 bp 113191; gap of 100 bp 113191; and specified in length 11391 13391; contig of 14441 bp in length 11393 13393; contig of 14441 bp in length 13393 137937; gap of 100 bp 13393 137937; gap of 100 bp 13393 137937; gap of 100 bp 13393 137937; gap of 100 bp 13393 137937; gap of 100 bp 13393 137937; gap of 100 bp 13938 137937; gap of 14192 bp in length.
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/clone_lib="RPCI-11 Human Male BAC"
1. .1005
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15144. .17123
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17224. .19466
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24420. .27059
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27160. .30170
.Anote="assembly_fragment"
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51386. 55871
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55972. 60595
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50696. ,66595
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    Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                      Center Clone name: 504.02.11

Sequencing vector: Mais; M77815.

Sequencing vector: Mais; M77815.

Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 135376 bases at least Q40

Consensus quality: 14503 bases at least Q30

Consensus quality: 14603 bases at least Q20

Insert size: 161000; agarose-fp

Insert size: 149029; sum-of-contigs

Quality coverage: 3.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4402: contig of 1297 bp in length
4403 2502: gap of 100 bp
2503 3823: contig of 1329 bp in length
3824 3923: gap of 100 bp
3924 5020: contig of 1321 bp in length
5021 5120: gap of 100 bp
5121 6161: contig of 1041 bp in length
6162 6261: gap of 100 bp
6262 7547: contig of 100 bp
7548 7647: gap of 100 bp
                                                                     Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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12657 15043; contig of 2387 bp in length
15044 15143; gap of 100 bp
15144 17123; contig of 1980 bp in length
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38179; contig of 4111 bp in length
38279; gap of 100 bp
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46365: contig of 3899 bp in length
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60595: contig of 4624 bp in length
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                                                                                                                    ----- Project Information
                                                                                                                                        Center project name:
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                                                  Center code: WIBR
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10084 1255
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ACUU9974 206854 bp DNA linear PRI 09-JAN-2002
Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
AC009974
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Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 206854)
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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4444 Forest Park Parkway, St. Louis,
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Catarrhini; Hominidae; Homo.
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459119
Unpublished (2001)
3 (bases 1 to 206854)
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                                                                                                                                                                                                                     100.0%; Score 61; DB 2; I
llarity 100.0%; Pred. No. 4.1e-10;
Conservative 0; Mismatches 0;
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/note="assembly_fragment"
85123 . 93314
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93415 . 101193
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/note="assembly_fragment"
101294. .113090
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73319. .77115
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Submitted (08-NOV-2001) Genome
University School of Medicine,
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Mammalia; Eutheria; Primates;
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Sulston, J.E. and Waterston, R.
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5 (bases 1 to 206854)
Waterston, R.H.
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenco, M., Catanese, J.J. and de Jong, P.J. (1988) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswall Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this
                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

Location/Qualifiers

1. 206854
                                                                                                                                                                                                                                                                                                                                                                                                                                           all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >> 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
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                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted:
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/note="match to EST BI059713 (NID:914467240)"
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/note="match to EST BG477625 (NID:913409904)"
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    .37
    /note="match to EST AW880850 (NID:g8042860)"

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/note="match to EST BE314060 (NID:99134719)"
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence, see http://genome.wustl.edu/gsc
                                                                                                            Center project name: H_NH0459119
                                                                             Summary Statistics
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/db_xref="taxon:9606"
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1. .37 /note="similar to Homo sapiens EST BI114348 (NID:q14565249)"

misc_feature

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LSPQAPFPKLGWDDELRKPGAQIYWRFIEEHTCYDAMATSSKLVIFDTMLEIKKAFFA
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LJGCFRPLVSISPNDSLFEBAYTLITNRIHRLDFVLDPVSGNVLHILTHRELKFRLHF
GSLLERPSTLZFTJODGIGTFRDLAVLETAPILTALDIFVDRRYSALPVVNCGQY
VGLYSRFDVIHLAAQQTYNHLDMSVGEALRKRTLCLEGVLSCQPHESLGEVIDRIARR
QVHRLVLVDFTQHLLGVVSLSDILQALVLSPAGIDPSGPEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit (AMPK gamma 3 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MEPGLEHALRRTPGWSSLGGSEHQEWSFLEQEWSSRPSPAVTS
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DPAGWGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthbria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2290)
Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of Amy-activated protein kinase gamma-subunit lisoforms and their role in Amy binding
Blochem. J. 346 Pt 3, 659-669 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
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/product="Auta-activated protein kinase gamma 3 subunit"
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                                       /note-"match to EST AA043371 (NID:g1521226) zk53e10.rl*
                  /note="match to EST A1656812 (NID:g4740791) tt54b06.x1"
                                                                                                                                                                                                                                                                                   1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
                                                                                                                                                                                                                                           Gaps
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Direct Submission
Submitted (12-00T-1999) Carling D., Cellular Stress Group, Mi
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
London, W12 ONN, UNITED KINGDOM

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="AMP-activated protein kinase regulatory
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                                                                                                                                                                                           Length 206854;
                                                                                   967. .1090
/note="similar to Homo sapiens EST BIll4348
(MD:914565249)"
967. .1085
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                                                                                                                                                                                           Score 61; DB 9; I
Pred. No. 4.1e-10;
                                                                                                                                                                                           Query Match 100.0%; Score 61; DB Best Local Similarity 100.0%; Pred. No. 4.1 Matches 61; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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22. .1500
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                                                                                                                                                      281. .344
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281. .344
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/note="match to EST AA043371 (NID:91521226) zk53e10.rl"
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594. .763
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                                         4 .37
/note="match to EST A1670836 (NID:94850567) wa04910.x1"
                                                                                                                                                                                                                                                                                                                            /note="match to EST BE047599 (NID:98364652) tz39c01.y1"
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594. .763
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/note="match to EST BG992568 (NID:g14396638)"
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281. .344
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/note-"match to EST BI059713 (NID:g14467240)"
594. .763
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                    'note="match to EST BE908408 (NID:g10402954)"
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281. .344
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281. .344
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281. .344
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/note="match to EST AW880850 (NID:g8042860)"
594. .763
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281. .344
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                                                                                                                                                                                                                                                                                   /note="match to EST AW880850 (NID:98042860)"
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(NID:914565249)"
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                                                                                   /note="match to EST C05773 (NID:g1502549)"
220. .221
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/product="AMP-activated protein kinase gamma subunit"
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HFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTI
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KNRIHRLPVLDPVSGAVLHILTHKRLIKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRYSALPVNETGGVVGLYSREDYIHLAQQITVHHDMNV
GEALRQRILCLEGVLSCQPHETLGEVIDRIYREQVHRIVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA*

580 c 535 g 376 t
                                                                                                                                               A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle Science 288 (5469), 1248-1251 (2000)
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Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 02-APR-2001
                                                       1 (bases 1 to 1873)
Milan, D., Geon, T., Looft, C., Amarger, V., Robic, A., Thelander, M.,
Rogel-Gaillard, C., Peul, S., Tannuccelli, N., Rask, L., Ronne, H.,
Luddstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P. L., Chardon, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGCTGGGATGAGGAACTGCGGAAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
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Sus scrofa
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Pred. No. 7.2e-06;
0; Mismatches 8; Indels 0
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AX099800
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/chromosome="15"
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mRNA, complete cds.
AF214520
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YRTIQDLGIGTFRDLAVVLETAPILTALDIEVDRRYSALPVVNETGQVVGLYSRFDVI
HLAAQQVTHLUMNVGEALNQRYLCLECVLSCQPHETLGEVIDRIVREQVHRLVLVDB
TQHLLGVYSLSDILQALVLSPRGIDALCA"
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/db_xref="G1:13538809"
/translation="MHRWQEHCYDAMATSSKLVIFDTMLEIKKRAFFALVANGVRAAP
LWDSKKQSFVGMLTITDFILVLHRYYRSPLVQ1YEIEEHKIETWREIYLGGGFKPLVS
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              same, and uses thereof
Patent: WO 0120003-A
PATENT: WO 0120003-A
PATENTIATUR NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variants of the gamma chain of ampk, dna sequences encoding the
                                                                         1 GGCTGGGATGACGAAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
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Pred. No. 7.2e-06;
0; Mismatches 8; Indels
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                                       Indels
Score 57.8; DB 9;
Pred. No. 4.1e-09;
0; Mismatches 2;
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/note-"unnamed protein product"
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/organism="Sus scrofa"
/db_xref="taxon:9823"
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GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAFLAEVDNPPTERDILPSDCAASAS
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
Patent: WW 0020360.A 1 14-WAR-2002;
Iowa State University Research Foundation, Inc. (US)
                                                                                                                                                                 Same, and uses thereof
Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                        Variants of the gamma chain of ampk, dna sequences encoding the
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                                                      Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus 1 (bases 1 to 1873)
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Best Local Similarity 86.9%;
Matches 53; Conservative
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TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALI
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GEALRQRTLCLEGVLSCQPHETLGEVIDRI VREQVHRLVLVDETQHLLGVVSLSDILQ
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Novel prkag3 alleles and use of the same as genetic markers reproductive and meat quality traits
Patent: WO 0220850-A 3 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
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Pred. No. 7.2e-06;
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 7 14 *MAR-2002,
IOWA State University Research Foundation, Inc. (US)
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 5 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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Sequence 5 from Patent W00220850.
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AX398337
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Matches 53; Conservative
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Search completed: June 13, 2003, 04:39:44 Job time : 194.613 secs

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GEALRGRILCLEGYLLGGVTLGGVTDRIVNETGQVHRLLGVVDSTGHLLGVVSESDILQ
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/note="unnamed protein product"
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PRKAG3 cDNA. Homo
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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AAD36459 AAD36460 AAD03321 AAA64228 AAT99682 AAT93737 AAS54367 AAS54367 AAS54367 AAS56883 AAL35338 AAL35338 AAL35338	AAZ27414 ABL19504 ABL19502 AAS74013 AAS74013 AAZ58005 AAZ58306 AAZ58306 AAZ58306 AAZ58306 AAZ58306 AAZ58306 AAZ58306 AAZ58306 AAZ58308 AAZ58308 AAZ58308 AAZ58308 AAZ58308 AAZ58308 AAZ61190 AAZ61190 AAZ61190 AAZ61190 AAZ61190	ALIGNMENTS BP. Kinase gamma obesity; sub	S 2 S
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/number= "Intron 4"

'note= "Causes P71A"

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                                                                                                                                                               New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                  The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a mino acid substitution of a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
 portion of intron 4"
                                                                                                                         Marklund S;
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230
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                                                                                                                                                                                                                  Example 1; Fig 2; 25pp; English.
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/label= "C230G"
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                                                           06-APR-2001; 2001WO-SE00765.
/note= "5'
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                                                                                                                         Luthman H,
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This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution of a G for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
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100.0%; Pred. No. 1.7e-12;
tive 0; Mismatches 0;
      /label= "T559C"
/note= "Silent variation"
1037
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/label= "C1037T"
/note= "Causes R340W"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 5; 25pp; English.
_ "T559C" -
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Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
                                                                                                      AAD03320 standard; cDNA; 2115 BP.
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                                                                                                                                        AAD03320;
                                                                     RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders sus diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalm E, Milan D, Robic A, Rogel-Gaillard C;
I, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is a cDNA encoding human adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 61; DB 22; Length 2109; 100.0%; Pred. No. 1.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
                                                                                                                                                       /*tag= b
/product= "Human Prkag3 protein"
1390..2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Fig 2; 71pp; English.
                                                                                                                                                                                                                                                                                                                  11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                  10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                                        /*tag= a
472..1389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Conservative
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                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Looft C,
                                                                                                                                                                                                                                                                                                                                                                                                                        ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-244810/25.
P-PSDB; AAE00221.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KALM E.
                                                                                                                                                                                                                                                WO200120003-A2.
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                                                   Homo sapiens.
                                                                                                                                                                                                                                                                               22-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KALM/)
                                                                                                                                                                                                                                                                                                                                                                                                                        (ANDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                          (LOOF/
                                                                                     Key
5'UTR
                                                                                                                                                                                         3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbobydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbobydrate metabolism disorders such as allabetes, obesity, and disorders associated with muscle metabolism countries in myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered aliele of PRKAG3 or activity and an animal and host call transformed with PRKAG3 or and it ransgenic animal and host call transformed with PRKAG3 or activity for detecting a functionally altered aliele of PRKAG3.
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in a sequence encoding the first cystathione beta synthase (CBS) domain
of PRKAG3 and is useful in gene therapy.
Human, gamma subunit; adenosine monophosphate-activated kinase; AMPK; FKKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Iannuccelli N, Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Human complete Prkag3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 65-68; 71pp; English.
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1..1395
/*tag= a
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                                                                                                                                                                                                                                            Homo sapiens
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(KALM/) KALM E.
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                                                                                                                                                                                                                                                                                   489 G 489
                                                                                                                                                                                                                                                                  61 G 61
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                                                                                                                                                                                                                                                                                                                                                                    13-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                   AAD03319;
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                               RESULT 6
AAD03319
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                                                                                                                                                                                                                                               PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robic A, Rogel-Gaillard C;
                                                             1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.
                                                                                                                                                                                                                                        gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                           0
                          Length 2115;
                                                                                                                                                                                                                      Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                           Indels
       Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                           "Sus scrofa PRKAG3 protein"
                         ch 100.0%; Score 61; DB 22; Similarity 100.0%; Pred. No. 1.8e-12; 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
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(ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..471
                                                                                                                                                              AAD03295 standard; cDNA; 1867 BP.
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18-MAY-2000; 2000EP-0401388.
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/product= ":
1390..1867
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472..1389
                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Looft C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-244810/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAE00220
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                                                                                                G 61
                                                                                                                  495 G 495
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                                                                                                                                                                                                   13-JUN-2001
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                                                                                                                                                                                                                                                                                             Sus scrofa
                         Query Match
Best Local S:
Matches 61,
                                                                                                61
                                                                                                                                                                                 AAD03295;
                                                                                                                                                                                                                                                                                                                 Key
5'UTR
                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                               RESULT 5
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Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRAG3 sequence and its functionally altered mutants are useful for the diagnostic preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dystunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMFK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robic A, Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48.2; DB 22;
Pred. No. 7.6e-08;
0; Mismatches 8;
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD03319 standard; cDNA; 1873 BP.
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86.9%;
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18-MAY-2000; 2000EP-0401388.
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/product= "
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nes 53; Conservative
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us-09-826-581-5_copy_529_589.rng

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1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCGTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
/standard_name= "Single nucleotide polymorphism (SNP)" replace (595, A /*tag= d
                                                                                                              /standard_name= "Single nucleotide polymorphism (SNP)"
                                                           "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger likely to The present sequence is pig wild-type PRRAG3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; plq; gene; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24; Length 1873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.0%; Score 48.2; DB 24;
86.9%; Pred. No. 7.6e-08;
Live 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                           Ciobanu DC, Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
                                                                                                                                                                                                                                                                                                                                      (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                         /standard_name=
replace (599, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Fig 1; 109pp; English.
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                                                                                                                                                                                                                                                            08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                          10-SEP-2001; 2001WO-US28283.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 86.9
mes 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAE22984.
                                                                                                                                                                                                                                                                                                                                                                         Rothschild MF,
                                                                                                                                                    WO200220850-A2
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                       variation
                                                                             variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD36457;
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                                                                                                                                                                                               The present sequence is a cDNA encoding pig adenosine monophosphate

(AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,

complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome

15. Mutation in Prkag3 results in an altered regulation of carbohydrate

metabolism, particularly in skeletal muscle PRKAG3 is useful as

therapeutic for treating carbohydrate metabolism disorders such

catabotty, and for restoring a normal AMPK function. PRKAG3 sequence

cutivity, and for restoring a normal AMPK function. PRKAG3 sequence

cutivity, and for restoring a normal AMPK function. PRKAG3 sequence

cutivity, and for restoring a normal AMPK function. PRKAG3 sequence

cutivity, and for restoring and prognosis of a metabolic disorder,

cutivity, and for restoring and prognosis of a metabolic disorder,

cutivity, and for restoring and prognosis of a metabolic disorder,

cutivity, and for activity altered metabolism cesulting

cutivity, and for a sequence encoding PRKAG3, are

greferably a carbohydrate metabolism resulting

cuseful for detecting a dysfunction of carbohydrate metabolism resulting

cuseful for detecting a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a

currently many consisting of PRKAG3 or its mutant, are useful for

screening compounds able to modulate AMPK activity, Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                     New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /standard_name= "Single nucleotide polymorphism (SNP)" replace (154, A) /*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.0%; Score 48.2; DB 22; Length 1873; 86.9%; Pred. No. 7.6e-08; Live 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Pig PRKAG3 wild-type protein" replace (89, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                              Claim 12; Page 62-64; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53; Conservative
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                   2001-244810/25.
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Best Local Similarity
Matches 53; Conserv
                                    P-PSDB; AAE00222.
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                                                                                                                                 myopathy
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                                                                                                                                                                                                                                                                                                                                                                                                Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                 /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
                                                  "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
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                                                                                                                                                                                                                                                                                                                       Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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    Location/Qualifiers
                                                                 replace (154, A)
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                                                                                                                                                                                                                      08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                                                                                                                       Rothschild MF, Ciobanu DC,
                                                                                                                                                                                          10-SEP-2001; 2001WO-US28283,
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                                                  /product-
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                                                                 variation
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AAD36459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase requlatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                           Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                               /*tag= a
/product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
replace (89, C)
                                                                                          /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                   Ciobanu DC, Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 89-91; 109pp; English.
                                                                                                                                                                                                                                                                                   (IOWA ) UNIV IOWA STATE RES FOUND INC
 Location/Qualifiers
1..1395
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Best Local Similarity 86.99
Matches 53; Conservative
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                                                              variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD36458;
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                                 /product= "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
replace (599, A)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                    /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Malek M, Plastow G;
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Pred. No. 7.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 102-104; 109pp; English.
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             Location/Qualifiers
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Matches 53; Conservative
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                                                                                             variation
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AAD03321
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                                                     /product= "Pig PRKAG3 polymorphic variant (PRKAG3-199)" replace (595, A) /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                    /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48.2; DB 24; Length 1873;
Pred. No. 7.6e-08;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Malek M, Plastow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 98-100; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            (IOWA ) UNIV IOWA STATE RES FOUND INC.
Location/Qualifiers
1..1395
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Best Local Similarity 86.9%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Rothschild MF, Clobanu DC,
                                                                                                                                                                                                                                                                                                      08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                                                                10-SEP-2001; 2001WO-US28283.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAE22987.
                                                                                                                                                                              WO200220850-A2
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                                                                                             variation
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AAD36460
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(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity, Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a sequence encoding the first cystathione beta synthase (CBS) domain PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                             monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
                                                                                                                                                                                                                                            Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMFK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered requiation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as suppathy and cardiovascular diseases, to modulate AMPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                             /product= "Sus scrofa Prkag3 splice variant"
                                                                                                                                                                                                                                                                                                                  New variants of the gamma subunit of vertebrate adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Chardon P;
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                                                                                                                                                                               (INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
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r, Le Roy P,
          Location/Qualifiers
1..1545
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                                                                                                                                             10-SEP-1999; 99EP-0402236
18-MAY-2000; 2000EP-0401388
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Matches 53; Conservative
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Gellin
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Iannuccelli N,
                                                                       WO200120003-A2.
                                                                                                                                                                                                                 (KALM/) KALM E.
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ID AAA6
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designated SMAK. SMAK is a caspase activated protein kinase. SMAK activated SMAK activated protein kinase. SMAK activated SMAK activated protein kinase. SMAK activates 2 signalling pathways that are involved in mediating apoptosis. It also mediates activate fiber dissolution through caspase-3-cleavage and functions to activate the stress activated protein kinases (cjun-amino terminal kinase (JMK) signalling pathway). SMAK proteins and polymucleotides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate SMAK production of antibodies, and in assays to identify modulators (aponists and antagonists) of SMAK expression and activity. The SMAK protein is associated with apoptosis and may play a role in preventing neoplasia development, lymphoproliferative conditions, inflammation, ischemia or strokes and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding a Ste20-related protein kinase designated SMAK, useful for the prevention, diagnosis and treatment of neoplasia development, lymphoproliferative conditions, inflammation, ischemia or strokes and autoimmune diseases.
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                                                                                                   caspase activated protein kinase; apoptosis; neoplasia development; actin stress fiber dissolution; lymphoproliferative condition; inflammation; ischemia; stroke; autoimmune disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a murine Ste20-related protein kinase
cDNA sequence encoding a Ste20-related protein kinase called SMAK.
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                                                                    Mouse; Ste20-related protein kinase; SMAK; caspase-3-cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.3%; Score 25.8; DB 21; Length 5259; 67.9%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_except= (pos: 4..5, aa: Ser)
/transl_except= (pos: 1373..1376, aa: Xaa)
/product= "SMAK"
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                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 66..3674
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AA199683/c
ID AA199683 standard; DNA; 4403765 BP.
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es 36; Conserv
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variation; epidemiology; patient treatment; epidemic monitoring;
                                                                                                         24-JUN-1998;
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                                                    US6294328-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (ARI99683) and H37Rv (ARI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6294328B1.
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                                                                                                                                                                                                                                                                                                                                                             determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M, tuberculosis strains CDC
                                                                                                                                                                                                                                                                                                                                                Evaluating strain variation of Mycobacterium tuberculosis, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                       variation; epidemiology; patient treatment; epidemic monitoring; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
                                                                                           Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4403765;
                                                                 Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
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                                                                                                                                                                                                                                                                                              Venter JC;
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63.9%; Pred. No. 33;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                             Fleischmann RD, White OR, Fraser CM,
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                                                                                                                                  Mycobacterium tuberculosis.
                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                       1551 and H37Rv differ
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            AA199683;
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AAI99682/
ID AAI9
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2322190 GGGGGGCAAGACCCCCAGGGCACCGCGGCGCCCAGCGTTACCCGGGCTATCCTGGG 2322131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37RV differ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser CM, Venter JC;
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                                                                       Mycobacterium tuberculosis.
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BJ005207 BJ005207 AQ641446 RPCT93-BC BB711478 BP711478 A1606158 VO15-02.x BH140228 ZMMBBB000 BH140663 ZMMBBB000

AW024446 wu76d09.x BE198211 ug76b11.y BG918873 602819380 BF120119 601756421 BM006421 603615139 AA519383 TgESTZZ54 AL240746 Terraodon BM468546 AGENCOURT W68459 Zd36603.r1 BF1616099 RH45605.5 BF1537568 416137 MA AW488804 U1.M-BH3-BJ060200 BJ060200 BF135856 601782168 BF135856 601782168 BF73519 CMZ-ITO03 AW501053 UT-HF-BPO AV392022 AV392022 AM395150 Zr34c12.r BI719961 1031046G1

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Database :

Scoring table:

Perfect score:

Sequence:

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Bos taurus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.

1 (bases 1 to 444)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
DO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 436
Email: Smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bryyu374 444 bp mRNA linear
291826 WARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF890374
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BB711478
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SOURCE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF890374
LOCUS
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BI775360 467815 MA
BB630381 BB630381
AL212510 Tetracdon
AL233007 Tetracdon
BG394974 602457369
                                                                                                                 (without alignments)
6506.409 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                   June 13, 2003, 02:37:44; Search time 151.839 Seconds
                                                                                                                                                                                         1 gggctgggatgacgaactgc.....acatgcgcttcatgcaggag
                                                                                                                                                                                                                                                                                              32308132
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                               16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                           hits satisfying chosen parameters:
                                                                                                                                                          US-09-826-581-5_COPY_529_589
61
                                                                        nucleic search, using sw model
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                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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gb_htc:*
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Match I
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Score

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45. 45.

AG130442 Pan trog1 AV753229 AV753229 BG70079 602681675 BE394076 601312450 BM011144 603634858 BF033403 601457923 AL262954 Tetraodon BQ508350 Esr615765 BM088002 501350 MA BG59496 EST504391 BE809466 21503 MA BE809496 21038

25-APR-2001

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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                             BB630381
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                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 548)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
v0.980904.e. Vector identified by cross_match with the -minscore 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 25-SEP-2001
                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence evaluation of four pooled-tissue normalized bovine cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.8%; Score 45.6; DB 12; Length 444; 85.0%; Pred. No. 3.2e-05; ive 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI775360 548 bp mRNA linear 467815 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TPI: 402 762 4366
Pax: 402 762 4390
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                                                                                                                                                                                                                                     /clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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/clone_lib="MARC 2BOV"
                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 57 row: H column: 11
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
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                    and -minmatch 12 options. PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .548
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 683)

RS Arakawa.T., Carninci.P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Rodaki,T., Maczaki,Y., Okldo,T., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shirzaki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-9222
Fax: 81-45-503-9226
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinaqawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,W., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
Waqi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watafiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsunra
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAG
                                      Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
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                                                                                                                                                                                                                                                                                 74.8%; Score 45.6; DB 13; Length 548; 85.0%; Pred. No. 3.4e-05; Live 0; Mismatches 9; Indels 0
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CNSU38S6 1010 bp DNA linear GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 005N22 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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1 (bases 1 to 1010)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
                                                           1. .910
/organism="Tetraodon nigroviridis"
/db.xref="taxon:99883"
/clone="163d17"
/clone_lib="6"
/note="Genoscope sequence ID : COAG163AD09LP1-end : T7"
a 263 c 305 g 160 t 3 others
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g 210 t l others
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genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/clone="note"
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Location/Qualifiers
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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/clone_lib="G"
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                                                                                                                                                                                 /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was cadadadadadadadaccretrrrrrrrrrrvv 3'1, cDNA was
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1 (bases 1 to 910)
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Roset-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Bllault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
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                                                                            /clone_lib="RIKEN full-length enriched, 6 days neonate
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Pred. No. 0.00012;
0; Mismatches 10;
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                                                                                                                      /tissue_type="skin"
/dev_stage="6 days neonate"
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                 /organism="Mus musculus'
/db_xref="taxon:10090"
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AL212510.1 G1:7871329
GSS; genome survey sequence.
Tetraodon njgroviridis.
Tetraodon nigroviridis.
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83.3%;
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Conservative
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Trypanosoma.

I (bases 1 to 442)

El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, Y., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ641446 442 bp DNA linear GSS 08-JUL-1999
RPC193-ECORI-4113.TJ RPC193-ECORI Trypanosoma brucei genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93
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Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences search
page: http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: SP6
Class: BAC ends.
                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha,
Beloniformes, Adianichthyidae, Oryzinae, Oryzias.
1 (bases 1 to 581)
                                                                                                                                                                         Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H. Medaka EST Project in Takeda's lab Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
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Other_GSSs: RPC193-EcoRI-4113.TV
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235 c 119 q 91 t. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="MF01SSA076B04"
/clone_lib="WR01SSA_CDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryzias latipes"
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73.9%; Pred. No. 71;
tive 0; Mismatches
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Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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/db_xref="taxon:8090"
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Best Local Similarity 73.9%
Matches 34; Conservative
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Trypanosoma brucei
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                                                  Oryzias latipes
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                                                                                       /note="Organ: eye; Vector: porB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GCACGAGGGG. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeicy) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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1 (bases 1 to 955)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the 1.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCML297 row: j column: 17
High quality sequence stop: 717.
Location/Qualifiers
                                                                1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
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                           21; Indels
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/lab_host="DH10B (phage-resistant)"
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65.6%; Pred. No. 50;
tive 0; Mismatches
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/db_xref-"taxon:9606"
/clone="IMAGE:4579696"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_MGC_16"
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Best Local Similarity 65.6
Matches 40; Conservative
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno, H., Fwunnuishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara Y. and Hayashizaki,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Al606158 349 bp mRNA linear EST 21-APR-1999 vol5c02.xl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1049954 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: Sall: Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGGACCAAGAGCTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Waller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="B020024106"
/clone_lib="RIKEN full-length enriched, 2 cells egg"
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Mus musculus"
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="egg"
/dev_stage="2 cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                            /clone="Replies Ecori-4113"
/clone="Replies Ecori-4113"
/clone="Replies Ecori-4113"
/clone="Wercio: Pakcijo: Site_1: Eco RI; Site_2: Eco RI;
/note="Wector: pakcijo: Site_1: Eco RI; Site_2: Eco RI;
Constructed for The Institute for Genomic Research by
Robui Zhao in Pieter de Jong's laboratory (Roswell Park
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
bruce; TREU927/4 GUTat 10.1 agarose embedded DNA was
partially digested with a combination of Eco RI and Eco RI
methylase (RPCI93-EcoRI segment) or Dpn II (RPCI93-DpnII
segment). High molecular weight fragments were ligated in
pBACe3.6 vector digested with Eco RI or Bam H1,
respectively. The average insert size is 141 Kb. Total
coverage (Doth segments): > 90 X the haploid
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,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
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RIKEN Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
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URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Wataliki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB711478 B8711478 IIKEN full-length enriched, 2 cells egg Mus musculus cDNA
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
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1ive 0; Mismatches 21; Indels 0
                                        /organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
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BB711478
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Fax: 81-45-503-9216
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Matches 39; Conservative
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/tissue_type="Young leaves"
/lab_host="E. coli"
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Fax: 864 656 4293
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ZMMBBb0001L18f Maize B73 Zea mays genomic clone ZMMBBb0001L18f, DNA
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                                                                                                                                                                                                                                                                 Tonkins,J.P., Main,D., Goicoechea,J.L., Frisch,D.A. and Wing,R.A. A Deep-Coverage BAC Library for Maize Unpublished (2001)
                                 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
High quality sequence stop: 326.
Location/Qualifiers
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IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                        /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4793
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Clemson University Genomics Institute
                                                                                                               1. .349
/organism="Mus musculus"
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Class: BAC ends
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/clone="ZMMBBb0001L18f"
/clone_lib="Maize B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 71 High quality sequence stop: 510.
                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:1049954"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
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вні40228.1 сі:15099289
                                                                                                                                                      /strain="C3H"
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Matches 38; Conservative
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BH140663 593 bp DNA linear GSS 07-AUG-2001 AMMBBb0001118f Maize B73 Zea mays genomic clone ZMMBBb0002118f, DNA
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                                                                                   http://www.genome.clemson.edu/projects/stc/maize/ZMMBBb * 221 c 138 g 146 t l others
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 593)
Tomkins, J. P., Main, D., Golcoechea, J. L., Frisch, D. A. and Wing, R. A.
A Deep-Coverage BAC Library for Malze
Unpublished (2001)
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/cultivar="873"
/db.xref="taxon:4577"
/db.xref="taxon:4577"
/clone="lb.Walize B73"
/tissue_type="Young leaves"
/lissue_type="Young leaves"
/lote="Vector: pcUGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation, ordering clones and sequence analysis see
/note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI; For more details on library preparation, ordering clones and sequence analysis see
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65.5%; Pred. No. 1.38+02;
tive 0; Mismatches 20; Indels
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
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1. .593
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Best Local Similarity 65.54
Matches 38; Conservative
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Best Local Similarity 65.54
Matches 38; Conservative
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BG918873
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the 1.M.A.G.E. Consortium/LINL at:
www-bio.lln.gov/bbrp/image/image.html
Insert Length: 878
Seq primer: -40UP from Gibco
AW024446 648 bp mRNA linear EST 09-MAR-2000 wu76d09.xl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2525969 3' similar to TR:043176 043176 PEPTIDASE HOMOLOG ;, mRNA sequence.
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Mammalia; Butheria; RodenLia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 680)
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 64,040,000)
NOLT-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:2525969"
                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adators (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library is normalized. Library
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 738)
                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:953633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was constructed by Bento Soares and M. Fatima Bonaldo.
137 c 187 q 103 t
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Email: cgapbsrcfmail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="infiltrating ductal carcinoma"
                                                                                                                                                                                                                                                   1. .680
/organism="Mus musculus"
/db_xref="taxon:10090"
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/clone="ImaGe:1548285"
/clone=lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
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Pred. No. 1.6e+02;
0; Mismatches 17;
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/clone_lib="NCI_CGAP_Mam6"
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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High quality sequence stop: 472.
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Best Local Similarity 67.9
Matches 36; Conservative
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/dev_stage="5 months"
//lab_host="DH10B"
//lab_host="DH10B"
//lab_host="DH10B"
//note="Organ: mammary: Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH*
Ouery Match

Query Green, M.D., NIH*

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Sequence 7, R
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Sequence 39,
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/barkorus_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/barkorus_Seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-518-914-1
US-09-518-914-3
US-08-804-227C-7
US-08-804-198-1
US-08-989-358A-1
US-08-993-558-1
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US-08-808-358-27
US-08-808-358-27
US-08-808-327-67-27
US-08-808-324-27
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US-08-147-023-4
US-08-447-570-4
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US-07-679-451-1
US-07-989-847-1
US-07-721-847A-3
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US-08-713-556F-39
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US-08-449-699A-4
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                                                                                                                                                                                                                    441362 seqs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                 - nucleic search, using sw model
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42.3 4411529 4

40.0 2327 4 0

38.4 1508 4 0

38.4 1508 4 0

38.0 441377 2 0

38.1 441377 2 0

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37.4 1320 3 0

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                                                                                                            Sequence 200, The Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 3, Appli 
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Sequence 9, Appli
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERBNCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
UNUMBER OF SEQ ID NOS: 2
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APPLICANT: FELESCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Obn C.
APPLICANT: PENSER, John C.
APPLICANT: PENSER, JOHN C.
APPLICANT: TILE OF INVENTION: UNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
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Sequence 3,
Patent No.
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Pred. No. 7.4;
); Mismatches 22;
US-08-469-411-1
19-08-925-779-3
5166058-3
15-09-027-337-9
US-09-644-600-9
US-09-365-6148-5
US-08-943-731-200
US-08-943-731-5
US-08-943-731-5
US-08-943-731-5
US-08-244-093-3
US-09-244-093-3
US-09-244-093-3
US-09-244-093-3
US-09-244-033-3
US-09-244-231-34
US-08-044-718-13
US-08-044-718-13
US-08-205-586-14
US-08-205-586-14
US-08-205-586-14
US-08-205-586-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECULT 2
US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09103840A, Patent No. 6294328, GENEBAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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OTHER INFORMATION: "n" bases at
OTHER INFORMATION: represent a,
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ilarity 63.9%;
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Best Local Similarity
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US-09-103-840A-2/c
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US-09-103-840A-2
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       Best Local Similarity 73.8%; Pred. No. 5.2;
Matches 31; Conservative 0; Mismatches 11; Indels
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                                                                                                                                                                                                                                 Sequence 1, Application US/08744231
Patent No. 6358722
GENERAL INFORMATION:
APPLICANT: Mitchell, David
TILLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             822 ACCAGCTGCGAGATCTGGGCGCCCAGTTCTACGAGCGCTACA 863
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                                                                         12 ACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCA 53
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
OCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patchtin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: Case Docket 9339 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ), NAME/KEY: CDS
; LOCATION: join(374..420, 469..1819)
US-08-744-231-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
21P: 07110
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US-09-518-914-1
; Sequence 1, Application US/09518914
; Patent No. 6413731
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhlani, Parul P.
; APPLICANT: Adham, Nika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (201) 235-4205
TELERAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2327 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Conservative
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STRANDEDNESS: double
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                                                                                                                                                                                        RESULT 4
US-08-744-231-1
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                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                           Query Match 42.3%; Score 25.8; DB 4; Length 4411529; Best Local Similarity 63.9%; Pred. No. 7.4; Matches 39; Conservative 0; Mismatches 22; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
APPLICANT: Witchell, David
TILLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFRENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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United States of America
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                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/744,231
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08868435
; Patent No. 6291221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                         LENGTH: 4411529
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US-08-868-435-1
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US-08-868-435-1
                                                                                                                                                                     TYPE: DNA
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LOCATION:
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LOCATION:
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FEATURE:
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; LOCATION:
US-08-804-227C-7
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Sequence 3, Application US/09518914

Fatent No. 6413731

GENERAL INFORMATION:

APPLICANT: BOTOWSKY, Beth E.

APPLICANT: GENERAL STAIN PARTICANT: APPLICANT: NUMBER: US/09/518,914

CURRENT APPLICATION NUMBER: US/09/518,914

CURRENT FILING DATE: 2000-03-03

ERALIER PELING DATE: 1999-05-03

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PATENTIN VET. 2.1
TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS FILE REFERENCE: 59138-A/JPW
CURRENT APPLICATION NUMBER: US/09/518,914
CURRENT FILING DAFE: 2000-03-03
EARLIER APPLICATION NUMBER: US 09/303,593
EARLIER FILING DAFE: 1999-05-03
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                     Query Match 38.4%; Score 23.4; DB 4; Length 1508; Best Local Similarity 67.3%; Pred. No. 11; Matches 33; Conservative 0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                       11 GACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGG
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GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Rubsches, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Button, Kimberly J.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 7, Application US/08804227C; Patent No. 5876991
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                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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ZIP: 46285
                                                                                                                                                              SEQ ID NO 1
LENGTH: 1508
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Pred. No. 26;
0; Mismatches 13; Indels 0;
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APPLICANT: Ruhstoss, Stuart A.
APPLICANT: Rac, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
FILING DATE: February 21, 1997
                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
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STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/08804198
; Patent No. 5945320
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 70.5%;
Matches 31; Conservative (
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36155..41830
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14046..20036
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31329..36071
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20110..31284
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STRANDEDNESS: single
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No. 60602980 No. 6060298disk of No. 6060298th America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.4%; Score 22.8; DB 3; Length 1320; Best Local Similarity 66.0%; Pred. No. 18; Matches 33; Conservative 0; Mismatches 17; Indels 0.
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APPLICATION NUMBER: US/08/989,358A FILING DATE: 12-DEC-1997 CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 1481/96 FILING DATE: 20-DEC-1996 APPLICATION NUMBER: 0529/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5101.200-US
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fuglsang, Claus
APPLICANT: Ohmann, Anders
APPLICANT: Breinholt, Jens
APPLICANT: Ostergaard, Peter
TITLE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                     5101.200-US
                                                                   FILING DATE: 07-MAY-1997,
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08989358A Patent No. 6060298
                                                                                                                                                                                                 NAME: Gregg, Valeta A
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5101.
TELECOMMULCATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 405 Lexington Avenue CITY: New York STATE: NY
      12-DEC-1997
IMBER: 0529/97
                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-MAY-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-MAY-1997 APPLICATION NUMBER: 60/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 212-867-0123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: NY
COUNTRY: U.S.A.
7TP: 10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lassen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-08-989-358A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-221-654-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 38.0%; Score 23.2; DB 2; Length 44377; Best Local Similarity 70.5%; Pred. No. 26; Matches 31; Conservative 0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27492 GGGCAGCGCGTCGAACTGCCGGAGTCCGGTGACCGGATGTACA 27535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOSTWARE: FREALSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Fuglasng, Claus
APPLICANT: Ornan, Anders
APPLICANT: Ornan, Anders
APPLICANT: Ostergaard, Peter
TITLE OF INVENTION: Periophora Phytase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/804,198
                                        ELLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION UNDERR: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDENESS: single
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APPLICATION NUMBER: 08/989,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/09221654
; Patent No. 6054306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLIATE: NY
COUNTRY: U.S.A.
CLOUTRY: U.S.A.
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COUNTRER: IBM COMPATIBLE
COUNTRER: IBM COMPATIBLE
COUNTRER: IBM COMPATIBLE
COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF COUNTRER: OF
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14046..20036
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20110..31284
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31329..36071
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350..14002
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
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US-08-804-198-1
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135 GGGCTGGGATGAGGGGCGGCCCGACGCCGCCGCGCGCAACTTCCTGCGGCCCA 83
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Pred. No. 21;
0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,670B
FILING DATE: December 22, 1994
FILING DATE: December 22, 1994
ATTORNEY AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
THENDERNEY POCKET NUMBER: 5202-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
CLONE: peptide
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APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Nell
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
                                                                                                                                                                                    APPLICANT: Melton, Douglas A. TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
                                                                                                                                                                                                                                                                              ADDRESSEE: GENETICS INSTITUTE, INC. STREET: 87 CambridgePark Drive
  Sequence 27, Application US/08362670B Patent No. 5658882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 27, Application US/08333576C
; Patent No. 6027919
                                             GENERAL INFORMATION: APPLICANT: Celeste, Anthony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celeste, Anthony J.
                                                                                       APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 52
TELECOMUNICATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
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64.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mat_peptide
847..1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 64.2 Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Celeste,
APPLICANT: Worney,
APPLICANT: Rosen,
APPLICANT: Wolfman,
APPLICANT: Thomsen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                           Cambridge
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LOCATION:
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; LOCATION:
US-08-362-670B-27
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                           482 CGGGGCTAACCAATCGCACCAAACCGGCACCGATATGTATACGCGCTACA 531
                                                                                                                                                                                                                                                                                                                                                 4 CTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCA 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 1593;
                                                                                                                                                                                                                                                         DB 3; Length 1320;
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                                                                                                                                                                                                                                                    37.4%; Score 22.8; Di
66.0%; Pred. No. 18;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lassen, Soren F.
APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Breinholt, Jens
APPLICANT: Breinholt, Jens
APPLICANT: Fuglsang, Claus C.
APPLICANT: Stergaard, Peter R.
TILE OF INVENTION: Phytase Polypeptides
FILE REFRENCE: 538 3.50-02
FILE REFRENCE: 538 3.50-02
FALLER APPLICATION NUMBER: 1480/96
EARLIER APPLICATION NUMBER: 1481/96
EARLIER FILING DATE: 1996-12-20
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-05-07
EARLIER FILING DATE: 1997-05-07
EARLIER FILING DATE: 1997-05-07
EARLIER FILING DATE: 1997-05-07
EARLIER FILING DATE: 1997-05-07
EARLIER FILING DATE: 1997-05-07
EARLIER FILING DATE: 1997-05-07
EARLIER FILING DATE: 1997-05-09
NUMBER OF SQL ID NOS: 32
NUMBER OF SQL ID NOS: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08993359A Patent No. 6039942 GENERAL INFORMATION:
                     TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
ILENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                          Best Local Similarity 66.03
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Peniophora lycii
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: mat_peptide
; LOCATION: (213)...(1439)
US-08-993-359-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (123)...(1439)
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LOCATION: (123)...(21;
                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
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US-08-362-670B-27/c
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                                                                                                                                                                                                                                                         Query Match
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PCT-1594-14030A-27/C
Sequence 27, Application PC/TUS9414030A
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVERTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
CLONE: peptide
                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
CLASSIFTCATION: 514
ATTORNEY, AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
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FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-N0Y-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: GENETICS INSTITUTE, INC. 87 CambridgePark Drive
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: Patentin Release #1.
                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 5202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1233 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 64.28 Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: mat_peptide
; LOCATION: 847..1233
US-08-808-324-27
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.0%; Score 22.6; DB 3; Length 1233; Best Local Similarity 64.2%; Pred. No. 21;
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                                                                                                                                                                                                   COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
SOFWRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/333,576C
FILING DATE: NO. 6027919ember 2, 1994
TLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-B
TELEPONMUNICATION INFORMATION:
TELEPONME: 617 498-8260
TELECOMMUNICATION INFORMATION:
TELEPONE: 617 498-8260
TELEPONE: 617 498-8261
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1233 base pairs
TYPE: nucleic acid
STRANDENDESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27, Application US/08808324

Patent No. 6284872
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Wozney, Vicki A.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding BMP2 propeptide/BMP-12 mature peptide
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STREET: 87 CambridgePark Drive
CITY: Cambridge
                     CORRESPONDENCE ADDRESS:
ADDRESSES:
STRET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: mat_peptide
LOCATION: 847..1233
  NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                      Massachusetts
                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                           USA
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US-08-808-324-27/c
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                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE:
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**RESERVATION NUMBER: 32.618
**RESERVATION NUMBER: 52020-PCT**
**RESERVATION NUMBER: 52020-PCT**
**RESERVATION NUMBER: 52020-PCT**
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**TELEMANTION NEW PROMINE NUMBER: 53056-S851
**TELEMANTION FOR SEQ ID NO: 27:
**SEQUENCE CRARACTERISTICS: LENGTH: 1233 base pairs
TYPE: nucleic acid
**SPRANDENES: 51ngle
**TOPCOCK: linear
**MOLECULE TYPE: DNA (genomic)
**TONE: Peptide
**TOPCOCK: linear
**MOLECULE TYPE: DNA (genomic)
**TONE: Peptide
**FRAUME: Poptide
**FRAUME: Poptide
**FRAUME: NAME/KEY: mat_peptide
**LCCATION: 1..1233
**FERAUME: NAME/KEY: mat_peptide
**LCCATION: 1..1233
**FRAUME: NAME/KEY: mat_peptide
**LCCATION: 847..1233
**PCT-US94-14030A-27
**Ouery Match
**Best Local Similarity 64.2%; Pred. No. 21:
**Matches 34; Conservative 0; Mismatches 19; Indeis 0; Gaps
**Ouery Match
**Matches 34; Conservative 0; Mismatches 19; Indeis 0; Gaps
**Ouery Match
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**Ouery Matches 34; Conservative 0; Mismatches 19;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1029858 seqs, 724030393 residues
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61
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                               OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 2, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 8004, Ap	Sequence 11, Appl	Sequence 19, Appl	Sequence 1, Appli	Sequence 17, Appl	Sequence 166, App	Sequence 84, Appl	Sequence 51, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 1694, Ap	Sequence 4, Appli	Sequence 23, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 12740, A
ID	0 US-09-826-581-2	.0 US-09-826-581-5	US-09-939-964-1	0 US-09-815-242-8004	US-09-909-567B-11	0 US-09-931-381A-19	US-09-898-751A-1	.0 US-09-931-381A-17	.0 US-09-764-864-166	US-10-108-605-84	.0 US-09-934-868-51	US-10-146-835-1	US-10-146-835-3	.0 US-09-917-800A-1694	US-09-927-827-4	US-10-007-270-23	US-09-927-827-1	US-10-265-593-3	LO US-09-960-352-12740
Query Match Length DB	989	1647 1	536165 9	1473 1	14917 9	1086	1089	1244	009	573	2760	1508	1541	1323	3627	4204	7356	27847	242
Query Match	100.0	100.0	41.6	41.0	40.7	39.3	39.3	39.3	39.0	38.7	38.7	38.4	38.4	38.0	38.0	38.0	38.0	38.0	37.7
Score	61	61	25.4	25	24.8	24	24	24	23.8	23.6	23.6	23.4	23.4	23.2	23.2	23.2	23.2	23.2	23
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6224, Ap 6227, Appl 67, Appl 2 2303, Ap 6 602, App 934, Appl 27, Appl	1, Appl 1, Appl 176, Apl 176, Apl 17, Appl 1330, Apl 1330, Apl 15, Appl 17872,		
ce 62 ce 62 ce 67 nce 2 nce 6 ce 93 ce 27	ce 1, ce 4, ce 4, ce 1, ce 1, ce 1, ce 4, ce 4, ce 1,	nce 3, 8	
Sequence 6224, Ap Sequence 6227, Ap Sequence 67, Appl Sequence 2303, Ap Sequence 602, Appl Sequence 934, App Sequence 17, Appl	Sequence 4, Appl1 Sequence 1, Appl1 Sequence 3, Appl Sequence 476, App Sequence 1, Appl Sequence 1, Appl Sequence 21143, A Sequence 310, Appl Sequence 31, Appl1 Sequence 31, Appl1 Sequence 7546, App Sequence 7546, App Sequence 7546, App Sequence 7546, App Sequence 7546, App Sequence 7546, App Sequence 7546, App Sequence 7546, App Sequence 7672, App Sequence 7672, App Sequence 7672, App Sequence 7672, App	Sequence	
S-09-764-891-6224 S-09-764-891-6227 S-09-373-688-67 US-09-923-876-2303 US-09-764-864-602 S-09-738-626-934 US-09-738-626-1 S-09-945-182-27	S-08-957-425-4 S-10-044-716-1 S-09-804-671-476 S-10-073-651-476 US-09-952-360-1 US-09-957-29143 S-09-988-574-5173 S-09-995-29143 S-09-988-751A-3 US-09-923-826-830A-330 S-09-764-891-7546 S-10-300-841-7546 US-09-923-876-3718 US-09-923-876-3718 US-09-923-876-3718 US-09-923-876-3718 US-09-923-876-3718 US-09-923-876-3718 US-09-923-876-3718	S-09-886-607-3 ALIGNMENTS 81 THE HUMAN AMP-ACTIVATED	
64-891 64-891 73-658 923-87 764-86 38-626 738-624	08-97-425-4 10-044-716-1 10-073-961-4: 2-09-184-887-3 2-09-18-987-3 2-09-18-987-3 2-09-18-991-3 2-09-88-514-0918-991-2 2-09-88-714-0918-991-2 2-09-88-714-0918-3 2-09-923-886-3 2-09-923-886-3 2-09-923-886-3 2-09-923-886-3 2-09-923-886-3 2-09-923-886-3 2-09-923-886-3 2-09-923-886-3 2-09-923-896-3 2-09-923-896-3 2-09-923-896-3 2-09-923-896-3	-09-886-60 ALIGNMENTS 1 HE HUMAN A	55 4.0
US-09-764-891-6224 US-09-764-891-6227 US-09-373-658-67 US-09-923-876-290 US-09-764-864-602 US-09-738-626-934 US-09-738-626-1 US-09-945-182-27	US-08-957-425-4 US-10-044-716-1 US-09-804-625-3 US-10-073-961-476 US-09-952-360-1 US-09-978-574-517 US-09-918-995-2914 US-09-898-751A-3 US-09-898-751A-3 US-09-898-751A-3 US-09-898-751A-3 US-09-898-751A-3 US-09-898-751A-3 US-09-898-751A-3 US-09-922-876-371 US-09-923-876-371 US-09-923-876-371 US-09-923-876-371 US-09-923-876-371 US-09-928-876-5260 US-09-228-876-5260 US-09-228-876-5260 US-09-228-876-5260 US-09-228-876-5260 US-09-228-876-5260 US-09-228-876-5260	JS-09-: ALIG 581 THE H	CURRENT APPLICATION NUMBER: US/09/826,581 CURRENT FILING DATE: 2001-04-05 PRIOR FILING DATE: 2000-04-07 PRIOR FILING DATE: 2000-04-07 NUMBER OF EGG ID NOS: 14 SOFTWARE: FastSEQ for Windows Version 4.0
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000 000	000000 0000	RESUS- US- SOS- SOS- SOS- SOS- SOS- SOS- S	

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APPLICANT: Macina, Roberto A.
APPLICANT: Macina, Roberto A.
APPLICANT: Mair, Manoj
APPLICANT: Chen, Seiyu
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REPERENCE: DEX-0214
CURRENT APPLICATION NUMBER: 05/09/9909,567B
CURRENT PILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-21
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Version 3.1
SEQ ID NO 11
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Matches 35; Conservative 0; Mismatches "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.0%; Score 25; DB 10; Length 1473; 64.9%; Pred. No. 2.7;
tive 0; Mismatches 20; Indels
APPLICANT: Trawick, John D.
APPLICANT: Garnt J.
APPLICANT: Gant J.
APPLICANT: Ganmoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPERBACE: ELITRA.011A
CURRENT APPLICATION NUMBER: U$/09/815,242
CURRENT APPLICATION NUMBER: 06/19/1,078
PRIOR APPLICATION NUMBER: 60/19/1,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/23/65
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-12-22
PRIOR PELLING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
SOFTWARE: FastEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09909567B Publication No. US20030022257A1 GENERAL INFORMATION:
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 64.9
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(1473)
US-09-815-242-8004
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ORGANISM: Homo sapien
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  APPLICANT: Marklund, Stefan
TITLE OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE PEPERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR PAPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NO 5
LENGTH: 1647
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APPLICANT: Perret, Xavier Philippe
APPLICANT: Perret, Xavier Philippe
APPLICANT: Perret, Xavier Philippe
APPLICANT: Propose Sequence of Rhizobium SP. NGR 234 Symbiotic
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARPOGG
CURRENT APPLICATION NUMBER: US/09/939,964
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR PILING DATE: 1999-06-22
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100.0%; Pred. No. 3.5e-14;
tive 0; Mismatches 0;
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Pred. No. 3.1;
0; Mismatches 21;
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/0993964
Publication No. US20030054522A1
GENERAL INFORMATION:
APPLICANT: ROSENTHAI, Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 41.6%;
Best Local Similarity 64.4%;
Matches 38; Conservative
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Best Local Similarity 100.0
Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5
                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1
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US-09-939-964-1/c
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TITLE OF INVENTION: Methof for Identifying Agents Which
TITLE OF INVENTION: Medulate Chemokine "MEC"-Induced Functions of CCR3 and/or
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
CURRENT ELER REFERENCE: 1855.2010-003
CURRENT APPLICATION NUMBER: US,099/931,381A
CURRENT FILING DATE: 2001-08-15
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1244
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Pred. No. 7.4;
0; Mismatches 17; Indels 0
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Pred. No. 6.6;
0; Mismatches 15; Indels (
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TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILLE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT APPLICATION DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 166
LENGTH: 600
                                                      DB 9; Length 1089;
                                                                                                 15; Indels
                                                39.3%; Score 24; DB 9 68.8%; Pred. No. 6.5; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09931381A, Patent No. US20020137107A1, Patent No. US20020137107A1, APPLICANT: Butcher, Eugene C. APPLICANT: Runkel, Eric J., APPLICANT: Pan, Juniang APPLICANT: Soler-Ferran, Dulce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 166, Application US/09764864; Patent No. US20020132753A1; GENERAL INFORMATION:
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68.8%;
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Best Local Similarity 68.85
Matches 33; Conservative
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Best Local Similarity 66.7'
Matches 34; Conservative
                                                Query Match 39.33
Best Local Similarity 68.83
Matches 33; Conservative
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US-09-764-864-166
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ORGANISM: Homo sapiens
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US-09-931-381A-17
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LOCATION: (5).
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US-09-898-751A-1
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                                                                                                                 GENERAL INFORMATION:
APPLICANT: Butcher, Engene C.
APPLICANT: Butcher, Engene C.
APPLICANT: Butcher, Engene C.
APPLICANT: Bran, Juniang
APPLICANT: Soler-Ferran, Dulce
TITLE OF INVENTION: Method for identifying Agents Which
TITLE OF INVENTION: Method for Identifying Agents Which
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
CURRENT APPLICATION NUMBER: US/09/931,381A
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: US. 09/638,914
PRIOR APPLICATION NUMBER: US. 09/638,914
SPRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Morales, Janine M.
APPLICANT: Morales, Janine M.
APPLICANT: McEvoy, Leslie M.
APPLICANT: Bowman, Edward P.
APPLICANT: Bowman, Edward P.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: CHEMOKINE AND RECEPTOR USES; COMPOSITIONS; METHODS
FILE REFERENCE: DX0882XK
CURRENT APPLICATION NUMBER: US/09/898,751A
CURRENT APPLICATION NUMBER: US/09/17,549
PRIOR APPLICATION NUMBER: US/09/17,549
PRIOR PELING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US/09/13,6570
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: US/09/113,858
PRIOR APPLICATION NUMBER: US/09/113,858
PRIOR APPLICATION NUMBER: US/09/113,858
SOFWWARE: PATENTLING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 16
SSOFTWARE: PATENTLING VERSION 3.1
SEQ ID NO 1
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                                                                        ; Sequence 19, Application US/09931381A
; Patent No. US20020137107A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09898751A
Patent No. US20020160024A1
GENERAL INFORMATION:
APPLICANT: Oldham, Elizabeth R.
APPLICANT: Soto, Hortensia
APPLICANT: Liu, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 68.88
Matches 33; Conservative
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Homey, Bernhard
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US-09-931-381A-19
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LOCATION: (1)..(1086)
OTHER INFORMATION:
                                                US-09-931-381A-19/C
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US-09-898-751A-1/C
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APPLICANT:
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APPLICANT:
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                                                                   GENERAL INFORMATION:
APPLICANT: Borowsky, Beth E.
APPLICANT: Borowsky, Beth E.
APPLICANT: Gazalek, Kristine L.
APPLICANT: Adham, Nika
TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
FILE REFERENCE: 59138-A/JPW
CURRENT APPLICATION NUMBER: US/09/518,914
PRIOR PAPLICATION NUMBER: US/09/518,914
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US/09/318,914
PRIOR FILING DATE: 1999-05-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.4; DB 9; Length 1508;
Pred. No. 11;
0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1541;
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US-09-917-800A-1694
S-69uence 1694, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
                        Sequence 1, Application US/10146835 Publication No. US20030073167A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.4%;
Best Local Similarity 67.3%;
Matches 33; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1508
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SEQ ID NO 3
LENGTH: 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-146-835-1
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ORGANISM: Homo sapiens
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APPLICANT: Blachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Randar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR PELLING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
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  GGCGAGCGGCCCTACCACTGCGCCGAGTGCGGCAAGCGGCTTCACGCAGAAG 132
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APPLICANT: Schenzle, Andreas J
TITLE OF INVENTION SCHENZER SHOW METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: CL1596 US NA
CURRENT APPLICATION NUMBER: US/09/7934, 868
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229, 858
PRIOR FILING DATE: 2000-09-01
SUMBER OF SEQ ID NOS: 81
SOFTWARE: Microsoft Office 97
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Best Local Similarity 64.8%; Pred. No. 10;
Matches 35; Conservative 0; Mismatches
                                                                                                                          ; Sequence 84, Application US/10108605; Patent No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 51, Application US/09934868
; Patent No. US20020137190A1
; GENERAL INFORMATION:
; APPLICANT: Koffas, Mattheos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Drosophila melanogaster US-10-108-605-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: ORF7; OTHER INFORMATION: nasA gene US-09-934-868-51
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US-09-934-868-51/c
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TYPE: DNA FEATURE:

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APPLICANT: Ranseier, Thomas M.
TITLE OF INVENTION: Directed Genetic Engineering of Xanthomonas campestris
TITLE REFERENCE: 38-10(15824)B
CURRENT APPLICATION NUMBER: US/09/927,827
CURRENT APPLICATION NUMBER: US 60/279,493
PRIOR APPLICATION NUMBER: US 60/279,493
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_022220 US-09-917-800A-1694
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                                                                                                                      APPLICANT: Endanolt, MICHORAL
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR PLING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,80
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,45
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR PRIOR DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-22
PRIOR PLING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-19
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Porter, Mark
Johnson, Kory
Castle, Arthur
Elashoff, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Rattus norvegicus
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LENGTH: 3627
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Maximum Match 100%
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A724957 Homo sapi A724957 Homo sapi AX099774 Sequence AX099800 Sequence AX39833 Sequence AX39833 Sequence AX39833 Sequence AX39833 Sequence AX39834 Sequence AX3981580 Sequence AX3981580 Sequence AX39814 Sequence AX09804 Sequence AX09804 Sequence AX09804 Sequence AX09804 Sequence AX09804 Sequence AX09974 Homo sapi AC127107 Rattus no AC127107 Rattus no AC12707 Rattus no AC128070 Rattus no AC12970 Rattus no AC12970 Rattus no AC12970 Rattus no AC1290 Homo sapi AC12501 Homo sapi AC125016 Homo sapi AC125016 Homo sapi AC125016 Homo sapi AC125016 Homo sapi AC125016 Homo sapi AC125016 Homo sapi AC125016 Homo sapi AC125016 Homo sapi AC125016 Homo sapi AC12616 Homo sapi AC12616 Homo sapi AC10805 Human DNA AC022226 Homo sapi PAT 02-NOV-2001 Andersson, L., Luthman, H. and Marklund, S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 5 18-OCT-2001; Oryza sat Human DNA Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AX281582 Sequence AX099776 Sequence AX099802 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AC105743 O AL034548 H AC018818 H linear DNA ALIGNMENTS SUMMARIES AX281582 1647 bp Sequence 5 from Patent W00177305. AX099802 AF214519 HSA249977 AX099774 HSJ894D12 AL663072 ΩI AX281582.1 GI:16608833 510 DB 100.0 100.0 100.0 100.0 2109 100.0 2210 92.1 1867 92.1 1873 92.1 1888 67.5 1988 1988 1 Length REFERENCE AUTHORS TITLE JOURNAL Pred. No. is the number of results predicted by chance to have a ~

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2115 bp mRNA linear PRI 03-JUN-2000 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3) mRNA, complete cds.
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/db_xref="GI:13538837"
/translation="MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTROKSVEEG
EPPGGGEGPRSRPTAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAG
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KNRIHRLEVLDPVSGNVLHILTHKRLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
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GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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                                                                        1 TICCTGCACATCITIGGITCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCCAA
                                        Gaps
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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100.0%; Pred. No. 9.4e-10;
iive 0; Mismatches 0;
Score 61; DB 6; 1 Pred. No. 9.4e-10;
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Sequence 29 from Patent W00120003.
AX099802
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match 100.
Best Local Similarity 100.
Matches 61; Conservative
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AF214519
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LISPQAPPTGWDCLLRRPGAGITWREWGEHTCVDAMAYSSKLVIFDYLLEIKKAFRA
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QVHRLVLVDFTQHLGGVYSLSDILGALVLSPAGIDALGA"

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ISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFL
YRIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLXSRFDVI
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TQHLLGVVSLSDILQALVLSPAGIDALGA"
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SSERIRGKRRAKALRWTRQKSVEBGEPPGQGEGPRSRPAAESTGLEATFPKTTFLAQA
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Patent: WO 0120003-A 3 22-MAR-2001;
INSTITU MATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
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Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
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Sequence 3 from Patent W00120003.
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/db_xref="taxon:9606"
                                                                                                                                                   /protein_id="CAD10589.1"
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Sus scrofa
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1867)
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., 1e Roy, P. and
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Variants of the gamma chain of ampk, dna sequences encoding the
                                                                                                        (bases 1 to 229)
Cheung, P.C., Salt, I.P., Davies, S.P., Hardle, D.G. and Carling, D. Chenng, P.C., Salt, I.P., Davies, S.P., Hardle, D.G. and Carling, D. Chenng, Indicated on the Ampactivated protein kinase gamma-subunit isoforms and their role in AMP binding
Biochem. J. 346 Pt 3, 659-669 (2000)
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 DNN, UNITED KINGDOM Location/Qualifiers

1. .2500 /ouganism="Homo sapiens" //db_xref="taxon:9606"
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AX099774
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22. .1500
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/gene="AMPK gamma
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Best Local Similarity 100.
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                          Carling, D.
Direct Submission
                                Homo sapiens
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EPPGGGEGRERPTAGEGENTPEAGDEAGGGTPPTGMDCLPSDCTRSAAG
ESTDOVELATEFPATEAWECELEGILEERPALCLSPQAPPFKLGWDDELKFPGAQIYM
ERWQBHTCYDAMATSKIVIEDTMLEIKKAFFALYANGYRAAPLWBSKKQSFYGMLTI
TDFILVLHRYYREPLVQIYELEQHKIETKHAFFALYGSLRFPSLYSTSRDNSLFEAVYTLI
KNRIFHELVLDPVGGVVLHITHKEKLKFLHFFSSLLPRFSLYFTGDLGIFFRDL
AVVLETAPILTALDIFVDRRVSALPVVNECGQVVGIYSRPDYIHLAAQCTXHLDMSY
GEALRORTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDFTQHLLGVVSLSDILQ
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AJ249977 AJ249977.1 GI:6688200
AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
                                                                                                                                                                                                                                                                                                                  A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Reinsch, N., Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N., Kalm, E., Le Roy, P., Chardon, P. and Andersson, L. Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              913 TTCCTGCACCTTGCTTGCTGCCCGGCCCTCCTTCTTCTTACGCACTATCCAA 972
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2115)

Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., lannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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/protein_id="AAF73987.1"
/db_xref="GI:8215682"
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1. .2115
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Science 288 (5469), 1248-1251 (2000)
20280150
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/db_xref="taxon:9606"
/chromosome="2"
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AF214519.1 GI:8215681
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                                                              Homo sapiens.
                                                                                         HOMO sapiens
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Best Local S.
Matches 61
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/translation="MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
DSNTDHLDLGIEFSASAASGDELGIVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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KNRIHELPUDPVSGAVLHILTHRELKEHLHFGTLLERSPETLKRIDDGLGIGFRED
AVVEETAPILTALDIFVDRAVSALPVVRETGQVYGIXSREPVIHLAAQOTYNHLDMV
GBALRQRTLCLEGVISCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDLLQ
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Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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Pred. No. 3.5e-08;
0; Mismatches 3;
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Sequence 27 from Patent WO0120003.
AX099800
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/db_xref="G1:13538835"
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/organism="Sus scrofa"
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                                                       /note="AMPKG3"
                                                                            /codon_start=1
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 /gene="PRKAG3"
                                   /gene="PRKAG3"
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/protein_id="CA358898"
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YRTIQDLGIGTRRDLAVLETAPILTALDIFVDRRYSALPVNNETGQVVGLYGRFDVI
HLAAQQTVHLDMNVGBALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDE
TQHLGVVSLSDILGALVLSAGIDALGA"

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Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
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Milan,D., Jeon,J.T., LoofL,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
               Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Pred. No. 3.5e-08;
0; Mismatches 3;
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/chromosome="15"
/map="15q"
/tissue_type="skeletal muscle"
1. 1873
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GPPGPREGEPGRRPVAESASTGGAPFEKTAPLAGAPLLAEVDRPPTERDLIESBCASASAS
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HENGEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKGSFVGMLTI
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GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220856-A 1 14-WAR-2002,
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
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           Score 56.2; DB 6; Length 1873;
Pred. No. 3.5e-08;
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/note="unnamed protein product"
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AX398333
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AX398331
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/db_xref="taxon:9823"
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Best Local Similarity 95.1%;
Matches 58; Conservative
              92.1%;
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/translation-"MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
GPPGPRESPORRPYESTGGATFRAFILAGAPALLAEVNPFTERILEBUCASASA
DSWTDHLDDGIESSASAASGEGGLYEEKPAPCPSPEVLLPEKGANDELGKPGAQYYM
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TDFILVLHRYTSPLVQTYEIEBEKIETWREITIQGCFKPLVSISPNDSLFEAYYALI
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AVVEETAPILTALIFVDRRVSALPVVNETGQVGYNHLAAQQTYHLLDMN
GEALRQRTLCLEGGVLSCQPHETLGEVIDRIVREQVHRLVLVDBFQHLLGVVSLSDILQ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 5 14 MAR-2002.
Iowa State University Research Foundation, Inc. (US)
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                                                                    Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G. Novel prkag3 alleles and use of the same as genetic markers reproductive and meat quality traits Patent: WO 0203650-A 3 14-MAR-2002, Iowa State University Research Poundation, Inc. (US)
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                      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
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Pred. No. 3.5e-08;
0; Mismatches 3
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/db_xref="G1:21261111"
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Sequence 5 from Patent WO0220850.
AX398335
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Best Local Similarity 95.1
Matches 58; Conservative
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PAT 27-MAY-2002

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/prodel_101261121261115"
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TDFILVLHRYTRSPLVQIYEIEERKIEFWRETYLIGGCFKPLVSISPNDSLEBAYYALI
AVRIERLPVLDPVSGAVHILTHKRLLKFLHIFGTLCHPRFSFLYRTIQDIGIGTFRDL
AVNLETAPLICHEGVLSCQPHETLGEVUNSTGVYVGLYSRFDVHLLAAQOTYNHLDMNV
GEALRQRATLCLEGVLSCQPHETLGEVUDRIVREQVHRLVLVDDETQHLLGVVSLSDILQ
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 2022)
                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                     Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 914-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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Patent: WO 0120003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product"
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Pred. No. 3.5e-08;
0; Mismatches
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Sequence 31 from Patent W00120003.
AX099804
          Sequence 9 from Patent W00220850.
AX398339
AX398339.1 GI:21261114
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/db_xref="taxon:9823"
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Matches 58; Conservative
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Sus scrofa
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GEALRQRTLCLEGVISCQPHETLGEVIDRIVBEQVHRLVLVDBTQHLLGVVSESDILQ
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Pred. No. 3.5e-08;
0; Mismatches 3; Indels 0;
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Pred. No. 3.5e-08;
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95.1%;
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Best Local Similarity 95.1%;
Matches 58; Conservative
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PAT 02-APR-2001

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Variants of the human amp-activated protein kinase gamma 3 subunit
Patent: WO 0177305-A 3 18-0cT-2001;
Arexis AB (SE)
Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                    Query Match 92.1%; Score 56.2; DB 6; Length 2022; Best Local Similarity 95.1%; Pred. No. 3.5e-08; Matches 58; Conservative 0; Mismatches 3; Indels 0.
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/db_xref="taxon:9606"
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Search completed: June 13, 2003, 04:39:46 Job time : 194.613 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human AMP-activate	PRKAG3 CDNA. Homo	Human AMPK gamma s	Human AMPK gamma s	Pig AMPK gamma sub	Pig AMPK gamma sub	Pig wild-type PRKA	Pig PRKAG3 polymor	Pig PRKAG3 polymor
SUMMARIES	ID		AAH43685	AAD03296	AAD03320	AAD03295	AAD03319	AAD36456	AAD36457	AAD36458
	DB	22	22	22	22	22	22	24	24	24
	Query Match Length DB	547	1647	2109	2115	1867	1873	1873	1873	1873
dФ	Query Match	100.0	100.0	100.0	100.0	92.1	92.1	92.1	92.1	92.1
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AAD36459 AAD36460 AAD36460 AAD321 AAR4363 AAR81194 AAR(81194 AAR(81699 AAD08199	AA134811 AAF20812 AAF20882 AAF20891 AAA34760 AAA34760 AAA34766 AAC208901 AAF20880 AAA34767 AAA34767 AAA34767 AAA34767 AAA34767 AAA34767	ALIGNMENT Rinase subun kinase subun issue growth insus; throm ancer; tumou boid cell dis con; prolifer vascular gr vascular gr vascular gr vascular gr infe j; gene thera j; gene thera j; gene thera j; gene thera j; denoctati
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	44444444444444444444444444444444444444	ALIGN 3485 ABA08485 standard; CDNA; 547 BP. ABA08485; 11-JAN-2002 (first entry) Human AMP-activated protein kinase is Human; cytokine; cell proliferation, haematopoiesis regulation; tissue grinhibin; chemotaxis; chemotaxis; proliferation; metastasis; cancer; proliferation; metastasis; cancer; proliferation; metastasis; cancer; proliferation; metastasis; cancer; proliferation; inclanmatory condition; proatheroic inflammatory condition; proatherosclerosis; coronary heart discondisorder; osteoporosis; vasculations regeneration; vound healing; cell culture; drug screening; gene antisthmatic; osteopathic; vasciropic, antifungal; vulnerary; antilloer; ss Homo sapiens. WO200157188-A2. 09-AUG-2001.
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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                              21-JAN-2002
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                                                               PRKAG3 CDNA.
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                                                                                                                                                                                                                                       Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides. C antibodies against the polypeptides, methods of detecting the nuclectides. C polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby cylving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, stem cell growth factor activity. C harmactopolesis regulatory activity; itssue growth activity; charmactopolesis regulatory activity; itssue growth activity. C hematopolesis regulatory activity; itssue growth activity or charmactopolesis regulatory activitie; hamocataic, thrombolytic activities; achemostatic, thrombolytic activities; achemostatic, thrombolytic activities; achemostatic, thrombolytic activities; achemostatic, thrombolytic activities; captor or liquid activities; or may be protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., mapolid call disorders), chronic inflammatory conditions (e.g., asthma or arthritis), arterial ischaemia, bone disorders (e.g., mapolid conditions (e.g., asthma or arthritis), arterial ischaemia, bone disorders (e.g., asthma or arthritis), arterial schaemia, bone disorders (e.g., mapolid conditions (e.g., asthma or arthritis), arterial and fungal infections and ulcress), while those with the allow (e.g., of burns, incisions and ulcress), while those with manipulate stem english growth. Polypeptides may be used to promote wound the promote cell growth. Polypeptides with growth growth growth activities may be used in the treatment of viral, and manipulate stem english or promote cell growth gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                     Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
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                                                                                                                                                                                                                    Claim 1; Page 429; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH43685 standard; cDNA; 1647 BP.
                                                                            Liu C, Drmanac RT;
03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                     e.g. arthritis and cancer -
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                                                                                                         WPI; 2001-457740/49.
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                                             (HYSE-) HYSEQ INC.
                                                                                                                           P-PSDB; ABB11241
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/label= "T559C" /note= "Silent variation"

r "T559C"

/*tag=

'note= "Causes P71A"

/*tag= b /label= "C230G"

Location/Qualifiers 20..1489 /*tag= a /product= "PRKAG3"

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMP-activated protein Kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon resulting in the amino acid substitution PIA; in exon 4 variation may be a substitution of a G for a C at nucleotide 320, be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may variation may be a substitution of a T for a C at nucleotide 1377,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the full length cDNA encoding the human
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hes 0;
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100.0%; Pred. No. 1.7e-10;
tive 0; Mismatches 0;
   /*tag= d
/label= "C1037T"
/note= "Causes R340W"
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d
"C1037T"
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                                                                                                                                                                                                                                                                                    06-APR-2001; 2001WO-SE00765.
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(KALM/) KALM E.
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                                                                                                                                                                                  PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
Iannuccelli N, Gellin J, Le Roy P, Chardon P;
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                                                                                                                                                                         gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                   Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA,
                                                                                                                                                                                                                                                            (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                    AAD03296 standard; DNA; 2109 BP
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18-MAX-2000; 2000EP-0401388.
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                                                                                                                              (first entry)
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                             G 1067
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5'UTR
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Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; strKRG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbolydacte metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                              ooft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                         Length 2109;
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                                                                                                                                                                                                                                   Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
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                                                                                                                                                                                                                                                                                                   100.0%; Score 61; DB 22;
100.0%; Pred. No. 1.8e-10;
ive 0; Mismatches 0;
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(ANDE/) ANDERSSON L.
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1..1395
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18-MAY-2000; 2000EP-0401388
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Best Local Similarity 100.
Matches 61; Conservative
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(KALM/) KALM E.

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complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism cutivity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primars that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3. are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. are ransgenic animal and host cell transformed with PRKAG3 or a neterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 and is useful for detecting mutations in a Prkag3 gene, or of PRKAG3 and is useful in gene therapy.
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1390..1867
                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 61; DB 22; 100.0%; Pred. No. 1.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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18-MAY-2000; 2000EP-0401388.
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472..1389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
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                                                                                                                                               New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                   Robic A, Rogel-Gaillard C;
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                                                                                                                                                                                                                                                                             The present sequence is a cDNA encoding pig adenosine monophosphate (AMPP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK
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Pred. No. 6.2e-09;
0; Mismatches 3; Indels 0;
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                                   ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of PRKAG3 and is useful in gene therapy.
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95.1%;
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                                     Looft C,
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                                                     Iannuccelli N,
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                                   Andersson L,
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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma subunit gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /standard_name- "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                            AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
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                                                                                                                                                                                                                                          /*tag= a
/product= "Pig PRKAG3 wild-type protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malek M, Plastow G;
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Pred. No. 6.2e-09;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                  replace (595, A
                                                                                                                                                                                                                                                                                replace (89, Č)
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95.1%;
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18-JUN-2001; 2001US-299111P.
                      Pig wild-type PRKAG3 gene.
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                                                                                                                                                     Sus scrofa
                                                                                                                                                                                                                                                                                  variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK cardivity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing an promosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transpenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid nordain as sequence encoding the first cystathions in a PrKaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain compounds and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                               Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 6.2e-09;
0; Mismatches 3; Indels 0;
/product= "Sus scrofa complete Prkag3 protein"
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                                                                                                                                                                                                                                      (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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95.1%;
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18-MAY-2000; 2000EP-0401388.
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Gellin J,
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nes 58; Conservative
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Query Match Best Loc Matches

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase requiatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant DNA (PRRAG3-30).
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                                                                                                                                                                                                                                                                                       /*tag= a
/product- "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
replace (89, C)
                                                                                                                                                                                                                                                                                                                                      /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                          AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rothschild MF, Ciobanu DC, Malek M, Plastow G;
                                                                                                                           Pig PRKAG3 polymorphic variant DNA (PRKAG3-30)
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1..1395
                            AAD36457 standard; DNA; 1873 BP
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                                                                                             (first entry)
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Matches 58; Conservative
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gene; variant; ds.
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                                                            AAD36457;
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Pred. No. 6.2e-09;
0; Mismatches 3; Indels 0;
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                                                                                                                                                             Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
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                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replace (154, A)
/*tag= b
  BP
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/product= "Pig
AAD36458 standard; DNA; 1873
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95.1%;
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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                                                                                                                                                                                                                                                                      gene; variant; ds.
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Matches
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Sus scrofa.

Key

AAD36459;

RESULT 10 AAD36459

variation

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The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase requiatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
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/product= "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
replace (599, A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malek M, Plastow G;
                                                                                                                                                           Pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
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Pred. No. 6.2e-09;
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                                     AAD36460 standard; DNA; 1873 BP.
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95.1%;
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                                                                                                                     (first entry)
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nes 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-393850/42.
                                                                                                                                                                                                                       screening; meat qu
gene; variant; ds.
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                                                                                                                   09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-2002
                                                                                                                                                                                                                                                                               Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                variation
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                                                                              AAD36460;
RESULT 11
AAD36460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199)
                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "Pig PRKAG3 polymorphic variant (PRKAG3-199)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma subunit gene
                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening animals to determine those likely to produce larger litters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                            AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56.2; DB 24; Length 1873; Pred. No. 6.2e-09; ); Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malek M, Plastow G;
                                                                                                                                                         Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 98-100; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                     AAD36459 standard; DNA; 1873 BP
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95.1%;
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                                                                                                                     (first entry)
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24; Length 1873; Indels

Query Match Best Local &

Matches

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Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such as myopathy and cardiovascular diseases, to modulate AMPK
activity, and for restoring a normal AWPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic disorder,
preferably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered allele of PRKAG3.
Transgenic animal and host cell transformed with PRKAG3 or a
heterotrineric AWPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AWPK activity. Nucleic acid
encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                       PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalm E, Milan D, Robic A, Rogel-Gaillard C;
J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                          Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                 /*tag= a
/product= "Sus scrofa Prkag3 splice variant"
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                               Sus scrofa PRKAG3 splice variant DNA.
                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                 AAD03321 standard; DNA; 2022 BP
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18-MAY-2000; 2000EP-0401388.
                                                                                                       (first entry)
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Gellin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-244810/25.
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                                                                                                      13-JUN-2001
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                                                                          AAD03321;
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                       RESULT 12
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                                          1 TICCIGCACAICTINGGITCCCIGCTGCCCCGGCCCTCCTCCTCTACCGCACTAICCAA
                        Gaps
                                                                                                                                                                                                                                                        Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ds.
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 Length 2022;
                       Indels
 DB 22;
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                                                                                                                                                                                                                                                                                                                                             'number = "Intron 4"
'note= "3' portion of intron 4"
Score 56.2; DB 22
Pred. No. 6.2e-09;
0; Mismatches 3
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r= "Intron 6"
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                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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'number= "Intron 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Intron 8"
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 92.1%;
95.1%;
                                                                                                                                                                                                                                   PRKAG3 intron 4 - intron 10.
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          Local Similarity 95.1 tes 58; Conservative
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2820 recrecaccicacceerracearcreccarecacrecrerrerececacreccare 2761
                                                                                                                                                                                                                                     polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) as useful in gene therapy techniques to restore normal activity of (II) as useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36006.
                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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Pred. No. 8.6;
0; Mismatches 20; Indels
                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3238 BP; 926 A; 915 C; 858 G; 539 I; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                          Claim 1; SEQ ID No 13137; 103pp; English.
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2000US-0189874.
2000US-0190076.
2000US-019123.
2000US-020515.
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ilarity 66.7%;
Conservative (
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2000US-0184664
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    2001-639362/73.
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nes 40; Conserv
                        P-PSDB; ABG13146
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19-MAY-2000;
07-JUN-2000;
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16-MAR-2000;
17-MAR-2000;
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                                                                                                                                      biodiversity
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24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2000;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                      New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRRAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the
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23-AUG-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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Search completed: June 13, 2003, 03:00:00 Job time: 22.1613 secs

us-09-826-581-5_copy_1007_1067.rst

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June 13, 2003, 02:37:44; Search time 151.839 Seconds (without alignments) 6506.409 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	æ	Query Match	56.2 92.1	48.2	45.9	45.2	44.9	44.9
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	4444444444	1000000000000000000	RESULT : B134452: LOCUS DEFINIT: ACCESSION VERSION KEYWORDS SOURCE ORGANI	REFEREN AUTHOI TITLE JOURNI COMMENT

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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                AQ997354 1inear GSS 24-FEB-2000 RPCI-23-271P21.TV RPCI-23-271P21
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musiae; Musiaes I to 389)
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Moubulished (1999)
Other_CSS: RPCI-23-271P21.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 638                                                                                                                                                                   5 TGCACATCTTTGGTTCCCTGCTGCCCGGCCCTCCTTCCTCTACCGCACTATCCA 59
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        70.9%; Pred. No. 1.5e+02;
tive 0; Mismatches 16;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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//incle="Organ: small intestine; Vector: pCMV-SPORT6;
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                                                                                                                                                                                      /organism="Sus scrofa"
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/tissue_Lype="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
a 190 c 151 g 124 t l others
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I. M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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11ve 0; Mismatches 3; Indels 0
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http://image.llnl.gov
High quality sequence.stop: 473.
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Plate: 119 row: I column: 11
Seq primer: ATTTAGGTGACACTATAG.
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BM556730
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Matches 58; Conservative
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Gaps

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/dev_gatge="1-5 day adult"
//dev_gatge="1-5 day adult"
//lab_host="SOLR (Stratagene)"
//note="Corgan: testis; Vector: pBlueScript SK (Stratagene);
Site_1: ECOR I: Site_2: Xho I: Testes dissected from 1-5
day adult y[*] w[67c1]/Y males raised at 25cc. RNA
isolated using Trizol (Life Technologies) and a single
round of Poly(A) + selection using Oligotex (Qiagen). CDNA
library constructed using Stratagene ZAP-CDNA syntesis
kit. Oligo dT-primed, size fractionated -1-6 kb, and
directionally cloned at Ecorg and XhoI in Uni_ZAP XR.
Following a single round of amplification pBlueScript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.

Requests for clones cannot be honored."
Email: oliver@helix.nih.gov,
http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).
Seq primer: MISRPI reverse primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Drosophila melanogaster adult testis library"
/sex="male"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 701)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov
Plate: LLCM336 row: g column: 03
High quality sequence start: 7
High quality sequence start: 7
High quality sequence
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/strain="y[*] w[67c1]/Y"
/db_xref="taxon:7227"
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Best Local Similarity 69.8%; Pred. No. 4.9e+02;
Matches 37; Conservative 0; Mismatches 16
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BE408262
BE408262.1 GI:9344712
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BE408262/c
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  BF528264 626 bp mRNA linear EST 11-DEC-2000 602043043F1 NCI_CGAP_Brn67 Homo sapiens CDNA clone IMAGE:4180619
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Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm Bl-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: brain, Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2:3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MgC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMA9492 row; f column: 12
High quality sequence start: 130
High quality sequence stop: 605.
Location/Qualifiers
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Drosophila melanogaster

Bukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster testis expressed sequence tags
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4180619"
/clone_lib="NCI_CGAP_Brn67"
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BE978092.1 GI:10609221
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                                                  5', mRNA sequence.
BF528264
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Mon Jun 16 09:56:16 2003

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fruit fly.

Drosophila melanogaster

Bukaryota; Merazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Boptera; Endopterygota: Diptera; Brachycera; Muscomorpha;

Bopydroidea; Drosophilae; Drosophila,

(Dassa 1 to 715)

Stapleton,M., Brokstein,P., Hong,L., Adbayani,A., Baxter,E., Berman, B., Carlson,J., Champe,M., Chavez,C., Chew,M., Dorsett,V., Farfan,D., C., Miranda,A., Misra,S., Mungall,C.J., Nunco,J., Parfsb., Miranda,A., Misra,S., Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S., Celniker,S. and Rubin,G.M.
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/sex="male"
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                                                                                                                                                                                                                                                                                                  BF488250
715 bp mRNA linear EST 23-APR-200 AT23475. prime AT Drosophila melanogaster adult testes pOTB7 Drosophila melanogaster cDNA clone AT23475 5 similar to CG4714:
EBan0004714 located on: 2R 49F15-50A1:: 04/09/2001, mRNA sequence.
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             Gaps
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hit genomic AEO03819: arm.2R [8082036,8314191]
hit genomic AEO03819: arm.2R [8082036,8314191]
Pate: Ar.234 row: G column: 3
High quality sequence stop: 674.
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/lab_host="Plates Ar.10-Ar.120: DH5-alpha. Plates
Ar.121-Ar.319: DH5-alpha TonA"
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      11;
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Unpublished (2000)
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/clone="AT23475"
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      Conservative
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/ tissue_type="natural killer cells, cell line"
/ tab_host="Publis (phage-resistant)"
/ note="Organ: blood; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI, cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/AhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH.MGC Library.

NIH.MGC Library.
                                                                                                                    /lab host="Drion Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 706)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consorthum/LLNL at:
http://image.llnl.gov
Plate: LLCM1689 row: i column: 02
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National Institutes of Health, Mammalian Gene Collection (MCC)
Unpublished (1999)
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Pred. No. 5e+02;
0; Mismatches 11; Indels 0
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Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
                                                             /clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_106"
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Location/Qualifiers
                              /clone="IMAGE:3637274"
/db_xref="taxon:9606"
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75.68;
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Best Local S.
Matches 34
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BG4/9U5/ 757 bp mRNA linear EST 21-MAR-2001 002526134F1 NIH_MGC_21 HOMO sapiens CDNA clone IMAGE:4649792 5',
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 757)
                                                                                                                                                                                                                                             Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
melanogaster cDNA clone GH03085 5 similar to CG4714: FBan0004714 located on: 2R 49F15-50A1;: 04/10/2001, mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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hit genomic AE003819: arm:2R [8082036,8314191]
estimated-cyto:49F2-50A3: 04/10/2001
Plate: GH.30 row: H column: 1
High quality sequence stop: 754
                                                                                                                                  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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/clone_lib="GH Drosophila melanogaster head pOT2"
                                                                                                                                                                              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 754)
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Other_ESTs: GH03085.3prime
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Pred. No. 5.1e+02;
0; Mismatches 16; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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Contact: Robert Strausberg, Ph.D.
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/dev_stage="adult"
/lab_host="DH5 - alpha"
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Tissue Procurement: ATCC
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Fax: 510 486 6798
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/lab_host="bH108" (phage-resistant)"
/note="organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 913)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Cloe distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAM10409 row: f column: 13
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
http://mage.lnl.gov
Plate: ILCM1430 row: c column: 09
High quality sequence stop: 757.
1. 757.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Notact: Strausberg, Ph.D.
Emall: ogapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/clone_lib="NIH_MGC_21"
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/clone="IMAGE:4517004"
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/Ugdistand. now!o Sapiens/
/Clone="InAGE:3346077"
/Clone=lib="NIH_MGC_20"
/Issue_type="melancitc melanoma"
/Iab_host="DHIOB (phage-resistant)"
/note="Organ: skin: Vector: pOTB7; Site_1: XhoI; Site_2:
/Organ: skin: Vector: pOTB7; Site_1: XhoI; Site_2:
//Organ: Skin: Vector: pOTB7; Site_1: XhoI; Site_2: Callifornia, Berkels, skin: Skin:
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Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 921)
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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High quality sequence start: 5
High quality sequence start: 5
High quality sequence stop: 742.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 5.2e+02;
0; Mismatches 11; Indels 0;
                                                                                                                  Length 913;
                                                                                                                                                                                                                                                                      1 INCCRECACATETTTGGTTCCCTGCTGCCCCGGCCCTCCTTCCTC 45
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                                                                                                            Score 27.4; DB 12; Length Pred. No. 5.2e+02; 0; Mismatches 11; Indels
Note: this is a NIH_MGC Library." 254 c 287 g 146 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BE275257
BE275257.1 GI:9150210
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1 Similarity 75.6%;
34; Conservative (
                                                                                                            ch 44.9%;
1 Similarity 75.6%;
34; Conservative (
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                                                                                                                  Query Match
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DEFINITION
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BE275257/c
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                           BASE COUNT
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cloue_lib="NIH MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/tab_nost="bHi0B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH—MGC Library."

a 229 c 328 g 145 t
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Sperimatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Zea.
                                                                                                             Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 926)
                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be flound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                        NIH'MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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Pred. No. 5.2e+02;
0; Mismatches 11; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TICCIGCACATCITIGGITCCCIGCIGCCCGGCCCTCCTICCIC 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    648.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mays cDNA, mRNA sequence.
BQ048516
BG291149
BG291149.1 GI:13048809
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11 Similarity 75.6%;
34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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ORIGIN
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                                                 /organism="zea mays"
/cultiva="zNS (Black Mexican Sweet)"
/db.xref="tasnscon:4577"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammaliai; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 887)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://mage.llnl.gov
Plate: LiAM10258 row: f column: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.6%; Score 27.2; DB 14; Length 569; 67.9%; Pred. No. 5.5e+02; Live 0; Mismatches 18; Indels 0.
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/clone_lib="WCI_CGAP_Mam1"
/clsue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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Location/Qualifiers
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Location/Qualifiers
1. .569
                                                                                                                                                                                                                                                         /lab_host="DH10B"
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Matches 38; Conservative
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Mus musculus
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BG174779/c
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TITLE
JOURNAL
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KEYWORDS
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Search completed: June 13, 2003, 05:58:32 Job time : 155.839 secs

Perfect score:

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Run on:

Scoring table:

Total number

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Sequence 10, A
Sequence 3, Ap
Sequence 3, Ap
Sequence 1, Ap
Sequence 7, Ap
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                                                            Sequence 3,
Sequence 3,
                                                                                                Sequence 3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strader, Catherine D
Strader, Joseph B
Borkowski, Joseph B
Ransom, Richard W
TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
BK-2 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARB: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,708
FILING DATE: 08-NO. 6407207-1993
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                        4 US-09-103-840A-2
4 US-09-103-840A-1
US-09-576-160B-10
US-09-576-160B-11
US-09-199-637A-164
US-08-200-016-4
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US-09-103-840A-1
US-08-852-091-3
US-08-822-091-3
US-08-956-652-3
US-08-956-869-3
US-08-948-547-3
US-09-364-970-10
US-09-956-653A-3
US-09-087-465-1
US-09-087-465-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 18713
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/860,709
FILING DATE: <01ANOWD-
ATTORNEY/AGENT INFORMATION:
NAME: CATUSO, Charles M
REGISTRATION NUMBER: 30161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-08-148-708-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7, Application US/08148708; Patent No. 6407207; GENERAL INFORMATION: APPLICANT: Hess, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: cDNA to mRNA
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                                  37.4 3943 37.4 3943 37.4 3943 37.4 3943 37.4 3943 37.4 3943 47.4 3943 47.4 3960 37.4 4411529 47.4 36.7 11613 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 36.7 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 4 4440 1.1013 
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STATE: NJ
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Best Local Similarity
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US-08-148-708-7
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Patent No. 5171671
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4027.262 Million cell updates/sec
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Sequence 3, Al
Sequence 3, Al
Sequence 7, Al
Sequence 25, J
Sequence 3, Al
Sequence 3, Al
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Sequence 7, A
Sequence 52,
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Sequence 9, 8
Sequence 3, 8
Sequence 2, 1
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Sequence 1
Sequence 1
Sequence 2
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Sequence 3
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-466-906B-3
US-08-706-281A-3
US-09-201-746-3
US-08-592-383-7
US-08-592-383-7
US-08-592-383-3
US-08-592-383-3
US-08-592-383-3
US-08-592-383-3
US-08-592-383-3
US-08-592-383-1
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US-08-729-955A-2
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US-08-759-848-2
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                                                                                                                                                                                                                                                                                                                                    441362 seqs, 153338381 residues
                                                                                                                                                                                US-09-826-581-5_COPY_1007_1067
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Maximum Match 100%
Listing first 45 summaries
                                                                                            using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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3258 2
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1929
1101
2051
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Match 1
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Score

Result Ş.

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TITLE OF INVENTION: Cloned and Expressed Human Bradykinin \ensuremath{\mathsf{BK-2}} Receptor
                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE:
ABTOR SEE:
BOO. BOX 2000
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (908) 594-4830
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                       COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1179 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: John W. Wallen III
STREET: 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                        NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rahway
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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US-08-759-848-2
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Strader, Catherine D
BOXKOWSKI, JOSeph B
ROXKOWSKI, JOSeph B
RAISOM, Richard W
RAISOM, Cloned and Expressed Human Bradykinin
BK-2 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 909;
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,708
FILING DATE: 08-No. 6407207-1993
CLASSIFICATION CUNNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/860,709
20;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: CUDKIDGED ATTORNEY/AGENT INFORMATION:
NAME: CATUGE, CHALLES M
REGISTRATION NUMBER: 30161
REFERENCE/DOCKET NUMBER: 18713
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (908) 594-4830
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-148-708-3
Sequence 3, Application US/08148708
Patent No. 6407207
GENERAL INFORMATION:
                                                                                                                                                                         Sequence 9, Application US/08148708
Patent No. 6407207
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hess, John W
38; Conservative
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
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Matches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARR: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,708
FILING DATE: 08-NO. 6407207-1993
CLASSIFICATION: CURNOWN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08759848
Patent No. 5750826
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Borkowski, Joseph A.
APPLICANT: Strader, Catherine D.
APPLICANT: Chen, Howard Y.
APPLICANT: Chen, Howard Y.
APPLICANT: Trumbauer, Myrna E.
TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED
TITLE OF INVENTION: NON-HUMAN ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURE SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUBBER: 07/860,709
FILING DATE: CIGNON:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              NAME: Caruso, Charles M
REGISTRATION NUMBER: 30161
REFERENCE/DOCKET NUMBER: 18713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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Score 26; DB 4; Length 1378; Pred. No. 4.5;
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BOrkowski, Joseph A.
APPLICANT: Strader, Catherine D.
APPLICANT: Hess, John W.
APPLICANT: Cheo, Howard Y.
APPLICANT: Trumbauer, Myrna E.
TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED
TITLE OF INVENTION: NON-HUMAN ANIMALS
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09383
FILING DATE:
CLASSIFICATION:
APPLICATION:
APPLICATION
FILING DATE:
APPLICATION NUMBER: US 08/281,393
FILING DATE:
                                                                                                                                                                                       20;
                                                                                                                                               Query Match 42.6%; Score 26; DB 4
Best Local Similarity 65.5%; Pred. No. 4.5;
Matches 38; Conservative 0; Mismatches
                                TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-148-708-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9509383 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wallen III, John W.
REGIGSRATION UNDHER: 35,403
REFERENCE/DOCKET NUMBER: 1923
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1378 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: John W. Marker empRET: 126 E. Lincoln Avenue
      TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 65.5
Matches 38; Conservative
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: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.6%; Score 26; DB 1; Length 1378; 65.5%; Pred. No. 4.5; tive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,708
FILING ADTE: 08-NO. 6407207-1993
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 18713 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
                                                     CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281,393
FILING DATE: 27-UUL-1994
ATTORNEY/AGENT INFORMATION:
                     APPLICATION NUMBER: US/08/759,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hess, John W
Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: <UDKNOWN>
ATTOREY/AGENT INFORMATION:
NAME: CATUSO, Charles M
REGISTRATION NUMBER: 30161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (908) 594-4830
TELERAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19234
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08148708
Patent No. 6407207
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1378 base pairs
                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-759-848-2
                                                                                                                                                                                                                                             TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 65.3%,
".hog 38; Conservative
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                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1378 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NJ
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-148-708-6
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; Sequence 3, Application US/08706281A; Patent No. 6100048
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APPLICANT: Fan, Wei
APPLICANT: Boston, Bruce A
APPLICANT: Kesterton, Robert A
APPLICANT: Lu, Dongsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 67.3*
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960..1260
                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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MEDIUM TYPE: Floppy
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1..14
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USA
   Chicago
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ZIP: 60606
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LOCATION:
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LOCATION:
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US-08-466-906B-3
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                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 8
                                                                APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melancoyte Stimulating Hormone Receptor TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION WUBBER: US/07/866,979 CLASSIFICATION: 435
                                                                                                                           STREET: 10 South Wacker Drive, Suite 3000 CITY: Chicago STATE: 111nois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: No. 5532347nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEX: 910-221-5317
TELEX: 910-221-5317
TELEX: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                Sequence 3, Application US/07866979
Patent No. 5532347
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1260 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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FEATURE:
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US-07-866-979-3
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APPLICANT: Chen, Wenbiao
APPLICANT: Chen, Wenbiao
TITLE OF INVENTION: Methods and Reagents for Discovering and
TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagon
TITLE OF INVENTION: To Modulate Feeding Behavior in Animals
NUMBER OF SEQUENCES: 19
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Pred. No. 11;
0; Mismatches 17; Indels 0
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PSTERM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPPLICATION NUMBER: US/08/466,906B
FILING DATE: OG-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: NO. 5849871nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154-H
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAX: 312-913-0002
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STREET: 300 South Wacker Drive
CITY: Chicago
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TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.7%; Score 24.8; DB 4; Length 1260; 67.3%; Pred. No. 11; tive 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/097,231
FILLING DATE: 12-Jun-1998
CIASSIFICATION: <a href="https://doi.org/10.10/10/19/98/">CIASSIFICATION: <a href="https://doi.org/10.10/19/98/">CIASSIFICATION: <a href="https://doi.org/10.10/19/">CIASSIFICATION: <a href="https://doi.org/10.10/19/">CIASSIFICATION: <a href="https://doi.org/10.10/">CIASSIFICATION: <a href="https://doi.org/10.10/">CIASSIFICATION: <a href="https://doi.org/10.10/">CIASSIFICATION: <a href="https://doi.org/10.10/">CIASSIFICATION: <a href="https://doi.org/10.10/">CIASSIFICATION: <a href="https://doi.org/10.10/">CIASSIFICATION: <a href="https://doi.org/10.10/">Octobarchion:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 300 South Wacker Drive
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US-09-097-231-3
US-09-097-231-3
Sequence 3, Application US/09097231
Patent No. 6278038
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Cone, Wenbiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001 TELEFAX: 312-913-0002
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                            INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1260 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60606
COMPUTER READABLE FORM:
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STATE: Illinois
            TELEFAX: 312-913-0002
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                                                                                                                                                                                                                                                                                                                       NAME/KEY: 5'UTR
LOCATION: 1..14
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; LOCATION:
US-09-201-746-3
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FEATURE:
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67.3%; Pred. No. 11;
Live 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
TITLE OF INVENTION: and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-DEC-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6268221nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                                         ALELING DATE: 04-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100048 nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                         JMBER: US/08/706,281A
04-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/201,746
FILING DATE: 01-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 300 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 3, Application US/09201746
; Patent No. 6268221
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 67.39
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               960..1260
                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15..959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-201-746-3
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Sequence 3, Application US/08592383
Patent No. 5830760
GENERAL INFORMATION:
APPLICANT: Tsai, S. and S.J. Collins
TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Rec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 TITICGECTCAAGCTCGCTACCCAGCTCCACAAGCTTCCTTCATCTAACAGGCTATGCAG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TICCIGCACATCITIGGITCCCIGCTGCCCGGCCCTCCTTCCTCTACCGCACTAICCAA 60
US-09-347-878-25/c
; Sequence 25, Application US/09347878C
; Patent No. Gardell
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAVING ANALYTES
; FILE REFERENCE: 25865-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 25
; LENGTH: 2561
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                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1131)..(2399)
OCHER INFORMATION: Bescherichia coli nucleic acid encoding
OTHER INFORMATION: folypolyglutamate synthetase-dihydrofolate
OTHER INFORMATION: synthetase
PUBLICATION INFORMATION:
DATABBASE ACCESSION NUMBER: M32445/GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.7%; Score 24.2; DB 4; Length 2561; 62.3%; Pred. No. 19; Live 0; Mismatches 23; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Christensen, O'Connor, Johnson and Kindness 2800 Pacific First Centre, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct) INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,242
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-7190
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WOLD FOUNDAMENT AS-DOS 4.01
SOFTWARE: WOLD FOR MINDOWS 5.01-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 62.39
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                   ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
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STREET: ZOUL
TIMY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-592-383-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tsai, S. and S.J. Collins
TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Recept
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: page 11, RAR-alpha N-terminal region; positions 103 to 363 of SEQ.
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                                                                                                                                                                                                          DB 4; Length 1260;
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Christensen, O'Connor, Johnson and Kindness STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
                                                                                                                                                                                                     Score 24.8; DB 4; Length 1:
Pred. No. 11;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31.332
REFERENCE/DOCKET NUMBER: PHCR-1-7190
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1.206.682-8100; 1-206-224-0709(direct)
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible
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                                                                                                                LOCATION: 960.,1260
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word for Windows 5.01-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08/099,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08592383
Patent No. 5830760
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MS-DOS 4.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.7%;
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Best Local Similarity 67.3%;
Matches 35; Conservative (
                                              15..959
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                           3'UTR
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Best Local Similarity 66.0
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                           NAME/KEY:
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                         NAME/KEY:
                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
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    FEATURE:
                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY:
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Gaps

18; Indels

66.0%; Pred. No. 20; tive 0; Mismatches

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6 GCACATCTTIGGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCC 58
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Job time: 9.64516 secs
    Best Local Similarity 66.03
Matches 35; Conservative
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                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to MRNA
DESCRIPTION: page 4,RAR-alpha403 dominant negative; deleted of 1311-1596 of SEQ.
                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: DMITROVSKY, ETHAN
APPLICANT: DMITROVSKY, ETHAN
APPLICANT: WARRELL JR, RAYMOND P
APPLICANT: MILLER JR, WILSON H
APPLICANT: MILLER JR, WILSON H
APPLICANT: MILLER JR, WETHODS FOR THE DETECTION AND
TITLE OF INVENTION: TRRATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                              39.7%; Score 24.2; DB 2; Length 2658; 66.0%; Pred. No. 19; 18; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-JUL-1993
CLASSIFICATION ATA:
APPLICATION NUMBER: US/07/673,838
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/673,838
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REDECRATION NUMBER: 28,678
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-052
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH 2928 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/08095728B; Patent No. 5843642
LENGTH: 2658 base pairs
                                                                                                                                                                                                                              Query Match 39.7%
Best Local Similarity 66.0%
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY; CDS
; LOCATION; 103..1488
; OTHER INFORMATION:
US-08-095-728B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
CLONE: hRAR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1185 AVEN
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                       ; IMMEDIATE SOURCE:
; LIBRARY: cDNA
US-08-592-383-3
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39.7%; Score 24.2; DB 2; Length 2928;

Query Match

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Sequence 129, App Sequence 1, Appl Sequence 59, Appl Sequence 2280, Appl Sequence 6987, Appl Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli
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Sequence 92, Appl
Sequence 21, Appl
Sequence 11, Appl
Sequence 11, Appl
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Sequence 7, Appli
Sequence 5, Appli
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Sequence 3, Appli
                                                                                       (without alignments)
4579.068 Million cell updates/sec
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                                                                           June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds
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/cgn2_6/ptodata/1/pubpna/US07_BUB.coms.pub.seq:*
/cgn2_6/ptodata/1/pubpna/US06_BUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_BUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_BUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_BUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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/cgn2_6/ptcodata/1/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptcodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptcodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 US-09-811-944-21

US-10-288-160-3

0 US-09-819-944-19

0 US-09-810-92

0 US-10-044-090-92

US-10-269-353-21

0 US-09-790-264-11

0 US-09-790-264-11
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US-09-826-581-3

US-10-255-356-159

US-10-045-815-7

US-10-045-815-7

US-09-925-297-129

US-09-979-593-1

US-09-979-593-1

US-09-764-891-2280

US-09-764-891-6987
                                                                                                                                                                                                                                         hits satisfying chosen parameters:
                                                                                                                                                                                                                 1029858 seqs, 724030393 residues
                                                                                                                    US-09-826-581-5_COPY_1007_1067
61
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                                                                                                                                                                                                                                                                                                                                                            Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                   Listing first 45 summaries
                                                   using sw model
                                                                                                                                                                                         Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 08
Maximum Match 1008
                                                                                                                                                                                                                                                                     DB seq length: 0
DB seq length: 2000000000
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APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 St
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR APPLICATION NUMBER: US 60/195,665
NUMBER OF SEQ ID NOS: 14
                                                                           Sequence 19, Appl Sequence 19, Appl Sequence 16, Appl Sequence 22, Appl Sequence 22, Appl Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 509, Appli Sequence 509, Appli
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Sequence 421, App
Sequence 146, App
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10 US-09-764-898-74
9 US-10-073-865-52
10 US-09-764-813-421
10 US-09-764-819-145
9 US-10-269-353-19
9 US-10-269-353-16
10 US-09-790-264-19
10 US-09-790-264-22
10 US-09-790-264-29
10 US-09-790-264-29
10 US-09-790-264-30
10 US-09-790-264-50
10 US-09-978-679-50
10 US-09-978-675-50
10 US-09-978-675-50
10 US-09-978-675-50
10 US-09-978-675-50
10 US-09-978-675-50
10 US-09-978-675-50
10 US-09-978-192A-50
10 US-09-998-192A-50
10 US-09-998-192A-50
10 US-09-998-192A-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Andersson, Leif
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; LOCATION: (20)...(1486)
US-09-826-581-5
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ORGANISM: Homo sapiens
 LENGTH: 1647
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 Query Match
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; Sequence 3, Application US/09826581; Patent No. US20020142310A1

us-09-826-581-3

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 43.6%; Score 26.6; DB 9; Length 2322; Best Local Similarity 71.4%; Pred. No. 2.3; Matches 35; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wadhwa, Renu
APPLICANT: Wadhwa, Renu
APPLICANT: SUGINATA, Takashi
APPLICANT: Oblide, Akiko
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REFERENCE: 06501 091001
CURRENT APPLICATION NUMBER: US/10/045,815
CURRENT PILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/JP00/02731
PRIOR FILING DATE: 1099-04-26
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 2416
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: JP 11/118806
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-10-045-815-5
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; OTHER INFORMATION: n = A,T,C or G
US-10-045-815-7
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NAME/KEY: CDS
LOCATION: (12)...(1637)
FEATURE:
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
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US-09-925-297-129
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US-10-045-815-5
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                                                 APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, Stefan
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILLE REFERENCE: 11145-007001
CURRENT FILLNG DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR PLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 159, Application US/1025536
| Publication No. US20030087807A1
| GENERAL INFORMATION:
| APPLICANT: Greenspan, Ralph J.
| TITLE OF INVENTION: Methods for Identifying Compounds for ITILE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to ITILE REFERENCE: P-NI 3864
| TITLE OF INVENTION: Balance and the Perception of Gravity FILE REFERENCE: P-NI 3864
| CURRENT APPLICATION NUMBER: US/10/255,536
| CURRENT FILING DATE: 2002-09-25
| PRIOR APPLICATION NUMBER: US 60/168,579
| PRIOR APPLICATION NUMBER: US 60/168,579
| PRIOR APPLICATION NUMBER: US 60/168,579
| PRIOR APPLICATION NUMBER: US 60/168,579
| PRIOR APPLICATION NUMBER: US 60/168,579
| PRIOR APPLICATION NUMBER: US 60/168,579
| PRIOR APPLICATION NUMBER: US 60/168,579
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| PRIOR APPLICATION NUMBER: US 60/168,579
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| PRIOR APPLICATION NUMBER: US 60/168,579
| PRIOR APPLICATION NUMBER: US 60/168,579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.7%; Score 46.2; DB 10; Length 1722; 86.4%; Pred. No. 3.1e-07;
Live 0; Mismatches 8; Indels 0;
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Query Match

Best Local Similarity 69.8%; Pred. No. 1.2;

Matches 37; Conservative 0; Mismatches 16;
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APPLICANT: Wadhwa, Renu
APPLICANT: Sugihara, Takashi
APPLICANT: Ohide, Akiko
ITILE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REFERENCE: 06501-091001
CURRENT APPLICATION NUMBER: US/10/045,815
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/JP00/02731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10045815
Patent No. US20020160498A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 86.49
Matches 51; Conservative
                                   APPLICANT: Andersson, Leif
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Drosophila
US-10-255-536-159
     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
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Score 25.8; DB 9; Length 12043; Pred. No. 4.4; 0; Mismatches 17; Indels 0;
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                                                              APPLICANT: Lee, Helen H
APPLICANT: Lee, Helen H
TILE OF INVENTION: HAPLOCYPES OF THE ICAM2 GENE
FILE REFERENCE: MHH-04.25 PCT ICAM2
CURRENT APPLICATION NUMBER: US/09/979,593
CURRENT FILING DATE: 2001-11.14
PRIOR APPLICATION NUMBER: PCT/US01/14714
PRIOR APPLICATION NUMBER: PCT/US01/14714
PRIOR APPLICATION NUMBER: 60/201,946
PRIOR FILING DATE: 2000-05-05
NUMBER OF FILING DATE: 2000-05-05
NUMBER OF FILING DATE: 2000-05-05
NUMBER OF SEQ. ID NOS: 83
SOFTWARE: PATENTIN Ver. 2.1
SEQ. ID NO 59
LENGTH: 12043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (7902)
OTHER INFORMATION: PS10: polymorphic base G or A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (8037)
; OTHER INFORMATION: PS12: polymorphic base G or A
US-09-979-593-59
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LOCATION: (4141)
OTHER INFORMATION: PS3: polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (3697)
OTHER INFORMATION: PS1: polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: (4110)
OTHER INFORMATION: PS2: polymorphic base C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: (7155)
OTHER INFORMATION: PS6: polymorphic base G
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OTHER INFORMATION: PS5: polymorphic base A
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OTHER INFORMATION: PS11: polymorphic base
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OTHER INFORMATION: PS8: polymorphic base
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OTHER INFORMATION: PS9: polymorphic base
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OTHER INFORMATION: PS7: polymorphic base
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Best Local Similarity 67.9%;
Matches 36; Conservative (
      Choi, Julie Y
Denton, R. Rex
Kliem, Stefanie E
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapien FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
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NAME/KEY: allele
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILE REFERENCE: PA105
CURRENT APPLICATION UNDER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SEQ ID NOS: 928
LENGTH: 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                       42.6%; Score 26; DB 10; Length 1682; 64.4%; Pred. No. 3.7; tive 0; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels
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APPLICANT: Lee, Helen H. Rest
APPLICANT: Lee, Helen H. Krishnan
TITLE OF INVENTION: HALFOOTYPES OF THE ICAM2
FILE REFERENCE: MMH-0425 PCT ICAM2
CURRENT APPLICATION NUMBER: US/09/979,593
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: PCT/US01/14714
PRIOR PRILING DATE: 2001-05-07
PRIOR FILING DATE: 2000-05-07
PRIOR FILING DATE: 2000-05-05
NUMBER OF ESQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.1
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Publication No. US20030082555A1
GENERAL INFORMATION:
APPLICANT: Genaissance Pharmaceuticals, Inc.
APPLICANT: Chew, Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Genaissance Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                LOCATION: (24)
OTHER INFORMATION: n equals a, t, g, or c
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Publication No. US20030082555A1
GENERAL INFORMATION:
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67.9%;
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Best Local Similarity 67.9%
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Matches 38; Conservative
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                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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CRGANISM: Homo sapien
US-09-979-593-1
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US-09-979-593-1/C
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SEQ ID NO 1

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us-09-826-581-5_copy_1007_1067.rnpb

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SEQ ID NO 21
LENGTH: 200
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tive 0; Mismatches 20; Indels
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2280
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                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT AFILICATION NUBBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6987, Application US/09764891
Fublication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUBBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
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                                                                                                                                 Sequence 2280, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
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Patent No. US20020038467A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
APPLICANT: Matthews, William
APPLICANT: Moore, Mark
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Matches 37; Conservative
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Best Local Similarity 64.9
Matches 37; Conservative
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US-09-764-891-2280
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                                                                                            RESULT 9
US-09-764-891-2280/c
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LOCATION: (9701)
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US-09-764-891-6987
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US-09-815-944-21
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TITLE OF INVENTION: Methods and Reagents for Discovering and Using Manmalian Melanocortin Receptor Agonists and Antag To Modulate Feeding Behavior in Animals
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Pred. No. 9.5;
0; Mismatches 17; Indels 0
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ADDRESSEE: ACCOUNCIL Boehnen Hulbert & Berghoff
ADDRESSEE: 300 South Wacker Drive
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ZIP: 60606
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 05-No. US20030105024A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: No. US20030105024Alnan, Kevin E
                                                                      FILE REFERENCE: R-654

CURRENT APPLICATION NUMBER: US/09/815,944

CURRENT FILING DATE: 2001-03-22

PRIOR PULICATION NUMBER: US 60/191,236

PRIOR FILING DATE: 2000-03-22

PRIOR APPLICATION NUMBER: US 60/215,214

PRIOR PELING DATE: 2000-06-29

PRIOR FILING DATE: 2000-06-29

PRIOR FILING DATE: 2000-06-29

PRIOR RELICATION NUMBER: US 60/219,167

PRIOR RELICATION NUMBER: US 60/219,167

PRIOR RELICATION NUMBER: US 60/219,167

PRIOR FILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FASTSEQ for Windows Version 4.0
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REFERENCE/DOCKET NUMBER: 96,886
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3, Application US/10288160; Publication No. US20030105024A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cone, Roger D
Fan, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 67.3%;
Matches 35; Conservative (
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Chen, Wenbiao
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SENERAL INFORMATION:
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Best Local S
Matches 37
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APPLICANT: Allen, Keith D.
APPLICANT: Matthews, William
APPLICANT: Matthews, William
APPLICANT: More, Mark
APPLICANT: More, Mark
APPLICANT: More, Mark
TITLE OF INVEWION: STIMULATING HORMONE RECEPTOR GENE DISRUPTIONS
TITLE OF INVEWION: STIMULATING HORMONE RECEPTOR GENE DISRUPTIONS
FILE REFERENCE: R. 654
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/191,236
PRIOR FILING DATE: 2000-03-22
PRIOR PAPLICATION NUMBER: US 60/215,214
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FEASTSEQ for Windows Version 4.0
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Pred. No. 9.7;
0; Mismatches 17; Indels 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-815-944-19; Sequence 19, Application US/09815944; Patent No. US20020038467&1
                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
IELEFAX: 312-913-0002
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Best Local Similarity 67.3%;
Matches 35; Conservative
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15..959
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                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                            LOCATION:
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GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVANTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REPERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
SEQ ID NO 92
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APPLICANT: Horne, Darci T.
APPLICANT: Horne, Joseph G.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe.
TITLE APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REPERBECE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US 60/214, 379
PRIOR PILING DATE: 2001-06-14
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-10-02
NUMBER OF SEX ID NOS: 3950
SOFTWARE: PALCHIN VER. 2.1
SEQ ID NO 3428
LIENGTH: 99014
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U78027
US-09-880-107-3428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24.4; DB 12; Length 733;
Pred. No. 13;
0; Mismatches 21; Indels 0
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 416842.32
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1 LOCATION: 665, 690, 698

7 OTHER INPORMATION: a, t, c, g, or other

US-10-044-090-92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cn 40.0%;
l Similarity 63.8%;
37; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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June 14, 2003, 11:14:11; Search time 4487 Seconds (Without alignments) 11168.939 Million cell updates/sec
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1722
I cctggcccctcagatcaaga......gatgagaggctcgggctgga 1722
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                OM nucleic - nucleic search, using sw model
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1. gb_ba:*

2. gb_bltg;*

3. gb_in:*

4. gb_om:*

5. gb_pl:*

9. gb_pl:*

9. gb_pr:*

9. gb_pr:*

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9. gb_ron:*

1. gb_sts:*

1. gb_sts:*

1. gb_sts:*

2. gb_ron:*

6. db_ron:*

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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AX281580 Sequence AC027416 Homo sapi AC009974 Homo sapi	Sus	Rattus	AX281582 Sequence	Seque	AF214519 Homo sapi AJ249977 Homo sapi	Rattu	AXVS5//4 Sequence AF214520 Sus scrof	AX099800 Sequence	AX398333 Sequence	AX398335 Sequence AX398337 Sequence	AX398339 Sequence	AX099804 Sequence G67375 A898 Human	Rattus	AL62/254 Danio rer aF329081 Ros tauru	Homo	Ношо	HOMO	Ношо	man : Homo	AK097606 Homo sapi	AX364914 Sequence	AF094763 Drosophil	AC019671 Drosophil	14 Drosophi	E003733	194 Sequence 1	AX482695 Sequence AF094764 Drosophil	34138 I			linear PAT 03-NOV-2001			Vertebrata; Euteleostomi; 1; Hominidae; Homo.	and Marklund,S. -activated protein kinase gamma 3 subunit -ocr-2001;
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ID	AX281580 AC027416 AC009974	AF214521 AF336381	AC128070	AX281582	AX099802	AF214519 HSA249977	AC127107	AF214520	AX099800 AX398331	AX398333	AX398335 AX398337	AX398339	AX099804 G67375	AC127107	AL52/254 AF329081	AC015613	AC019242	AC073610	AC025256	HSU4 24 12 BC000358	AK097606	AX364914 ACOO6966	AF094763	AC019671	AC009344	AE003733	166494	AX482695 AF094764	38413	ALIGNMENTS		1722 bp at W00177305.	31		Chordata; Cran Primates; Cata	н. алпр 18
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Page 2

		1081 ACAGTCCCTTCCCCAGTCCCAGTCTGAACTCACCTCTTCATCCTAGGCGGCACA 1140 	1141 CAGACAAGGGACCTIGGIGCCCTGCCTTTTIAGGGGCCTGGGAIGGAGGTTGTCT 1200 	1201 CTCCCTAGGCTGCCCCGAGGCTCACCTCCCATCTTGCAGCCTGTTGAAGCTGTTA 1260	1261 CACCCTCATCAAGAACCGGATCCATGCCTGCTGTTCTTGACCCGGTGTCAGGCAACGT 1320	1321 ACTCCACATCCTCACACACACCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGG 1380 	1381 CCCAGGTGGGAGGAGGAGCAGCAGGTGATCAGAGGCCTGAGGAGTCTTCAG 1440 	1441 CCCTAGCAGTCGTGGGGAAGAGCTGGGAGCCCTCTTGAAGCTGCTGGATCCCTGATCTCC 1500	1501 ACCTGGTCCCCATCCTAACCAGGTTCCCTGCTGCCCGGCCCTCCTCTCTCT	1561 TATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGTGCTGGAGACACCC 1620	CATCCTGACTGCACTGGACATCTTTGTGGACCGGGGTGTGTCT	1681 CGAATGTGGTACCCACCACGATGAGAGCTCGGGCTGGA 1722 	AC027416/c AC027416 152129 bp DNA linear HTG 07-JUN-2000	ON HOME Sapiens clone KPII-504GII, WOKKING DRAFT SEQUENCE, unordered pieces. N AC027416 AC027416.2 GIS317289	SW	Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo. REFERENCE 1 (bases 1 to 152129) AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E. TITLE Homo sapiens, clone RP11-504G11 JOURNAL Unpublished REFERENCE 2 (bases 1 to 152129)
90 40	oy Q	čo da	QY DP	oy Q	QY	o o	Š G	QY	Qy	QQ	Qy Ob	Qy	RESULT AC0274 LOCUS	ACCESSI VERSION	SOURCE ORGANI	REFER AUT TIT JOC REFER
FEATURES Location/Qualifiers 1172. source 1172. /db_xref="taxon:9606" DEASE COUNT 321 a 504 c 534 g 363 t	y Match Local Similar: hes 1722; Cons	CCTGGCCCCTCACATCAAGACGCCTTCTTTGCTCTGGTGGCGAACGGTGGCGCATGCGCGTGTTTTTTTT		ATCTCTGATAT 	ACCACAAGCTTGGCTTCAGCCCAAGCCCAGCCAGGGCCAGGGTGAAGAAGTCCATCC	241 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300 241 GGAGTCTGCAPTGGCCAGCTGGGAGACCCTGGGGCCTCAATTTCCCCATCTGTGGAGCCGT 300	301 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCATAGGTGCTAGGG 360	GGGCTGCCCC GGGGCTGCCCC	ACTGTCCTGTTCCCAAGGCCCACTGTGTCTCAGCACAAGGACACTGGCAGGGTGGGGAAH	GGGGATCTGACCTCAACCTGCCTTCCACCAAAGGCCCGGGGCTGACCTCCTCCCGCC		601 GGTCCCCCTGGTGAGGAGTGGGCAAATCTTATGGGCACCCAGAGGGGGGGG	661 AGGGAGTCCTCTGGAGCCTGGTGCCCTAGAAGCCCACGTCTTTCTGACTTCTGGAGTC 720	OY 721 CTGTCGATGTCTCTAGGTCCAGATCTATGAGATTGAACAACATGAGATTGAGACTGGAG 780 	781 GGGTGGGGGGGGAGGAACCCGGAAAGGGCTGTTGGTGATGGTGGCCCAGGCCTTAAG 840 	841 GTGGAGGATGGGCAGTGGGGATGTCCTGGAGTGAACAGGGGAGGGA

* 15044 15143; gap of 100 bp * 15144 17123; contig of 1980 bp in length 1724 17223; gap of 100 bp 1724 17233; gap of 100 bp 19467 19566; contig of 2362 bp in length 21929 20203; gap of 100 bp 24320 24319; contig of 2291 bp in length 24320 24419; gap of 100 bp 24320 24419; gap of 100 bp 24320 24419; gap of 100 bp 27160 7159; gap of 100 bp 27160 7159; gap of 100 bp 30271 33968; contig of 3011 bp in length 33969 34068; gap of 100 bp 33969 34068; gap of 100 bp 43869 24486; contig of 4087 bp in length 38280 42366; contig of 4087 bp in length 42367 42466; gap of 100 bp 42367 42466; gap of 100 bp 42367 42466; gap of 100 bp	#6366 46465; gap of 100 bp	contree (1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.
Birren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bouslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Colymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Gardgan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand, C., Harton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Looke, K., MacKernan, R., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, R., McPheeters, R., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, R., Peterson, R., Raymond, C., Hiey, K., Rogov, P., Rothman, D., Peisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Tafalamas, J., Ves, J., Viel, R., Vo, A., Tirrell, A., Travels, M., X., Wwman, D., Ye, M. J., Ves, J., Ves, J., Wassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wwman, D., Ye, M. J.	YOURGAG., Zainouu, J., Zimmer, A. and Zody, M. JOURNAL. Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome COMMENT On Jun 7, 2000 this sequence version replaced gi:7342115. Research, 320 Charles Street, Cambridge, MA 02141, USA ON Jun 7, 2000 this sequence version replaced gi:7342115. All repeats were identified using RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Center project Information Center project name: L7458 Center clone name: 504_G.11 Center project clone name: 504_G.11 Consensus quality: 145503 bases at least Q20 Insert size: 161000; agarose-fp Consensus quality: 145503 bases at least Q20 Insert size: 149029; sum-of-contigs Quality coverage: 3.1 in Q20 bases; sum-of-contigs	* NoTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. * 1006 1005: contig of 1005 bp in length 1006 2402: contig of 1297 bp in length 1106 2402: contig of 1297 bp in length 2403 2502: gap of 100 bp 2403 2502: gap of 100 bp 2503 3823: contig of 1321 bp in length 2503 15120: gap of 100 bp 2503 15120: gap of 100 bp 2503 5020: contig of 1041 bp in length 15120: gap of 100 bp 2503 5020: contig of 1041 bp in length 1548 7647: gap of 100 bp 7548 7647: gap of 100 bp 7548 1000 bp 7548 1000 bp 7548 1000 bp 7548 1000 bp 7548 12550: contig of 2473 bp in length 12557 12656: gap of 100 bp 100 bp 7548 12557 12656: gap of 100 bp 1000 bp 1

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                                                           PRI 09-JAN-2002
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                                                                                                                          1680
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                        TATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACC
                                                                                                                        CATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAA
                                                                                                                                                                                                                                                                                                                                    ACOU9974 206854 bp DNA linear PRI 09-JA
Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
ACO09974
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459I19
                                                                                                                                                                                                                            1681 CGAATGTGGTACCCACCCCAGGATGAGAGGCTCGGGCTGG 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: H_NH0459119
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Submitted (08-SEP-1999) Genome
University School of Medicine,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-NOV-2001) Genome
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Sulston, J.E. and Waters
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3 (bases 1 to 206854)
Waterston, R.H.
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5 (bases 1 to 206854)
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all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted: restriction digest

MAPPING INFORMATION:

a ò qq

Louis Mapping information for this clone was provided by Dr. John D. McPherson. Department of Genetics, Mashington University, St. I MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Gosegawa, K., Woon, P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J., and de Jong,P.J. (1988) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 208854 of RR11-459119. NEIGHBORING SEQUENCE INFORMATION: (http://bacpac.med.buffalo.edu) VECTOR: pBACe3.6

Data from AC079810 and AC073128 was used to finish this clone.

AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing. Location/Qualifiers

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'note="match to EST BE047599 (NID:g8364652) tz39c01.y1"
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                                                                                                                                                                                                                        /note="match to EST AL567345 (NID:g12920610)"
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/note="match to EST AW880850 (NID:g8042860)"
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'note="match to EST BF304755
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                                                                                      /chromosome="2"
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220 ..221 70cte="match to EST BG470047 (NID:g13402322)" 710...344 70ote="match to EST A1670836 (NID:g4850567) wa04g10.x1"

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Length 206854;

DB 9;

Score 1697;

98.58;

Query Match

166578 166278 166039 165919 165979 166638 166518 166398 166218 165860 165740 165680 166338 165800 1020 1080 3; 840 180 240 480 540 900 099 720 780 CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGTGAGGAGGAGGCTGGGGAGGTGAAG 120 300 360 420 900 960 9 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT AGGGGAGTCCTCCTGGAGCCTGGTGCCCTAGAAGCCCACGTCTTTCTGACTTCTGGAGTC CTGTCGATGTCTCTAGGTCCAGATCTATGAGATTGAACAACATAAGATTGAGACCTGGAG CTCCATCTCTCTAATGATAGGTGGCTGTCTCTGCTCATTCACCTGAGCCTCCTCCTCCCC GGGGATCTGACCCTCAACCTGCCTTCCACCCAAAGGCCCCGGGCTGACCTCCCCCGCC CCTCCCCTGCAGGGATGCTGACCATCACTTCATCCTGGTGCTGCATCGCTACTACA GTGGAGGATGGGCATGTCCTGGAGTGAACAGGGGAGGGACAATAGGAGCCTCG 165739 TGGCCTGACTCTGCTCTTTCTGCAGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGT CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCAGC **ACCACAGGTTGGCTTCAGGCCAAGCCCAGGGGCCCAGGGTGGAGGAAAGTCCATCC** GGAGTCTGCATGGCCAGCTGGGAACCCTGGGGCCTCAATTTCCCCCATCTGTGGAGCCGCT ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG ACTGTCCTGTTCCCACAGTCCCCACTGTGTCTCAGCACAAGGACACTGGCAGGGTGGGGA GGTGCCTGACGGAAGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGTGACCGGCTCCCC TGGCCTGACTCTGGCTCTTTCTGCAGAATCTACCTGCAAGGCTGCTTCAAGCCTCTGGT Gaps Indels ö Pred. No. 0; 0; Mismatches Conservative Best Local Similarity datches 1719; Conserv 421 661 1021 61 121 241 301 481 541 601 721 781 841 901 961 181 166457 Š

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2771. .2825,3027. .3153,3286. .3451,4578. .4615,4791. .4937,
5294. .>5410)
                                                                                                                                                                                                                                                                                      /product-"AMPK gamma subunit"
join(1. 154,515. 918,1809. 1890,2349. 2407,2509. 2554,
2771. 2825,3027. 3153,3286. 3451,4578. 4615,4791. 4937,
5294. 5410)
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DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGMDDELQKPGAQVYM
HFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLMDSKKQSFVGMLTI
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KNRIHHLPULDVSGAVALHITHRKLLKFLHFGTLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRAVALLVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMN
GEALRQRTLCLEGGVLSCQPHETLGEVIDRIYREQVHRAVLVDFTQHLGVVSLSDILQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC Box 597, Uppsala 751 24, Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGCTTGGCTTCAGGCCAAGCCCAGGGCCAGGGTGGAGGAAAGTCCATCCGGAG 244
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Pred. No. 1.9e-140;
0; Mismatches 484;
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/protein_id="AAF73989.1"
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                                                       Location/Qualifiers
1. .5888
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                                                                                                               /db_xref="taxon:9823"
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165679 CTCCATCTCTCCTAATGATAGGTGGGGGTGTCTCTGCTCATTCACCTGAGCCTCCTCCTCCT 165620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa AMPK gamma subunit (PRKAG3) gene, complete cds.
AF214521.1 GI:8215685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1620
                                   1081 ACAGTCCCCTTCCCCAGTCCCACTCAGCTCTGAACTCACCTCTTCATCCTAGGCGGCACA 1140
                                                                                                                                                                                          CTCCCTAGGCTGCCCCGAGGCTCACTGCTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTA 1260
                                                                                                                                                                                                                                                                      CACCCTCATCAAGAACCGGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCACAGGCAACGT 1320
                                                                                                                                                                                                                                                                                                                                                                                                                         CCCAGGTGGGAGGAAGGGGGAGACCTGGGCAGGTGATCAGAGGGCCTGAGGAGTCTTCAG 1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 5888)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 5888)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalin,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      excess glycogen content in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGACAAGGGAGCCTTGGTGCCCTGCCCTCTTTTTAGGGGCCTGGGATGGAGGTTGTCT
                                                                                                                                                                                                                                                                                      ACTCCACATCCTCACACACACACGCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Andersson, L. A mutation in PRKAG3 associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 288 (5469), 1248-1251 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                          5585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC128070 146577 bp DNA linear HTG 19-JUL-2002
Rattus norvegicus clone CH230-262H11, *** SEQUENCING IN PROGRESS
                                         1459 AGAGCTGGGAGCCCTCTTGAAGCTGCTGGATCCCTGATCTCCACCTGGTCCCCATCCTAA 1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CTAGATCAAGTGTCTTGATCTGATGAGATCACTACCATGTCCCATCTA 5536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1519 CCAGGGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCAT 1578
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1279 GATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCCACATCCTCACACA 1338
                                                                                                                                                           1339 CAAACGCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGGCCCAGGTGGGAGGAAGGG 1398
                                                                                                                                                                                                         GGAGACCTGGGCAGGTGATCAGAGGCCTGAGGAGTCTTCAGCCCTAGCAGTCGTGGGGGA 1458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5475 CGGCACATTCCGAGATTTGGCTGTAGTTCTGGAAACAGCTCCTGTCCTGACTGCGCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1639 CATCTTTGTGGACCGGCGTGTCTGCACTGCCTGTGGTCAACGAATGTGGTA 1691
                                                                                                                                                                                                                                                                                                                                                                                                     5603 GAGACCCACGGAGACACT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ***, 65 unordered pieces. AC128070
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Rattus norvegicus
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KEYWORDS
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pleces is not known and their order in this sequence record is
Peters, L., Pickens, R., Primus, E., Pu, L.L., Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, K., Tomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Mang, G., Walliamson, S., Warren, R., Washington, C., Watlington, S., Walliamson, A., Wille, W.Y. R., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid;
Assembly program: Phrap; version 0.990329
Consensus quality: 77418 bases at least Q40
Consensus quality: 77614 bases at least Q30
Consensus quality: 77614 bases at least Q30
Consensus quality: 7952 bases at least Q30
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-262H11
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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HTG: HTGS PHASE1.
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ANIBRO, D. Marie., Metzker, M. Lee., Abramzon, S., Addams, C., Aller, J., Alabbrooks, S., Adin, A., Angulano, D., Anyalebechi, V., Allan, H., Ababrooks, S., Adin, A., Angulano, D., Anyalebechi, V., Asyagi, A., Ayodeji, W., Baca, E., Baden, H., Balardanale, D., Barder, M., Barnstead, M., Benahmed, F., Barderin, D., Bandaranale, D., Barder, M., Crewn, M., Bryant, M., and J., Chen, E., Corner, M., Carter, K., Cavacos, I., Casar, H., Comer, A., D'Soura, L., Charderon, E., Chen, C., Coyle, M., Crew, D., D'Soura, L., Davila, M., Chen, S., Chen, R., Chen, Y., Chen, Z., Charder, M., Crewn, M., Davila, M., D
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On Aug 3, 2002 this sequence version replaced gi:22038439.
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Worley, K.C.
Direct Submission
Submitted (01-AuG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/denbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 consensus quality: 141109 bases at least Q40 Consensus quality: 148891 bases at least Q30 Consensus quality: 155675 bases at least Q20
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ILVANOYRAAPLWOSKGSYGWLTTIPDFILVLHRYYRSPLYOYIETBOHKIETREIY
LQGCFRPLYSISPHOSIFEAVYTLIKNRIHRLPVLDPVGDPVGNYLHITHKRLLKFLHIF
GSLLPRPSFLYRTIODLGIGTFRDLAVVLETAPILTALDIFVDRNSALPVVNBCGQV
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Primates; Catarrhini; Hominidae; Homo.
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                                                             TGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGG
                                        CTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGT
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Pred. No. 1.1e-30;
0; Mismatches 8;
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/db_xref="taxon:9606"
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AX281582
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0120003-A 3 22-WAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
1. 2109
/organism-Homo sapiens*
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
                                                                                                                                                                                                                                       Variants of the gamma chain of ampk, dna sequences encoding
                                                                                                                                                                                       Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 168.2; DB 6; Length 2109;
Pred. No. 1e-30;
0; Mismatches 8; Indels 0;
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                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product"
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AX099802
                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAC35799.1"
/db_xref="GI:13538811"
                               AX099776 2109 bp
Sequence 3 from Patent W00120003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX099802.1 GI:13538836
                                                                            AX099776.1 GI:13538810
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Best Local Similarity 95.6°
Matches 173; Conservative
                                                                                                                                                                                                                      Chardon, P.
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RESULT 9
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TDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLI
KNRHHELPULDVLDVOSNVHALLTHFRIKLKFLHFRSLLLRSPSELYRTIODAGGGFRDA
AVVLETAPILTALDIFUDRRVSALPVVNECQOVGIYSREDVIHLDAQOTVHHDASA
GEALRQRTLCLEGVISCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
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                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG
EPPGGGERERPRAFGARAFFYTPLAGADPAGVGFPTGWDCLDSCTASAAG
SSTDDVELATERPATEAMPCELEGLLEERPALCLSPQAPPFKLGWDDELRKPRQIYN
RFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLIT
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1 (bases 1 to 2115)
Milan, D., Jeon, J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P. and Andersson,L.
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Chardon, P.
Variants of the gamma chain of ampk, dna sequences encoding the
                                                                                   , well (SE); Looft, Christian (DE); Kalm, Ernst (DE) 1. .2115
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                                            same, and uses thereof
Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
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8
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/note="unnamed protein product"
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Pred. No. 1e-30;
0; Mismatches
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Science 288 (5469), 1248-1251 (2000)
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/db_xref="G1:13538837"
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/db_xref="taxon:9606"
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622 c 56
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/organism="Homo sapiens"
/db_xref="taxon:9606"
22. .1500
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22. .1500
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HTG; HTGS_PHASE1.
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     (bases 1 to 2290)
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Rattus norvegicus
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AC127107/c
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/translation="MSTSTELEGENSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG

/translation="MSTSTELEGENSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG

/translation="MSTSTELEGENSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG

STPOGGEGERSRTPAESVELEGENEGENEGENEGENEGENEGENEGWDELRKPGAQIYM

SSTDOVELATERPATEAWECELEGILEBRRPALCLSPQAPFPRLGWDDELRKPGAQIYM
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AVVLETAPILTALDIFVDRYSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSV
GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
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HOMO Sapiens mRNA for AMP-activated protein kinase gamma 3 subunit
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Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dasss 1 to 2290)

Cheung, P.C., Salt, LP., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
Biochem. J. 346 pt 3, 659-669 (2000)

20164049

10698692
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/protein_id="AAF73987.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
                                                                                                                                                                                                 /tissue_type="skeletal muscle"
1. .2115
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                                                                                      Location/Qualifiers
1. 2115
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                           /note="AMPKG3"
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AJ249977
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Homo sapiens
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GSLLPRPSTLYRIYOLGIGTFRDLAVVLETAPIHTALDIFVDRRVSALPVVNBCGQV
VGLYSRPSVVIHLAAQQYYNHLDMSVGBALRKRTLCLEGVLSCQPHESLGEVIDRIARE
QVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDPSGPEKI"
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LSPQAPFPKLGWDDELRYPGAQIYWRFIEEHTCYDAMATSSKLVIFDTWLEIKKAFFA
LVANGVRAAPLWDSKKQSFVGMLITIDFILVLHRYYRSPLVQIYEIEQHKIETWREIY
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Rattus norvegicus clone CH230-206A13, *** SEQUENCING IN PROGRESS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=experimental
/product="Amb-activated protein kinase gamma 3 subunit"
/protein_id="CAMES117.1"
/db_xref="GI:6688201"
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Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Harmersmith Hospital, DuCane Road, London, W12 ONN, UNITED KINGDOM
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Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Coyle, Coy, C., Coyle, M.D., Dathorne, S.R., David, R., David, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, C.D., Cox, C., Coyle, M.D., Dathorne, R.J., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flags, N., Ford, J., Esoter, P., Frantz, P., Garell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Harris, K., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, K., Hart, M., Hallyk, S., Hume, J., Jackson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, L., Kratcovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegd, H., Lozado, R.J., Lucier, R., Martindale, A., Martinez, E., Manhimer, E., Martin, R., Svatek, A., Rojubokan, I., Rolle, M., Martin, R., Martin, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 74 contisg. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 1105 bp in length
gap of unknown length
contig of 1170 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: GNHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 192968)
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JOURNAL
REFERENCE
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TITLE
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/translation-*MHFMORHTCYDAMATSSKIVIFDTMLBIKKAFFALVANGVRAAP
LWDSKKQSFVGMLTITDFILVLHRYRSPLVQIYEIEEHKIETWREIYLGGCFKPLVS
ISPNDSLFRAYYALIKNKTHRLPYLDPVSGAYLHILTHKRLIKFLHIFGTLLPRPSFL
YRTIODIGIGTFRDLAVVLETPPILTALDIFVDRNYSALPVVNETGQVVGLYSRFDVI
HLAAQQTYNHLDAWVGEALRORTLCLEGVLSCQPHETIGEVIDRIVYREQVHRLYLVDE
TQHLLGVVSLSDILQALVLSPAGIDALGA*
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Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A mutation in PRKAG3 associated with excess glycogen content in pig
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Chardon, P.

Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gailland,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Falm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
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Pred. No. 1e-25;
// Mismatches 20; Indels
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/codon_start=1
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0; Mismatches
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                                                                                                                                                                                                                                                     /protein_id="CAC35798.1"
                                                                                                                                                  /organism="Sus scrofa"
/db_xref="taxon:9823"
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Best Local Similarity 88.9
Matches 160; Conservative
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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/translation-"MSFLEQGESRSWPSRAVTTSSERSHGDGGNKASRWTRQEDVEEG
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KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
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Search completed: June 14, 2003, 16:15:58 Job time: 4498 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAH43681-84 represents genomic fragments encoding the human AAP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of a T for a C at nucleotide wariation and be a amino acid substitution of a T for a C at nucleotide wariation acid substitution R340W. There may also be nucleotide variation
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/note= "5' portion of intron 10"
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1689..1722
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                                                                                                              CATCCTGACTGCACACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAA 1680
                                                    ACTCCACATCCTCACACACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGG 1380
                                                                                                                                                          TATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACC
                          CACCCTCATCAAGAACCGGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New spatially-addressable set of single exon nucleic acid probes,
                                                                                                                                                                                                                                                                                                               microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                     CGAATGTGGTACCCACCCCCAGGATGAGAGGCTCGGGCTGGA 1722
                                                                                                                                                                                                                                                                                                 Human breast cell single exon nucleic acid probe #3401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank
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2000US-0207456.
2000US-0608408.
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2000US-0236359
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                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                     disease; cancer; ss.
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unclair acid probes for measuring gene expression in a sample derived from breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical cyprobes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for the measuring gene expression, with far less bias consist production of functional information from genomic sequence. The resquence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the proposition, but was obtained in electronic format directly consistence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGTGAGGAGGCTGGGGGAGGTGAAG 120
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                                                                                                                                                                                    relates to a spatially-addressable set of single
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useful for measuring gene expression in sample derived from breast, comprises number of single exon nucleic acid probes
                                                                                                           SEQ ID NO 3401; 327pp + sequence listing; English.
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ID ABA55162 standard; DNA; 378
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                                        23-JAN-2002 (first entry)
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                                                                                                                                                                                                                                                                                    26-MAY-2000; 30-JUN-2000; 20-JUN-2000; 21-SEP-2000; 27-SEP-2000; 24-OCT-2000; 2
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                                                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
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                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.4%; Score 351; DB 22; Length 378; 99.7%; Pred. No. 9e-83; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3467; 639pp + sequence listing; English.
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                                                                                                                                                                                                                                Rank DR;
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2000US-0608408.
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2000US-0234687.
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les 362; Conservative
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ABA24907/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGGCCAGGGTGGAGGAAAGTCCATCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
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Probe #3373 for gene expression analysis in human heart cell sample.
                                                            Human, gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCC 240
                                                                                                       241 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
                                                                                                                                                                                                ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG 360
                                                                                                                                                           GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO: 3431; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone marrow expressed single exon probe SEQ ID NO: 3431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DR;
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ID AAK28874 standard; DNA; 378 BP.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-02366.
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                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488900/53.
                                                                                                                                                                                                                                                  361 AGC 363
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27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTGGCCCCTCACATCAAGAAGCCTTCTTGCTCTGGTGGCCAACGGTGTGCGGGGAGC 60
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GGAGTCTGCATGGCCAGCTGGGAGCCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
                                                  ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG 360
                         63
                                                                62 ATGACCAGCTGACACTTTCACCTCGCTACTGCATGGCCCTGTG-CATAGGTGCTAGGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
             1; Gaps
                                                                                                                                                                                                                                                                                                   Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                           Human brain expressed single exon probe SEQ ID NO: 3414.
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11 Similarity 99.7%; Pred. No. 9e-83;
362; Conservative 0; Mismatches
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2000US-0234687.
2000US-0236359.
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                             epilepsy; cancer; ss.
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                                                                                                    AGC 363
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21-SEP-2000;
27-SEP-2000;
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30-JUN-2000;
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Probe; microarray;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
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                                                                                                                                          ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCC 240
                                                                                                                                                     GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT 300
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                                                                                                                                                                                                                         62 ATGACCAGCTGACATTTCACCTCCGCTACTGCATGGCCCTGTG-CATAGGTGCTAGGG 4
                                                                                                                                                                                                                                                                                                                                                                     gene expression analysis in human cervical cell sample.
                                   1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
                                           CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGGCTGGGGAGGTGAAG
                                                                                                        121 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \ensuremath{\mathsf{Human}} genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
20.4%; Score 351; DB 22; Length 378; 99.7%; Pred. No. 9e-83;
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                  0; Mismatches
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-06084008.
03-AUG-2000; 2000US-052366.
21-SEP-2000; 2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                     (first entry)
                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   cervical cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488901/53.
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         Similarity
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04-OCT-2000;
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The present invention relates to human single exon nucleic acid probes (SENF). The present sequence is one such probe. The SENFS are derived from human HeLa cells. The SENPS can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                   Length 378;
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                                                                                                                                                                                                                                                                                                                           Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                Query Match 20.4%; Score 351; DB 22
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI34821 standard; DNA; 378
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ABS03407/c
ID ABS03407 standard; DNA; 378 BP.
2001WO-US00661
                                                03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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29-JAN-2001;
                            26-MAY-2000;
30-JUN-2000;
                                                                             04-OCT-2000;
                   04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                   183
                                                                                                                                                                                                                                                                                                                                                                                ATGACCAGCTGACACCTTTCACCTCCGCTACTGCCATGCCCCTGTGCCATAGGTGCTAGGG 360
                                                                                                                                                                                                                                                                    303
                                                                                                                                                                                                                                                                                        CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGAGGCTGGGGAGGTGAAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; human, breast disease; breast cancer; development disorder; ss;
inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT
                                                                                                                                                                                                                                                                                                                                                                      ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCC
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                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #3335 used to measure gene expression in human breast sample.
                                                                              Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                1;
                                                                                                                                                                                                           20.4%; Score 351; DB 22; Length 378; 99.7%; Pred. No. 9e-83;
                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                       Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                         analyzing gene expression in human placenta
                                                                                                                                                                                                                               0; Mismatches
                                                                                                          Claim 25; SEQ ID No 3507; 654pp; English.
                                      Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                   (MOLE-) MOLECULAR DYNAMICS INC
                                      Chen W,
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI03344 standard; DNA; 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                               Matches 362; Conservative
                                      Hanzel DK,
                                                          WPI; 2001-488897/53.
                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGC 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
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                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                           Query Match
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases of the breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, prollferative breast disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                   Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 351; DB 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID No 3335; 322pp; English.
                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.48;
                                                       20000S-0632366.
20000S-0234687.
20000S-0236359.
2000US-0207456.
2000US-0608408.
                                                                                                                                                   2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.73
Matches 362; Conservative
                                                                                                                                                                                                                                                                  Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                         WPI; 2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                                                                                  in a human breast
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sarcoidosis, pulmonary

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DB 24; Length 378; Indels

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(MOLE-) MOLECULAR DYNAMICS INC
                                                                                                26-MAY-2000; 2000US-207456P.
30-JUN-2000; 2000US-0608408.
03-MG-2000; 2000US-23466P.
27-SEP-2000; 2000US-234687P.
04-OCT-2000; 2000US-0024263.
                                                                                     30-JAN-2001; 2001WO-US00665
                                                       hyaline membrane disease.
                                                                                                                                          WPI; 2002-114183/15.
                                                                                                                                   Hanzel
                                                                      WO200186003-A2.
                                                               Homo sapiens.
                                                                                            04-FEB-2000;
          19-AUG-2002
                                                                              15-NOV-2001
   ABS03407;
                                                                                                                                  Penn SG,
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DK,

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Human, cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis requiation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphold cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial isohaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CCCTCTATGGGACAGCAAGAAGCAGAGGCTTTGTGGGTGAGAGAGGGCTGGGGAGAGGTGAAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 ATGACCAGCTGACACTTTCACCTCGCTACTGCATGGCCCTGTG-CATAGGTGCTAGGG 4
                                                    paemosiderosis, pulmonary histiocytosis, lymphangioleiomyomicosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinfiammatory; antiasthmatic; antiarthritic; hemostatic; antiarteriosolerotic; cytostatic; osteopathic; vasctropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GGAGICIGCAIGGCCAGCIGGGAGACCCIGGGGCICAAITICCCCCAICIGIGGAGCCGCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.4%; Score 351; DB 24;
99.7%; Pred. No. 9e-83;
tive 0; Mismatches 0;
                            Niemann-Pick disease, Hermansky-Pudlak syndrome,
                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA08485 standard; cDNA; 547 BP.
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hes 362; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived concleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 sprobes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, comprising (a) identifying exons from genomic sequence by the method a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method in the above mentioned microarray; assigning exons to a single exon microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, patticularly cusing human lung derived mRNA and for the study of lung diseases cusing human lung derived mRNA and for the study of lung diseases cusing human lung derived mRNA and for the study of lung diseases cusing human lung derived mRNA and for the exons in the study of lung diseases cusing human lung derived mRNA and for the exons comm
                                                                                                                                                                                                                                                                                                                                                              Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicocytošis; lymphangiolejomyomicosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                            chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                 Human genome-derived single exon probe from lung SEQ ID No 3398.
                                                                                                                                                                                                                             Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       measure gene expression in human lung samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 3398; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
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                                                                                              (first entry)
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1630 TGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGG 1689
                                                      New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMP-activated protein kinase gamma 3 subunit (PRRAG3). Detecting the presence of the PRRAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon resulting in the amino acid substitution PIIA; in exon 4 variation may be a substitution of a G for a C at nucleotide 320, be a substitution of a T for a C at nucleotide 560; and in exon I variation may be a substitution of a T for a C at nucleotide 1037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the full length cDNA encoding the human
                                                                                                                             1690 TACCCACCCCCAGGATGAGAGGCTCGGGCTGG 1721
                                                                                                                                                             /*tag= c
/label= "T559C"
/note= "Silent variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= d
/label= "C1037T"
/note= "Causes R340W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andersson L, Luthman H, Marklund S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/label= "C230G"
/note= "Causes P71A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "PRKAG3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d "C1037T"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 5; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C "T559C"
                                                                                                                                                                                                                                                                                                          AAH43685 standard; cDNA; 1647 BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2001; 2001WO-SE00765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-2000; 2000US-195665P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; 00B47679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                         AAH43685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
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                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell afferentiation activities; stem cell growth factor activity; hammatopolesis regulatory activity; tissue growth activity; immunomodulatory activity; activity; tissue growth activities; chemotactic or chemokinetic activities; haemostatic, thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or amelicating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclensis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth, polypeptides involved with tissue regeneration and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1570 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 196; DB 22;
Pred. No. 9.6e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 429; 1963pp; English.
                                                                                                                                                                                                                                                                                rang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.4%;
95.3%;
                                                                                                   05-FEB-2001; 2001WO-US03800.
                                                                                                                                                  03-FEB-2000; 2000US-0496914
27-APR-2000; 2000US-0560875
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                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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WO200157188-A2.
                                                 09-AUG-2001
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13-JUN-2001
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                                      myopathy
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                                                                                                   1570 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTCCTGGAGACAGCACCCATCCTGAC 1629
                                                                                                                                                           1069 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1128
                                                                                                                                                                             1630 IGCACIGGACATCTITGIGGACCGGCGTGTGTCTGCACIGCCTGTGGTCAACGAATGTGG 1689
                                                                                                                                                                                        Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; perKKA3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrare metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Lannuccelli N, Gellin J, Le Roy P, Chardon P;
                                                                                    Gaps
resulting in the amino acid substitution R340W. There may also be nucleotide variation in introo 6. The numbering of these variations is based on the full length ODKA as given, rather than on position 1 of the open reading frame.
                                                              9.8%; Score 168.2; DB 22; Length 1647; 95.6%; Pred. No. 3.3e-34; Live 0; Mismatches 8; Indels 0;
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                                                                                                                                                                                                                                                                                                                                         Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                             Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human Prkag3 protein"
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(ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..471
                                                                                                                                                                                                                                                                                   AAD03296 standard; DNA; 2109 BP.
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18-MAY-2000; 2000EP-0401388.
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472..1389
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/product= "1
1390..2109
                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                          Best Local Similarity 95.6
Matches 173; Conservative
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                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAE00221
                                                                                                                                                                                                                 1690 T 1690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                      13-JUN-2001
                                                                                                                                                                                                                                    1189
                                                                                                                                                                                                                                                                                                    AAD03296;
                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                             Key
5'UTR
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The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMEK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in PrkAg3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism cut as diabetes, obesity, and disorders associated with muscle metabolism activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3 or transgenic animal and host cell transformed with PRKAG3 or a preservable compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 and is useful for detecting mutations in a PrkAG3 gene, or encoding PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bunnan AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  909 CCTGCACATCTTTGGTTCCCTGCTGCCCCGGCCTTCCTCTACTCACGCACTATCCAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1570 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGCTGCAGACAGCACCCATCCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.8%; Score 168.2; DB 22; Length Best Local Similarity 95.6%; Pred. No. 3.6e-34; Matches 173; Conservative 0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
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                                                                                                                                                                                                  Claim 12; Fig 2; 71pp; English.
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BP.

AAD03295 standard; cDNA; 1867

AAD03295;

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AAD03295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a cDNA encoding human adenosine monophosphate

(AMP)-activated kinase (AMEK) gamma subunit muscle-specific isoform,

complete PRKAG3. Mutation in Prkag3 results in an altered regulation of

carbobydrate metabolism, particularly in skeletal muscle. PRKAG3 is

useful as therapeutic for treating carbobydrate metabolism disorders such

as diabetes, obesity, and disorders associated with muscle metabolism

sy diabetes, obesity, and disorders associated with muscle metabolism

cutvity, and for restoring a normal AMFK function. PRKAG3 sequence

and its functionally altered mutants are useful for the diagnostic

evaluation, genetic testing and prognosis of a metabolic disorder,

preferably a carbobydrate metabolism disorder. Primers that can detect

a genetic polymorphic marker linked to a sequence encoding PRKAG3. are

useful for detecting a dysfunction of carbobydrate metabolism resulting

from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or are

neterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for

cercening compounds able to modulate AMPK activity. Nucleic acid

encoding PRKAG3 and is useful for detecting mutations in a prkag3 gene, or

of PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disc associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 2115;
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0; Mismatches 8; Indels
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95.6%; Pred. No. 3.6
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J, Le Roy P,
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                                                                                                                                                                                                                     10-SEP-1999; 99EP-0402236
18-MAY-2000; 2000EP-0401388
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Gellin J,
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LOOFT C.
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Iannuccelli N,
                           WO200120003-A2.
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The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, prkAd3 brkad3 gene is located in the RN locus of chromosome 15.

Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3 or a perecriment AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid cencoding PRKAG3 is useful for detecting mutations in a PrkAg3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
                                                                                                         PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                                                        gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                     Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
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/product= "Sus scrofa PRKAG3 protein"
1390..1867
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                                                                                                                                                                                                                                        Location/Qualifiers
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18-MAY-2000; 2000EP-0401388.
                 (first entry)
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                                                                                                                                                               chromosome 15; ss.
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                 13-JUN-2001
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                                                          0; Gaps
                                    Query Match 8.6%; Score 148; DB 22; Length 1867; Best Local Similarity 88.9%; Pred. No. 7.5e-29; Matches 160; Conservative 0; Mismatches 20; Indels 0
                   Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;
of PRKAG3 and is useful in gene therapy.
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AJ46118 AJ36118
AV608257 AV608257
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AA558845 n169b09.s
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRimers
FORMARD: AGGAAACAGCTATGACCAT
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 572)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Design and use of two pooled tissue normalized cDNA libraries for
BST discovery in swine
Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B1344527 572 bp mRNA linear 373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence. B1344527
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NO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4336
Fax: 402 762 4390
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AL047390
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BI821538
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COMMENT
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AUTHORS
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                                                                                               June 14, 2003, 11:14:11 ; Search time 2562 Seconds
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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em_gss_mam:*
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Maximum DB seq length: 200000000
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gb_htc:*
gb_est3:*
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BI819312 603037761 BI821538 603038457 BE871189 601448767 BQ216967 AGENCOURT

EST 30-JUL-2001

132.4 116.8 88.8 84.6 82.6

Score

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Direct Submission Submitted (12-ARR-2000)
Submitted (12-ARR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                           1543 CTCCTTCCTCACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGT 1602
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Roest-Crollius; H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Winoker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
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2 (bases 1 to 1042)
Roset-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Wetssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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/note="Genoscope sequence ID : C0BG033CF07LP1-end : T7"
1 282 c 241 g 271 t 6 others
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                                                                                                                                                                                                                                                                                                                                                                                                                  1603 GGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTC
                                                                                                                                                                                                                               Score 132.4; DB 9; Length 413;
Pred. No. 5e-21;
0; Mismatches 3; Indels 1
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/db_xref="taxon:99883"
/clone="033113"
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GSS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Best Local Similarity 97.3%;
Matches 144; Conservative (
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1 (bases 1 to 413)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylae, T., Waterston, R. and Wilson, R., Theising, B., Upublished (1997)

Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1570 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 CGCACTGGACATCTTCGTGGACCGGCGTGTCTGCGCTGCCTGTGGTCGACGAAACTGG 350
                                                                                                                                                                                                                               /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalmus, pituitary, and placenta." 1 190 c 151 g 124 t l others
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2588410...1 Stratagene muscle 937209 Homo sapiens CDNA clone
IMAGE:611731 5' similar to SW:AARG_RAT P80385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ;, MRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
TTE: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                      Score 148; DB 13; Length 572;
Pred. No. 1.1e-24;
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/tissue_type="muscle"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.1e-
0; Mismatches
                                                                                                                                   /db_xref="taxon:9823"
/clone_lib="MARC_2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="GDB:4643570"
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       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 119 row: I column: 11
Seq primer: ATTTAGGTGACACTATAG.
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                                                                         Location/Qualifiers
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AA178898.1 GI:1760259
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Matches 160; Conservative
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                                                                                                                                                                                                                           1358 CTGCACATCTTTGTAAG------CCTGGGCCCCAGGTGGGAGGGAAGGGGAAACCTGG 1408
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostoi; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
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Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics National Institute of Genetics For East, Mishima, Shizuoka 411-8540, Japan Fel: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  556 GTACATACCGGGACATIGCTTICATTCACCCCGACACGCCCATCATCAAAGCGCTCAACA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         673
                                                                                               17; Gaps
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                 Pred. No. 3.9e-17;
0; Mismatches 192; Indels
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/tissue_type="whole embryo"
/dev_stage="fry stage 40"
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/organism="Oryzias latipes"
     Score 116.8;
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/clone_lib="MF01FSA cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BJ495978.1 GI:22147904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="d-rR"
tch 6.8%;
al Similarity 56.3%;
269; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 591)
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     Query Match
                     Best Local
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                                   Matches
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JOURNAL
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KEYWORDS
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BJ495978
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BJ504184 728 bp mRNA linear EST 08-AUG-2002 BJ504184 MF01FSA CDNA Oryzias latipes CDNA clone MF01FSA006A14 3',
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                                                                                                                             1228 CTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCG 1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryzias latipes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.

1 (bases 1 or 728)
Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H. Whobblished (2001)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416 CACACCTGAGTCCAGCCTGTTTGACGCCATCTACTCGCTGCTGAAGAACAAGATCCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1241 AGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGCCTGCTTCTT
                                                                                               Gaps
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                                                        Length 591;
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   1 others
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  others
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National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                1348 GCICAAGTICCIGCACATCITIGIAAGCCIGGGCCC 1383
                                                    Score 88.8; DB 13;
Pred. No. 1.5e-10;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                                     male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.9%; Score 84.6; DB 13;
Best Local Similarity 77.9%; Pred. No. 1.6e-09;
Matches 102; Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="mixture of female and
/tissue_type="whole embryo"
/dev_stage="fry stage 40"
161 c 174 g 210 t
 ų
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 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="MF01FSA006A14"
/clone_lib="MF01FSA cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smail: tshini@genes.nig.ac.jp.
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130
                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BJ504184
BJ504184.1 GI:22156146
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                                                      5.28;
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                                                    Query Match
Best Local Similarity 73.13
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1361 CACATCTTTGT 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 CAACTGTTTAT 226
177
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150
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BASE COUNT
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BJ072114 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL096j16 5', mRNA sequence.
                                        1599 CIGIGGIGCIGGAGACAGCACCCAICCIGACIGCACIGGACAICITIGIGGACCGGCGIG 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1228 CTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATCCATCG 1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 AGCCGGAATTCATGTCTAAGTCTCTCCCAAGAGCTGCAGATTGGCACCTATGCCAATATTG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 crcccagcagacagccrrrrccaagcrgrgrarrcacrcarcaagaaraagarccacg
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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73.4%; Pred. No. 5.8e-09;
tive 0; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Context: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL096j16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Wellcome/CRC Institute).
                                                                                                                      1659 IGTCTGCACTGCCTGTGGTCAACGA 1683
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                                                                                                                                                          426 TCTCCGCCTTACCTGTAGTGGATGA 450
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                             BJ072114
BJ072114.1 GI:17502303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kenopodinae; Kenopus.
1 (bases 1 to 633)
                                                                                                                                                                                                                                                                                                                                                                                    African clawed frog.
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105; Conservat
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KEYWORDS
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BM488662
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                                                                            BG919314 100 933 bp mRNA linear EST 05-JUN-2001 602817782F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4946661 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1362 ACATCTTTGTAAG----CCTGGGCCCCAGGTGGGAGGAGGGGGAGACCTGGGCCAGGTGATC 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGGGCCTGAGGAGTCTTCAGCCCTAGCAGTCGTGGGGAAGAGCTGGGAGCCCTCTTGA 1478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH" 292 c 238 9 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 AGAGCGGTTGGGGACAGAGGAGCGGTGTTGGTGATGATGATGATGAGCGTAGCACCTCCATG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 CTCT-ATCCGGAAAGCACCTGCAAGCCAATGCCCCCTTCCTCAGATCACGGAGTTCCCA 305
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                         Email: gqapbs.r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMI0895 row: d column: 22
Bigh quality sequence stop: 498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 GICCGGTTGATGCTCTTCTTCATTAATTCGAAATAAGATCCACAGGCTCCCAGTTATCG
                                                                                                                                                                                                                                                                                1 (bases 1 to 933)
MHH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:4946661"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, Virgin"
/tssue_Lype="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"/strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .933
                                                                                                                                                          BG919314.1 GI:14299790
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=
                                                                                                                    mRNA sequence.
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                                                                                                                                                                                                  house mouse
                                                                                                                                       BG919314
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AUTHORS
TITLE
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                                                                                                                                       ACCESSION
                                   RESULT 6
BG919314
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/dev_stage="Breast, leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,1,1 weeks);growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coli Embil0B"
/note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1228 CTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATCCATCG 1287
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                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Cogburn, L.A. and Monsonego-Ornan, E.
ESTS from Normalized Chicken Breast Wuscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFARS Animal Genome
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Pred. No. 1.7e-08;
0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
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/strain="Commercial broiler
Strains 90 & 21"
                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
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BG713637
BG713637.1 GI:14007587
                                    GI:18608720
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BM487789.1
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BG713637
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/lab_host="E. coli EMDH10B"
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pgm2n.pk008.g21 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate obna library (pgm2n, plus gallus gallus cona clone pgm2n, pk008.g21 5' similar to gblAAC52580.1 (U42413) 5'.-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus
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/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
                                                                                                                                                                                                                                                    chicken.

Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Calliformes; Phasianidae;
Phasianinae; Gallus.

1 (bases 1 to 536)
Cogburn,L.A. and Monsonego-Ornan,E.
ESTS from Normalized Chicken Breast Muscle, Leg Muscle, and
EPiphyseal Growth Plate CDNA library, USDA/IFAFS Animal Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cogburn@udel.edu, www.chickest.udel.edu
Location/Qualifiers
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Strains 90 & 21"
/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Larry A. Cogburn
University of Delaware
Universed Hall, Newark, DE 19717, USA
Tel: 302-831-2822
Fax: 302-831-2822
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/organism="Gallus gallus"
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                                                                                                                                 , mRNA sequence.
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VERSION
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Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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AJ385115 dkfz426 Gallus gallus cDNA clone 21c2r1, mRNA sequence.
AJ395115.
AJ395115.1 GI:7125706
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.7%; Score 80.2; DB 13; Length 647; 69.4%; Pred. No. 1.7e-08; tive 0; Mismatches 48; Indels 0
                                                       /organism="Gallus gallus"
/strain="Commercial broiler and layer"
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/clone_11b="dkfz426"
/tissue_type="Bursa of Fabricius"
/cell_type="bursal lymphocyte"
/dew_stage="2-3 weeks old"
127 c 155 g 137 t
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      Location/Qualifiers
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BM440762

BM440762

BM5002.19 Normalized Chicken Reproductive Tract CDNA Library (pgrln) Gallus gallus CDNA clone pgrln.pk002.19 5' similar to gil4506061 ref|NP_002724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subbnit; AMP gamma 1; Protein kinase, AMP-activated, noncatalytic, gemma 1 | Homo sapiens| gil12737489 ref|xP_006778.2| protein kinase, AMP-activated, gamma 1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429 CTCCCCCAATGCCAGCCTTTTTGATGCCGTCTCCTCCCTGATGCGCAATAAGATCCACCG 488
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus; (bases I to 636)

Burnside,J.; Morgan,R.W. and Cogburn,L.A.
Chicken Esrs from a normalized liver library
Unpublished (2001)
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Cogburn, L.A. and Nys, Y.
ESTs from Normalized Chicken Reproductive Tract cDNA library-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 4.7%; Score 80.2; DB 12; Length 636; Similarity 69.4%; Pred. No. 1.7e-08; 09; Conservative 0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Gallus gallus"
/db_xefe="reaxon:901"
/clone="polln.pk008.cd3"
/clone_lib="Normalized Liver Library"
/sex="Male and Female"
/tissue_type="liver"
/lab_host="E.coli EMDH108"
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                                                                                                                                                                                                                                                                                                                                                                                                               Email: joan@UDel.Edu, www.chickest.udel.edu.
Location/Qualifiers
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University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
TEL: 302 831-1345
Fax: 302-831-3411
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215 c 167 g 119 t
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Tel: 302-831-1335
Fax: 302-831-2822
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University of Delaware
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                                                                                                                                                                                                                                        Contact: Joan Burnside
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Matches 109;
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AV603335 57-NOV-2001
AV603335 Bos taurus kidney fetus Bos taurus cDNA clone ELKI015F02
5', mRNA sequence.
AV603335
AV603335.1 GI:9725661
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Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 758)
Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.M.
A.J. Korn,B. and Buerstedde,J.M.
and Buerstedde,J.M.
and Jysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                  Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Bursa of Fabricius"
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/dev_stage="2-3 weeks old"
238 c 186 g 166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 4.6%; Score 78.6; DB 9; al Similarity 68.8%; Pred. No. 4.5e-08; 108; Conservative 0; Mismatches 49;
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Animal Genetics Division
Shirakawa Institute of Animal Genetics

    758
    /organism="Gallus gallus"

                                                                                                                                                                                                                                                                                                                                                                                            /strain="CB"
/db_xref="taxon:9031"
/clone="25f16r1"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="dkfz426"
                                                                                                                                                                                                                              20568495
Contact: Buerstedde JM
AJ396118.1 GI:7127728
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                                chicken.
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AV603335
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                                                                                                                      46 crececcaargecagecrrrrrgargecgrerecreerearcegearaagarceacg 105
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Gallus gallus
Gallus sallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
I (bases 1 to 687)
Buerstedde, J.M.
                                                                                                                                                                                                                                                                                                                                                          AJ451523 AJ451523 rikenl Gallus gallus cDNA clone 29a6r1, mRNA sequence.
AJ451523
                                                    0; Gaps
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                  Length 649;
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="298671"
/clone_lib="riken"
/cel_Ltypo="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
?28 c 191 g 125 t
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                Score 80.2; DB 9;
Pred. No. 1.8e-08;
0; Mismatches 48;
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Unpublished (2002)
Contact: Buerstedde JM
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                  4.78;
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                  Query Match
Best Local Similarity 69.49
Matches 109; Conservative
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TITLE
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Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan Tel: 81-248-25-5641

Fax: 81-248-25-5725

Email: kazusugiecoco.ocn.ne.jp
Single pass sequencing.
This clone was Obtained from a polyA-deleted cDNA library.
Location/Qualifiers
1. 576
1. 576
Ab_Arsf="taxon.9913"
/clone="ElKinDEFQ2"
/clone="ElKinDEFQ2"
/clone="ElKinDEFQ2"
/tissue_type="kidney"
/de_stage="fetus"
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Sequence 160,
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/cgn2_6/ptcdata/1/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
/cgn2_6/ptcdata/1/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptcdata/1/ina/bcAtiles1.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-467-781-3
US-08-195-487-3
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Sequence 11, App
Sequence 11, App
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TITLE OF INVENTION: NO. 6124125el AMP Activated Protein Kinase NUMBER OF SEQUENCES: 64
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                        PCT-0S93-06160-3

US-08-687-080-115

US-09-155-7618-1

US-08-455-543A-8

US-08-223-305C-8

US-08-149-097D-8

US-08-149-097D-8

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US-09-452-007-1
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ADDRESSEE: Jane Massey Licata, Esq. STREET: 66 E. Main Street
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
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TELEFAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: DISKETT
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TI-SENSE: NO
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Marlton
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US-09-101-146-63
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CITY: N
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Gaps

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4.0%; Score 68.8; DB 3; Length 1576; 57.4%; Pred. No. 4.9e-09; ve 0; Mismatches 47; Indels 0

67.48;

97; Conservative

Best Local Similarity Matches 97; Conserv

US-09-101-146-63 ANTI-SENSE:

Query Match

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; Patent No. 5885803
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NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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; CLONE: 1452972
US-08-878-989-14
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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ZIP: 94304
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US-08-878-989-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1026 TCTCTCCTAATGATAGGTGGTGTCTCTCTCATTCACCTGAGCCTCCTCCTCCTCCACAGT 1085
                                                           501 CAGCTTGTTTGATGCTGTCTCTTCATTAATTCGCAACAAGATCCACAGGCTGCCAGTTAT 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             906 CTGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGTGACCGGCTCCCCTGGCC 965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: 1BM PC COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CNORMENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.9%; Score 67.6; DB 1; Best Local Similarity 6.2%; Pred. No. 1.9e-08; Matches 25; Conservative 223; Mismatches 152;
                                                                                                                                                                                                                                         Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: FALKNER, F. G.
APLICANT: FALKNER, F. G.
APLICANT: FALKNER, F. G.
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: APPLICATION NUMBER: EP 91 114 300.6
                                                                                                           1360 GCACATCTTTGTAAGCCTGGGCCC 1383
                                                                                                                                               621 CAAATTGTTTATCACTGAGTTCCC 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
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(703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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ZIP: 22313-0299
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1086 CCCCTTCCCCAGTCCCACTCAGCTCTGAACTCACCTCTTCATCCTAGGCGGCACACAGAC 1145
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                                                                                                                                                                                      1206 TAGGCTGCCCCGAGGCTCACTGCTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCC 1265
                                                                                                                                                                                                                                                                             1266 TCATCAAGAACCGGATCCATCGCCTGCTGTTCTTGACCC 1305
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Neil G.
APPLICANT: Gorley, Neil G.
APPLICANT: Gorley, Neil G.
APPLICANT: Jan, Preeti
APPLICANT: Shah, Purvi
ITILE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
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SOFTWARES FASTESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
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671 TCCTGGAGCCTGGTGCCCTAGAAGCCCACGTCTTTCTGACTTCTGGAGTCCTGTCGATGT 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZUP: 22313-0299
ZUP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FATKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOoley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               US-08-232-463-14/c
; Sequence 11, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A. REGISTRAITON NUMBER: 29,768
REPERENCE/DOCKET NUMBER: 30,768
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE: CHARACTERISTICS:
LENGTH: 7218 base pairs
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(703)683-4109
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US-08-232-463-14
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   Length 1435;
Query Match 3.7%; Score 63.8; DB 2; Length 1 Best Local Similarity 67.9%; Pred. No. 1e-07; Matches 89; Conservative 0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09272796;
Sequence 14, Application US/09272796;
Patent No. 6207148
GENERAL INFORMATION:
APPLICANT: Bandman, Jennifer L.
APPLICANT: GOLLEY, Nell C.
APPLICANT: Golegler, Rarl G.
APPLICANT: Golegler, Rarl G.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES: Incyte Pharmarentis.
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SOFTWARES: RastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
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RECISTRATION NUMBER: 36,749
REFERENCE/COCKET NUMBER: PF-
FELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                         1361 CACATCTTTGT 1371
                                                                                                                                                                                                                                              629 CAGCTTTTAT 639
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CLONE: 1452972
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COUNTRY: USI
ZIP: 94304
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187 GTGGGGAGAGGAACCCGGAAAGGGGCTGTTGGTGATGGTGGGGCCAGGGCTTAAGGTGGAG 846
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                                       791 GGAGAGGAACCCGGAAAGGGGCCTGTTGGTGATGGTGGGCCCAGGGCTTAAGGTGGAGGATG 850
                                                                                                                                                                                                     851 GGCAGTGGGGATGTCCTGGAGTGAACAGGGGAGGGACAATAGGAGCCTCGGGTGCCTGAC 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          847 GATGGGCAGTGGGGATGTCCTGGAGTGAACAGGGGAGGACAATAGGAGCCTCGGGTGCC 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 RURARURURURARCRARARURURARCRARARURGRNRNRSRNRNRSRNRNRSRNRNRSRN 82
                                                                                                                                                                                                                                                                                                                911 GGAAGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGTGACCGGCTCCCCTGGCCTG 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPELICANT: SZOSZAK, Jack W.

APPLICANT: SZOSZAK, Jack W.

APPLICANT: SLOSZAK, JACK W.

APPLICANT: ROBERTS, Richard W.

APPLICANT: Liu, Rihe

TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN

TITLE OF INVENTION: FUSIONS

FILE REFERENCE: 00786/350003

CURRENT APPLICATION NUMBER: US/09/007,005B

CURRENT FILING DATE: 1998-01-14

EARLIER APPLICATION NUMBER: 60/005,963

EARLIER APPLICATION NUMBER: 60/005,491

EARLIER PILING DATE: 1997-01-27

EARLIER FILING DATE: 1997-11-06

NUMBER: PSEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 2.7%; Score 39.4; DB 4; Length 289; Similarity 2.7%; Pred. No. 0.19; 6; Conservative 107; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          907 TGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGTG 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 RNRSRNRNRSRNRNRSRCRARGRCRURGRCRGRURARARCRUR 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09007005B Patent No. 6258558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)...(289)
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Best Local Similarity
Matches 6; Conserv
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RESULT 7 US-09-244-796-17

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787 GIGGGGAGAGGAACCCGGAAAGGGGCIGITGGIGAIGGIGGGCCAGGGCIIAAGGIGGAG 846
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                  Partent No. 288344.

GENERAL INFORMATION:
APPLICANT: SZOSTAK, Jack W.
APPLICANT: SZOSTAK, Jack W.
APPLICANT: SZOSTAK, Jack W.
APPLICANT: ROBERTS, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROPEIN
TITLE OF INVENTION: PESLOCATION OF PROTEINS USING RNA-PROPEIN
TITLE OF INVENTION: PESLOCATION OF PROTEINS USING RNA-PROPEIN
CURRENT APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
SARLIER APPLICATION NUMBER: 09/007,005
SARLIER APPLICATION NUMBER: 09/007,005
SARLIER APPLICATION NUMBER: 09/007,005
SARLIER APPLICATION NOWS: 33
SOFTWARE: FASSEQ for Windows Version 4.0
SEQ ID NO 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 2.3%; Score 39.4; DB 4; Length 289; Similarity 2.7%; Pred. No. 0.19; 6; Conservative 107; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   907 TGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGTG 949
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APPLICANT: GCNNORSI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QLAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
CORPERCONDUCCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Translation template
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STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
Sequence 17, Application US/09244796 Patent No. 6281344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

: LOCATION: (1)...(289)

: OTHER INFORMATION: n = A,T,C or G

US-09-244-796-17
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APPLICANT: KLINGER, KATHERINE I
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA ORGANISM: Artificial Sequence
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COUNTRY: USA
ZIP: 01701
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Best Local Similarity
Matches 6; Conserv
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FEATURE
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APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY W
APPLICANT: BURN, TIMOTHY C
APPLICANT: BOUNDES, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GREMINO, GREGORY
APPLICANT: GINNENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
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APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                2.3%; Score 39; DB .52.1%; Pred. No. 2; tive 0; Mismatches
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ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8410
TELEPHONE: 508-872-8415
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Patent No. 6071717
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MOLECULE TYPE: DNA (genomic)
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ATTORNEY/AGENT INFORMATION:
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Matches 87; Conservative
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MEDIUM TYPE: Floppy
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777 GGAGGGGTGAGTGGGGAGGAACCCGGAAAGGGGCTGTTGGTGGTGGTGGGCCAGGGCT 836
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.3%; Score 39; DB 3; Length 53577; Best Local Similarity 52.1%; Pred. No. 2; Matches 87; Conservative 0; Mismatches 80; Indels
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Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
ITILE OF INVEWTION: Multi-Loci Genomic Analysis
FILE REPRENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT PILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
                                                       GEN4-17.8
                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-840
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
STREE: SEQUENCES: SINGLE
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN
                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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897 CTCGGGIGCCIGACGGAAGGGAAGCTGCCTGGGACTGCAAGGIGAGGCAGGTGACCGGCT 956
                                   APPLICANT: Vinayagamoorthy, Thuraiayah TITLE OF INVENTON: Milti-Loci Genomic Analysis CURRENT FILE REFERENCE: 4747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DAME: 1998-10-01
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                            APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
TITLE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT TILING DAPE: 1998-10-01
SOFTWARE OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09165264 Patent No. 6197510 GENERAL INFORMATION:
                                                                                                                                                                                                     Sequence 13, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
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Best Local Similarity
Matches 87; Conserv
                                                                          CCC 929
                                                                                                           310 CCC 312
                                                                                                                                                                                                                                                                                                                                                            NUMBER SOFTWARE: Pate SEQ ID NO 13
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US-09-165-264-11
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LENGIH: 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION; Description of Artificial Sequence:Primer sequence
US-09-165-264-8
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Best Local Similarity 50.3%; Pred. No. 0.68;
Matches 92; Conservative 0; Mismatches 91;
                                                                GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuralayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44/47
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEG ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Vineyagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 GGGGGGGGGGGTGTGCATGTACAGCAGAGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         957 CCCCTGGCCTGACTCTGCTTTCTGCAGAGA 989
                           ; Sequence 14, Application US/09165264
; Patent No. 6197510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-165-264-8
; Sequence 8, Application US/09165264
; Patent No. 6197510
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                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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           US-09-165-264-14
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                                                                                                                                                                                                                       SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                              777 GGAGGGGTGAGTGGGGAAGGAACCCGGAAAGGGGGCTGTTGGTGGTGATGGTGGGCCCAGGGCT 836
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                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
; OTHER INFORMATION: Description of Artificial Sequence: Primer sequence US-09-165-264-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-11
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                                                               Length 320;
                                                          Query Match 2.1%; Score 36.2; DB 4; Length 32
Best Local Similarity 50.3%; Pred. No. 1.4;
Matches 89; Conservative 0; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 36; DB 4; Length 320; 50.6%; Pred. No. 1.6; tive 0; Mismatches 85; Indels
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          0; Gaps
                                                                           897 CTCGGGTGCCTGACGGAAGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGT 948
                                                                                                   Score 36; DB 1; Length 2278;
Pred. No. 3.6;
0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 CTCTAGGTCCAGATCTATGAGATTGAACAACATAAG 766
                                                                                                                                                                                                                                             APPLICANT: Blakely, Randy D.
APPLICANT: Fremeau Jr., Robert T.
APPLICANT: Caron, Marc G.
ITLE OF INVENTION: Serotonin Transporter cDNA
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31,665
3R: 5405.38a
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Post Office Drawer 31107 CITY: Raleigh STATE: No. 5418162th Carolina COUNTRY: U.S.A.
                                                                                                                                                                                              Sequence 6, Application US/07959943
Patent No. 5418162
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEPAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2278 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; 51.9%;
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 51.9
Matches 81, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
POSITION IN GENOME:
UNITS: 2278 basepairs
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STRANDEDNESS: single
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48..1868
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ADDRESSEE: Gibson
                                                                                                                                                                              US-07-959-943-6/c
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; LOCATION:
US-07-959-943-6
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1823 ITCAGGAGTGATACITITAATAATGCGCTCCTTAAG 1788
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Search completed: June 14, 2003, 16:24:53 Job time : 93 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June 14, 2003, 16:16:05; Search time 288 Seconds (without alignments) 8658.197 Million cell updates/sec Run on:

US-09-826-581-3

1722 1 cctggcccctcagatcaaga......gatgagaggctcgggctgga 1722 Perfect score:

Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY_NUC Scoring table:

1029858 seqs, 724030393 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_NA:* Database :

I. (1902_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
(1902_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
(1902_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
(1902_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
(1902_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
(1902_6/ptodata/1/pubpna/NEON_NEW_PUB.seq:*
(1902_6/ptodata/1/pubpna/NEON_NEW_PUB.seq:*
(1902_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
(1902_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
(1902_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
(1902_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
(1) (1902_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

;	pli	Ap	pli	Appli	Appl	Ą	Appl	dd	dd	App	p]	dd	dd	dd	p]	li	ppl	pli	Appli
Description	Sequence 3, Appli	Sequence 3373, Ap	Sequence 5, Ap	-	-	016	Sequence 29, A	Sequence 112, A			18, A		Sequence 346, A	Sequence 394, A	Sequence 47, App.	Sequence 8, App	Sequence 15, App	Sequence 9, App.	Sequence 2, Ap
01	US-09-826-581-3	US-09-864-761-3373	US-09-826-581-5	US-09-925-297-2	US-10-108-605-70	US-09-864-761-20146	US-09-804-682-29	US-10-123-155-112	US-10-184-644-346	US-10-184-634-346	US-09-984-271-18	US-10-184-644-346	US-10-184-634-346	US-10-123-155-394	US-10-032-393-47	US-10-032-393-8	US-09-827-998-15	US-09-827-998-9	US-09-827-998-2
HQ.	10	10	10	10	σ	10	10	9	σ	σ	σ	δ	0	6	σι	6	10	10	10
% Query Aatch Length DB	1722	378	1647	1691	11527	92	1064	910	671	671	1512	671	671	1184	12733	12739	4158	5313	5376
Query Match	100.0	20.4	8.6	4.1	3.9	3.8	2.6	2.5	2.5	2.5	2.4	2.4	2.4	2.3	2.3	2.3	2.3	2.3	2.3
Score	1722	351	168.2	70.4	89	65	44.2	43	42.4	42.4	40.8	40.6	40.6	40.2	40	40	39.8	39.8	39.8
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		Sequence 1, Appli	574,	858	Sequence 49, Appl	Sequence 49, Appl	Sequence 348, App	Sequence 348, App	~	Sequence 5509, Ap	Sequence 22281, A	Sequence 2835, Ap	Sequence 20, Appl	Sequence 6, Appli	Sequence 202, App	Sequence 202, App	33,	g.	Sequence 28, Appl	312.	312,	20,
10 US-09-827-998-8 10 US-09-827-998-1	10 US-09-820-004-3	9 US-09-904-968A-1 9 US-10-184-644-574	9 US-10-184-634-574	9 US-10-198-846-8585	9 US-10-125-540-49	10 US-09-764-870-49	9 US-10-184-644-348	9 US-10-184-634-348	9 US-10-123-155-10	10 US-09-864-761-5509	10 US-09-864-761-22281	10 US-09-764~877-2835	_	9 US-10-026-188-6	9 US-10-184-644-202	9 US-10-184-634-202	10 US-09-804-682-33	9 US-10-017-724-3	9 US-10-123-155-28	9 US-10-184-644-312	9 US-10-184-634-312	10 US-09-804-682-20
5461 1	40090	882	882	931	٠.	2531 1	777	777	594		531		659158	55074	440	•	• •	98829	765	802	802	987 1
6.62	, e, e	. c.	2.3	2.5	2.5	2.5	2.5	2.3	2.5	2.5	2.5	2.5	~	2.1 1	2.1	2.1	2.1			2.1	2.1	2.1
39.8 39.8	39.5	38.8	38.8	38.4	38.2	38.2	37.6	37.6	37.4	37.2	37.2	37.2	37.2	37	36.8	36.8	36.8	36.6	36.4	36.4	36.4	36.4
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Sequence 3. Application US/09826581
; Sequence 3. Application US/09826581
; Patent No. US20020142310A1
; GENERAL INCORMATION:
APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Markind, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 S
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR APPLICATION NUMBER: US 60/195,665
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; FENCENT 1200-04-07
; FENCENT 1200-04-07
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGATGGAGGAGGTGAGGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1722; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA; ORGANISM: Homo sapiens
US-09-826-581-3
RESULT 1
US-09-826-581-3
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	1381 CCCAGGTGGGAGGGAAGGGGAACCTGGCAGGTCATCAGAGGGCCTGAGAGTCTTCAG 	Qy 1441 CCCTAGCAGTGGGGAAGAGCTGGGGAGCCCTTTGAAGCTGGTGGTGATCTCC 1500	QY 1501 ACCTGGTCCCATCCTAACCAGGGTTCCCTGCTGCCCGGCCCTCCTTCCT	1561 TATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGGGTGCTGGAGACACCCCTGGAGACACCCCTGGAGACACCCCTGGAGACACCCCTGGTTGTTTTTTTT	1621	OY 1681 CGAATGTGGTACCCACCCCAGGATGAGAGCTCGGGCTGGA 1722 	RESULT 2 US-09-864-761-3373/c ; Sequence 3733, Application US/09864761	; FACENT NO. US. UD. US. US. US. US. US. US. US. US. US. US	; APPLICANT: Hanzel, David K. ; APPLICANT: Chen, Wensheng ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL. ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY	FILE REFERENCE Accounts - X-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312	; PRIOR FILING DATE: 2000-02-04 ; PRIOR APPLICATION NUMBER: US 60/207,456 ; PRIOR FILING DATE: 2000-05-26 ; PRIOR APPLICATION NUMBER: US 09/632,366	; PRIOR FILING DATE: 2000-08-03 ; PRIOR APPLICATION NUMBER: 02 24563.6 ; PRIOR FILING DATE: 2000-10-04 ; PRIOR APPLICATION NUMBER: US 60/236,359	; PRIOR FILING DATE: 2000-09-27 ; PRIOR APPLICATION NUMBER: PCT/US01/00666 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00667	; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00664 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00669	; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00665 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00668	; PRIOR FILING DATE: 2001-01-30 ; PRIOR PEPLICATION NUMBER: PCT/US01/00663 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00662	PRIOR PRIOR PRIOR	
241 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGGGCCGCT 300 	301 AIGACCAGCIGACACCTTICACCICCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG 360	361 AGCAAATGGGGGAGGAGGAAGAAAGAGCCCCACTTCTCAGGCCTGGGGGCTGCCC 420	CCCACTGTGTCTCAGGACAGGACACTGGCACTGGCACTGGCACTGGCACTGCACTGGCAAGGACACTGGCAA	CAAAGGCCCCGGGCTGACCTCC 	541 CCTCCCTGCAGGATGCTGACCATCACTGACTTCATCCTGGTGCTGCATCGCTACTACA 600	601 GGTCCCCCTGGTGAGGAGTGGGAATCTTATGGCACCCAGAGGGCGGGGGGG 60 	661 AGGGGAGTCCTCGGAGCCTGGTGCCCTAGAAGCCCACGTTTTCTGACTTGTGGAGTC 720	721 CTGTCGATGTCTCTAGGTCCAGATCTATGAGATTGAACAACATAAGATTGAGACTGGAG 780 	781 GGGTGAGTGGGGAGAACCCGGAAAGGGCTGTTGGTGATGGTGGGCCAGGCTTAAG 840 	841 GTGGAGGATGGCCAGTGGGGATGTCCTGGAGCAACAGGGGAGGGA	901 GGTGCCTGACGGAAGGTAACTGCCTGGACTGCAAGGTGAGGCAGCTGACCGGCTCCCC 960	961 TGGCCTGACTCTGGCTCTTTCTGCAGAGATCTACCTGCAGGCTGCTTCAAGCCTCTGGT 1020	1021 CTCCATCTCTCTAATGATAGGTGGTGTCTCTCTCTCACCTGAGCCTCCTCCTCC 1080 (1081 ACAGTCCCCTTCCCCAGTCCCACTCAGCTCTACACTCTCATCATCCTAGGCGGCACA 1140	1141 CAGACAAGGGAGCCTTGGTGCCCTGCCCTCTTTTAGGGGCTGGGATGGAGGTGGTT 1200	1201 CTCCCTAGGCTGCCCCGAGGCTCACTGCTCTCTGCAGCCTGTTTGAAGCTGTCTA 1260	1261 CACCCTCATCAAGAACCGGATCCATCGCCTGCTGTTCTTGACCCGGTGTCAGGCAACGT 1320 	1321 ACTCCACATCCTCACACACACACACGCCTGCTCCAAGTTCCTGCACATCTTTGTAAGCCTGGG 1380

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Fatent No. US20020081659A1

GENERAL INFORMATION:

TITLE OF INVERTION: Nucleic Acids, Proteins and Antibodies

TITLE OF INVERTION: Nucleic Acids, Proteins and Antibodies

TITLE OF INVERTION: NUMBER: US/09/925,297

CORREMY APPLICATION NUMBER: US/09/925,297

CORREMY FILING DATE: 2000-08-10

FRIOR APPLICATION NUMBER: PCT/US00/05989

FRIOR FILING DATE: 2000-03-08

FRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928

SOFTWARE: Patentin Ver: 2.0
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                                                                                                                                                                                                                             9.8%; Score 168.2; DB 10;
95.6%; Pred. No. 2.7e-39;
tive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.1%; Score 70.4; DB 10;
Best Local Similarity 68.1%; Pred. No. 1.3e-10;
Matches 98; Conservative 0; Mismatches 46;
         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: n equals a,t,g, or c US-09-925-297-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 GCACATCTTTGTAAGCCTGGGCCC 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568 CAAATTGTTTATCACTGAGTTCCC 591
                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.69
Matches 173; Conservative
                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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                                                    LENGTH: 1647
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US-09-925-297-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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APPLICANT: Marklund, Stefan
IITE OF INVENTION: VARIATS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REFERENCE: 11145-007001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 ACCACAGGAGCTTGGCTTCAGGCCCAGGCCAGGGCCAGGGTGGAGAAAGTCCATCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 AIGACCAGCIGACACCITICACCICCGCIACTGCAIGGCCCIGIGCCAIAGGIGCIAGGG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 180
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FORTHER INFORMATION: MAP TO AC009974.3
FOTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN HELIOO, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 378;
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 3373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.4%; Score 351; DB 10;
99.7%; Pred. No. 4.6e-93;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-04-05
PRIOR PPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09826581
Patent No. US20020142310A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.79
Matches 362; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                             TYPE: DNA
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1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGGGGCCAACGGTGTGCGGGGCAGC 60
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Patent No. US20020106765A1
GENERAL INCORMATION:
APPLICANT: Kinders, Robert
APPLICANT: Corey, Michael J.
TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS
TITLE OF INVENTION: BAL-18 POLYPEPTIDES, NUCLEIC ACIDS
TITLE OF INVENTION: BAL-18 POLYPEPTIDES, NUCLEIC ACIDS
TITLE OF INVENTION: MODULATING THE SAME AND METHODS FOR SCREENING FOR OR
TITLE OF INVENTION: MODULATING THE SAME
FILE OF INVENTION: MODULATING THE SAME
CURRENT APPLICATION NUMBER: US/09/804,682
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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OTHER INFORMATION: EXPRESED IN HELA, SIGNAL = 4

OTHER INFORMATION: EXPRESED IN HERA, SIGNAL = 4.1

OTHER INFORMATION: EXPRESED IN PLACENTA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESED IN PLACENTA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESED IN HALIOO, SIGNAL = 3.9

OTHER INFORMATION: EXPRESED IN BLIOO, SIGNAL = 3.8

OTHER INFORMATION: EXPRESED IN BT474, SIGNAL = 3.8

OTHER INFORMATION: EXPRESED IN BOND MARROW, SIGNAL = 4.8

OTHER INFORMATION: EXPRESED IN LUNG, SIGNAL = 4.2

OTHER INFORMATION: EXPRESED IN BRAIN, SIGNAL = 4.2

OTHER INFORMATION: BY HIT: 9111430122, EVALUE 2.00e-22

OTHER INFORMATION: BY HIT: 911430122, EVALUE 3.00e-05

US-09-864-761-20146
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APLICATION NUMBER: PCT/US01/00665
PRIOR APLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
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Best Local Similarity 100.0
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 20146, Application US/09864761

Sequence 20146, Application US/09864761

Patent No. US2002004876341

GENERAL INFORMATION GENERAL SHATTON G.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR STITLE OF INVENTION: HUMBR: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-02-06

PRIOR FILING DATE: 2000-02-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-27

                                                                                                                                                                                FACEURANT STARMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Stam, Lynn
APPLICANT: Stam, Lynn
APPLICANT: Bachwann, Jane
APPLICANT: Bachwann, Jane
APPLICANT: Bachwann, Jane
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 311338
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT APPLICATION NUMBER: US 99/761,142
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2000-01-14
PRIOR PELING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
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APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                       Sequence 70, Application US/10108605
Patent No. US20020160934A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Drosophila melanogaster US-10-108-605-70
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US-09-864-761-20146/c
                                                      RESULT 5
JS-10-108-605-70
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US-10-184-644-346/c; Sequence 346, Application US/10184644; Publication No. US20030044930A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P.; APPLICANT: Chen, Jian; APPLICANT: Desnoyers, Luc
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Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                     Query Match 2.5%
Best Local Similarity 13.2%
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-346
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US-10-123-155-112
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            897 CTCGGGTGCCTGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGTGACCGG 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wood, William APPLICANT: Dang, Zenin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED FING THE SAME
                                                                                           209, 214, 231, 232, 292, 297, 306, 319, 363, 372, 376, 378, 459, 468, 470
                                                                                                                                                                                                      CCATION: 485, 487, 488, 494, 496, 499, 511, 524, 527, 552, 557, 562, 100CATION: 583, 600, 611, 613, 623, 624, 652, 654, 681, 681, 681, 681, 691, 100CATION: 694, 701, 713, 716, 726, 721, 725, 731, 734, 735, 739, 743, 100CATION: 744, 781, 782, 785, 789, 799, 803, 821, 823, 847, 852, 783, 100CATION: 744, 781, 782, 785, 789, 799, 803, 821, 823, 847, 852, 839, 743, 743, 744, 781, 782, 785, 789, 799, 803, 821, 823, 847, 852, 839, 743, 844, 886, 896, 897, 901, 917, 926, 932, 939, 948, 100CATION: 858, 878, 884, 886, 896, 897, 901, 917, 926, 932, 939, 948, 100CATION: 957, 961, 965, 981, 991, 993, 1001, 1002, 1005, 1011, 1018, 0THER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                    2.6%; Score 44.2; DB 10; Length 1064; 47.8%; Pred. No. 0.0058; ative 0; Mismatches 93; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See Palm or File Wrapper
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CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
                                                                                           6, 16, 21, 24, 25, 33, 39, 5, 237, 238, 244, 245, 246, 1, 323, 330, 334, 340, 349, 7, 405, 432, 437, 454, 455,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 112, Application US/10123155
Publication No. US20030068794A1
GENERAL INFORMATION:
                                                                                                                                                                      OTHER INFORMATION: n = A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
Wood, William
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 112
LENGTH: 910
TYPE: PRT
ORGANISM: Homo Sapien
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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Best Local Similarity 47.89
Matches 85; Conservative
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APPLICANN: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Psilvaroff, Ellen
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                                                                                                                                                                                          misc_feature
                                     ORGANISM: Homo sapiens
                                                                             misc_feature
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US-09-804-682-29
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APPLICANT:
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984 CAGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTCTCCATCTCTCTAATGATAGGT 1043
                                                                                                                                   71 GACAGCAAGAAGCAGAGCTTTGTGGGGTGAGGAGGCTGGGGGAGGTGAAGGGAGATGGAG 130
                                                                                                                                                                                                                                                            131 GAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATATACCACAAGCT 190
                                                                                                                                                                                                                                                                                                                       596 LRGPOPRRELLSSGPDLTLQFQAPPGPPNPGLGQGFVLHFKEVPRNDTCPELPPPEWGWR 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 TASHGDLIRGTVLTYQCEPGYELLGSDILTCQWDLSWSAAPPACQKIMTCADPGELANGH 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 TGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCCATCTGTGGAGCCGCTATGACCAGCT 310
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                                                                                                                                                                            191 TGGCTTCAGGCCAAGCCCAGGCCAGGGCCAGGGTGGAGGAAAGTCCATCCGGAGTCTGCA
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                                                                            Gaps
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2.5%; Score 43; DB 9; Length 910;
13.2%; Pred. No. 0.013;
Live 93; Mismatches 224; Indels
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1164 TGCCCTCCTTTTTAGGGGCCTGGGATGGAGGTTGTCTCTCCCTAGGCTGCCCCGAGGCTC 1223

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1224 ACTGCTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCC 1283
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                                                                                                                       215 .TYBITHMM..A.H.HSAM.S.SSS.SN...S.SBST.H.HSSTWYTYMSBSKW.T.AMYM 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 AAGAGCCCCACTTCTCAGGCCTGGGGGGCTGCCCCACTGTCCTGTTCCCACAGTCCCCAC 445
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APPLICANT: ROSEN et al.

TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PLO3091
CURRENT APPLICATION UNBER: US/09/984,271
CURRENT APPLICATION NUMBER: 09/482,273
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 1990-07-14
PRIOR APPLICATION NUMBER: 09/092,921
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR APPLICATION NUMBER: 60/092,925
PRIOR FILING DATE: 1998-07-15
PRIOR PRIOR PRIOR NUMBER: 60/092, 956
PRIOR FILING DATE: 1998-07-15
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-984-271-18
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; Publication No. US20030040088A1
                                                                                                                                                                                           1284 ATCGCCTGCCTGTTCTT 1300
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Best Local Similarity
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OTHER INFORMATION:
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                                                                                                                                                                   1104 TCAGCTCTGAACTCACCTCTTCATCCTAGGCGGCACACAGACAAGGGAGCCTTGGTGCCC 1163
                                                                                                                                                                                                                                                                    1164 TGCCCTCCTTTTTAGGGGCCTGGGATGGAGGTTGTCTCCCCTAGGCTGCCCCGAGGCTC 1223
                                                                                                                                                                                                                                                                                                                                                                       1224 ACTGCTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCC 1283
                                                                   1044 GGGTGTCTCTGCTCATTCACCTGAGCCTCCTCCTCCCACAGTCCCCTTCCCCAGTCCCAC 1103
                                                                                                                                                                                                                                                                                                275 Y..MMASBHSHSSSSSSSSSTSYTKTB...MTCHSHTMSHSHSTS.TMMAMYCC..CYY 216
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                                                                                                                                                                                                335 ..YYYYT...YYYT.HYYMW.S.YHB.HSHSHSSSSS..Y..M.MYCY.M...M.T.MYC 276
                                                                                                                                                                                                                                                                                                                                                                                              215 .TYBTTMM. A.H.HSAM.S.SSS.SN...S.SBST.H.HSSTWYTMSBSKM.T.AMYM 156
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CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 671;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1284 ATCGCCTGCCTGTTCTT 1300
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Smith,Victoria
Watanabe,Colin K.
Wood,William I.
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Gurney, Austin L.
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Goddard, Audrey
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US-10-184-634-346/c
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US-10-184-644-346

APPLICANT: APPLICANT:

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P34430R1C217 CURRENT APPLICATION NUMBER: US/10/184,634 CURRENT FILING DATE: 2002-06-28
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Best Local Similarity 7.5%; Pred. No. 0.059;
Matches 25; Conservative 135; Mismatches 173; Indels
                                                                                                                 Prior Application removed - See File Wrapper or Palm UNBER OF SEQ ID NOS: 612
SEQ ID NO 346
LENGTH: 671
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CURRENT FILING DAFFE: 2002-04-15
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
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Publication No. US20030068794A1
GENERAL INFORMATION:
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Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
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DeForge, Laura
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Filvaroff, Ellen
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US-10-184-634-346
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US-10-123-155-394/c
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LENGTH: 1184
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CURRENT FILING DATE: 2002-06-28
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 346
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                 Sequence 346, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
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Publication No. US20030068684A1
GENERAL INFORMATION:
                                                                                                                                                              APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Matanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
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Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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Gurney, Austin L.
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Publication No. US2030027286A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA.010A
CURRENT FILING DATE: 2001-12-21
PRIOR PPLICATION NUMBER: 60/259,434
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/259,434
PRIOR FILING DATE: 2000-10-66
PRIOR FILING DATE: 2000-09-66
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                 Best Local Similarity 8.8%; Pred. No. 0.089;
Matches 57; Conservative 175; Mismatches 412; Indels
                                                             2.3%; Score 40.2; DB 9;
8.8%; Pred. No. 0.089;
ORGANISM: Homo Sapien
                    US-10-123-155-394
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                                                                                                                                                                        777 GGAGGGGTGAGTGGGGAGGAACCCGGAAAGGGGCTGTTGGTGGTGGTGGGCCAGGGCT
                                                                                                                                                Gaps
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                                                                                                                  Length 12733;
                                                                                                                Score 40; DB 9; Length 127
Pred. No. 0.18;
0; Mismatches 105; Indels
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Job time: 292 secs
                                                                      ; OTHER INFORMATION: Vector peper 14 US-10-032-393-47
                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                               Query Match 2.3%;
Best Local Similarity 49.5%;
Matches 103; Conservative
SEQ ID NO 47
LENGTH: 12
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June 13, 2003, 01:49:14; Search time 192.613 Seconds (without alignments) 9216.782 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    2054640 seqs, 14551402878 residues
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61
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM nucleic - nucleic search, using sw model
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em_htg_mam:*
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Maximum DB seq length: 200000000
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1. gb_ba:*

2. gb_htg;*,

4. gb_om:*

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2. gb_ph:*

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2. gb_vi:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ID	AX281580	AC009974 AC027416	AC106624	AC118404	MMU276505	AC121886	AC094964	G75185	G74939	AC128911	AC113756	AC111883	PM7F7B	AL138688	AC094543	AP004938	AC090435	AC119661	CNS07YPU	APU04862 AC115443	CNSO7EFU	AC103544 AC098460	AC103128	AC094512	AC013606	AX411543	AC010758 AC021669	AC096454	AC103081	AC109908	AC011747	AP002893	AC096340	ALIGNMENTS	1700	1/22 bp int WO0177305	831		rdata; mates;	i. and
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AC009974 206854 bp DNA linear PRI 09-JAN-2002
Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
AC009974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-NoV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Louis,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459119
(Upublished (2001)
3 (bases 1 to 206854)
Waterston,R.H.
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Contact: sapiens@watson.wustl.edu
------------ Sunmary Statistics
Center project name: H_NH0459119
                                                                                                                                            Score 61; DB 6; 1
Pred. No. 3.8e-09;
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                                                 /organism-"Homo sapiens"
/db_xref="taxon:9606"
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Sulston, J.E. and Waters
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Waterston, R.H.
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Waterston, R.H.
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donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromsome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer Institute (http://www.resgen.com) or Pleter de Jong (http://pacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Louis
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                            This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between AS02.38903. Am unresolved tandem in the HERV SVA exists between 184390-185163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEIGHBOAING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-1077K22; the clone
sequenced to the right is RP11-64705. Actual start of this clone
is at base position 1 of RP11-459119; actual end is at base
position 206854 of RP11-459119.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mapping information for this clone was provided by Dr. John D. McPherson. Department of Genetics, Mashington University, St. I. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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/note-"match to EST BG477625 (NID:913409904)"
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Location/Qualifiers

    37
    Anote="similar to Homo sapiens EST BI114348
(NID:g14565249)"

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/db_xref="taxon:9606"
/chromosome="2"
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Gaps

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We continued to the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (30-MAR-2000) Whitehead Institute/NIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Unn 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 152129) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-504G11
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                                                                                                                                                   ch 100.0%; Score 61; DB 9; Length 206854; 1 Similarity 100.0%; Pred. No. 2e-09; 61; Conservative 0; Mismatches 0; Indels 0;
   967. .1090
//note="similar to Homo sapiens EST BI114348
(NID:g14565249)"
967. .1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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AC027416.2 GI:8317289
HTG; HTGS_PHASE1; HTGS_DRAFT.
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KEYWORDS
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588. .929
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/note="match to EST AA481361 (NID:92210913) zv44e01.rl"
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/note="match to EST AA043371 (NID:91521226) zk53e10.r1"
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'note-"match to EST AI670836 (NID:94850567) wa04910.x1"
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/note="match to EST BE047599 (NID:g8364652) tz39c01.y1"
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note="match to EST BE047599 (NID:98364652) tz39c01.yl"
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/note="match to EST BI059713 (NID:g14467240)" 594...763
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note="match to EST BG470047 (NID:gl3402322)"
594. .763
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//note="match to EST AL567345 (NID:912920610)"
281. .344
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281. .334
//note="match to EST BF183086 (NID:g11061273)"
281. .344
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/note="match to EST BG477625 (NID:g13409904)"
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/note="match to EST BE908408 (NID:910402954)"
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/note="match to EST AL567345 (NID:g12920610)"
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                                                                                  /note="match to EST BG470047 (NID:913402322)"
281. .344
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281. .344
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/note="similar to Homo sapiens EST BIll4348
(NID:914565249)"
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note="similar to Homo sapiens EST BI114348
NID:914565249)"
164. .662
/note="match to EST C05773 (NID:g1502549)"
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/note="match to EST
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Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 135376 bases at least Q40 Consensus quality: 143264 bases at least Q30 consensus quality: 143564 bases at least Q30 Insert size: 161000; agarose-fp Insert size: 161009; sqarose-fp Quality coverage: 3.1 in Q20 bases; sum-of-contigs Quality coverage: 3.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                        22028: gap of 100 bp
24319: contig of 2291 bp in length
24419: gap of 100 bp
27059: contig of 2640 bp in length
27159: gap of 100 bp
30170: contig of 3011 bp in length
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66696 73218: contig of 6523 bp in length
73319 73318: gap of 100 bp
73319 77115: contig of 3797 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12557 12656; gap of 100 bp
12657 1264 15143; contig of 2387 bp in length
15044 15143; gap of 100 bp
15144 17123; contig of 1980 bp in length
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17224 19466: contig of 2243 bp in length
19467 19566: gap of 100 bp
19567 21928: contig of 2362 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p of 100 bp contig of 3698 bp in length
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contig of 3899 bp in length
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55871; contig of 4486 bp in length
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0595: contig of 4624 bp in length

95: gap of 100 bp

66595: contig of 5900 bp in length
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85022: contig of 7807 bp in length
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101194 101293: gap of 100 bp
101294 113090: config of 11797 bp in length
113191 123496: config of 10306 bp in length
113191 123496: config of 10306 bp in length
123497 12356: gap of 100 bp
123597 137937: config of 14241 bp in length
1137838 152129: config of 14192 bp in length.
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51386. 55871
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                                                                                                                              Location/Qualifiers
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TITLE
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By Muzny, D. M., Adams, C., Are, J. B., Ayele, M., Banks, T., Alabrocks, S. L., Amaratunge, H. C., Are, J. B., Ayele, M., Banks, T., Bardaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Burbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Burbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bundy, C., Burch, P., Burda, N. C., Carter, M., Cavacos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, R., Chayle, M. D., Dathores, R., David, R., Davila, M. L., Davis, C., Davy-Carroll, L., Daderich, D. A., Davis, C., Davy-Carroll, L., Dederich, D. A., Davis, C., Davis, C., Edan, M., Canrer, P., Frantz, P., Farls, T., Ferraquto, D., Flags, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraquto, D., Flags, N., Ford, J., Foster, P., Frantz, P., Gorrell, J. G., Garcia, A., Garner, T., Garra, N., Gill, R., Goris, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. Garcia, A., Garner, T., Garza, N., Gill, R., Karlsson, E., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnes, M., Hollye, P., Marcia, J., Kovar, C., Kartisson, E., Mayliney, E., Martin, R., Martin, R., Mar, Martin, R., Mar, M., Mayliney, B., Mitchell, T., Morbad, M., Maylen, N., Muyuen, N., Mukerson, M., Sason, J., Reves, M., Ron, Y., Rives, M., Ron, Y., Ruse, M., Tabor, P., Tamerisa, A., Tamerisa, R., Tang, H., Sodely, Sodely, Sonaike, T., Sparks, A., Tabor, P., Tamerisa, A., Tamerisa, N., Tang, Y., Wull, Y., Wu, Y. W., Wu,
                                                                                                                                                                                                    ACLUD624 91247 bp DNA linear HTG 13-JUL-2002 Rattus norvegicus clone CH230-22513, *** SEQUENCING IN PROGRESS ***, 52 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                           0; Gaps
                                                       Length 152129;
                                                                                                                 1; Indels
                                                    Score 59.4; DB 2;
Pred. No. 6.7e-09;
0; Mismatches 1;
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60; Conservative
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Rattus norvegicus
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Worley, K.C.

REFERENCE AUTHORS

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgs.bcm.tmc.edu/docs/denbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                        Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:18139148.
                                    Department
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Departmen
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases I to 91247)
Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 Consensus quality: 46677 bases at least Q40 Consensus quality: 50328 bases at least Q30 Consensus quality: 53862 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s: contig of 1038 bp in length

s: gap of unknown length

contig of 1175 bp in length

s: gap of unknown length

s: contig of 1182 bp in length

s: contig of 1182 bp in length

contig of 1182 bp in length

s: contig of 1102 bp in length

s: gap of unknown length

s: gap of unknown length

s: contig of 1147 bp in length

s: contig of 1179 bp in length

s: contig of 1179 bp in length

s: contig of 1188 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Ratury, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C., Alabaratung, H. C., Are, J. R., Ayele, M., Banks, T., Barbaria, J., Banda, S., Briewe, H. C., Are, J. R., Ayele, M., Banks, T., Barbaria, J., Bencho, J., Bilankenburg, K., Bonnin, D., Barbaria, J., Bencho, J., Bilankenburg, K., Bonnin, D., Bubak, S., Briewe, M., Brown, B., Baryant, N. P., Bubak, S., Briewe, M., Brown, B., Baryant, N. P., Bubak, C., Davrell, K. L., Byrd, N. C., Carren, R., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, R., Chon, R., Chowall, K., Davis, C., Coyle, M. D., Dathorne, S. R., David, R., Davis, C., Coyle, M. D., Dathorne, S. R., David, R., Davis, C., Coyle, M. D., Dathorne, S. R., David, R., Davis, C., Davis, C., Elah, C., Escorto, M., Davis, C., Elah, C., Escorto, M., Davis, C., Elah, C., Escorto, M., Earnhart, C., Edgar, D., Flagy, N., Ford, J., Poutbin, K. J., Earnhart, C., Edgar, D., Flagy, N., Ford, J., Baves, A., Hennadez, J., Harris, K., Harris, K., Hatt, M., Havlak, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hatt, M., Havlak, P., Hawes, A., Harris, C., Harris, K., Haber, J., Hulyk, S., Hume, J., Jackson, L. E., Jackson, E., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jackson, E., Liu, Y., Liu, W., Loulesed, H., Lozado, R. J., Li, Y., Lidharge, C., Lieu, C., Liu, J., Liu, M., Loulese, L., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martin, S., Martin, S., Martin, S., Savery, G., Mawhiney, E., McLoed, M. P., Meader, M., Neide, M., Ren, Y., Micchell, T., Wolabbat, K., Mayuen, M., Noidecrson, E., Nack, A., Pathor, S., Tamerisa, K., Tang, R., Peters, L., Peters, L., Peters, L., Woster, M., Peter, M., Peter, L., Woster, M., Peter, M., Peter, M., Peter, J., Woster, M., Ren, Y., Tangor, P., Tamerisa, A., Tamerisa, M., Wais, S., Marten, Y., Weiser, M., Wais, S., Marten, Y., W
                                                                                                                             "Nolly by DNA linear HTG 18-JUL-2002 Rattus norvegicus clone CH230-150G18, *** SEQUENCING IN PROGRESS AC118404
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Submitted (17-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 127181)
Worley,K.C.
Direct Submission
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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              16; Indels
Best Local Similarity 71.4%; Pred. No. 8.8; Matches 40; Conservative 0; Mismatches
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HTG; HTGS_PHASE1.
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Rattus norvegicus
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49.8%; Score 30.4; DB 2; Length 91247;

Query Match

### Space Property Property Property Description	34276: gap of 35685: contig 37408: contig 37508: gap of 37508: gap of 3866: gap of 4065: gap of 4065: gap of 42067: gap of 43956: contig 42073: contig 47073: gap of 50301: contig 50301: gap of 50301: gap of 50301: gap of	52400: contiq of 1999 52400: contiq of 1999 52500: gap of unknown 52633: contiq of 1354 56187: gap of unknown 56187: gap of unknown 57599: contiq of 1412 57599: contiq of 1412 57699: gap of unknown 61551: gap of unknown 61551: gap of unknown 61651: gap of unknown 61651: gap of unknown 61651: gap of unknown 61651: gap of unknown 68892: contig of 1843 66883: gap of unknown 68892: contig of 1843 66883: gap of unknown 75995: contig of 2463 74099: gap of unknown 78998: contig of 2463 74899: contig of 2203 81231: gap of unknown 78998: contig of 2203 81231: gap of unknown 78998: contig of 2203 81231: gap of unknown 87594: contig of 2303 81231: gap of unknown 87594: contig of 2303 81231: gap of unknown 87594: contig of 2303 81231: gap of unknown 87594: contig of 2325 90359: gap of unknown 93882: contig of 3523 93882: contig of 3377 10246: contig of 4307 10246: gap of unknown 93882: gap of unknown 93882: gap of unknown 93882: gap of unknown 93882: gap of unknown 10245: gap of unknown 10745: contig of 4884	48.9%; Score 29.8; DB 2 70.2%; Pred. No. 13; vative 0; Mismatches 1 60GCTGGGAATCTTATGGCACCACAGGGGGGGGGGGGGGGG
Submitted (18-JUL-2001) Human Genome Sequencing Center, Department Day Cor Data a monomom Caption, Rayor Collage of Meditine, One Day Cor Data a monomom Caption, Rayor Collage of Meditine, One Conters and Caption Collage of Meditine Center: Supplication of the Sequence Version caption of the Caption Collage of Meditine Center Collage Collage of Meditine Center Collage Collage Collage Collage Collage Center Collage Collage Collage Collage Collage Center Collage Collage Collage Collage Collage Center Collage Collag	34409 35586 355866 375866 37509 387509 388674 4700666 413854 471075 447175 447175	50400 504010 5224010 53634110 540000 540000 5400000 540000000000	imilaritt; Conse GTGAGGAG
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.3	Geac	NOTE: Estimated insert size may differ from sequ NOTE: Estimated insert size may differ from sequ NOTE: This is a "working draft" sequence. It cut consists of 56 contigs. The true order of the pils not known and their order in this sequence rarbitrary. Gaps between the contigs are representums of N, but the exact sizes of the gaps are uthis record will be updated with the finished seas soon as it is available and the accession numbe preserved. 1248: gap of unknown length 1348: gap of unknown length 2555: contig of 1207 bp in length 2556 4350: contig of 1695 bp in length 2556 4350: contig of 1695 bp in length 2556 4350: contig of 1695 bp in length 2569 4350: contig of 1695 bp in length 2569 4350: contig of 1098 bp in length 2569 5748: gap of unknown length 2574 5777 526: gap of unknown length 2569 9727: gap of unknown length 2569 9729: gap of unknown length 2569 1767: contig of 1462 bp in length 1769 9728 9729: gap of unknown length 2560 1767: contig of 1865 bp in length 2560 1767: contig of 186 bp in length 2560 1767: contig of 186 bp in length 2560 1767: contig of 186 bp in length 2560 2346: contig of 187 bp in length 2560 2346: contig of 187 bp in length 2367: contig of 187 bp in length 2367: contig of 187 bp in length 2368: contig of 187 bp in length 2368: contig of 187 bp in length 2366: contig of 187 bp in length 2367: contig of 187 bp in length 2367: contig of 187 bp in length 2367: contig of 187 bp in length 2368: contig of 187 bp in length 2368: contig of 187 bp in length 2369: contig of 187 bp in length 2360: contig	27137: contig of 1529 bp in 27237: gap of unknown length 28297: contig of 1060 bp in 28397: gap of unknown length 29809: contig of 1412 bp in 29909: gap of unknown length 32067: contig of 2158 bp in 32167: gap of unknown length 34176: contig of 2009 bp in

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cars gene; Cdknlc gene; cyclin-dependent kinase inhibitor 1C;
cars gene; Cdknlc gene; cyclin-dependent kinase inhibitor 1C;
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receptor p60 homologue 1; tumor nepressing subtransferable candidate 5.
western European house mouse.
                                                                 ROD 06-MAR-2002
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Submitted (17-MAR-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
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Max-Planck-Institut fuer Molekulare Genetik, Innestrasse 73, 14195
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Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
                                                                                                                                                                                                                                                                                                                     Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Engemann, S., Strodicke, M., Paulsen, M., Franck, O., Reinhardt, R.,
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Sequence and functional comparison in the Beckwith-Wiedemann
region: implications for a novel imprinting centre and extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin, GERMANY
On Jan 27, 2001 this sequence version replaced g1:11191799, related accession numbers AJ300452-AJ300460
has a 1000 bp overlap with AJ271885.
Location/Qualifiers
                                                                 MMU276505 281000 bp DNA linear ROD
Mus musculus genomic fragment, 281000 bp, chromosome 7.

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DEFINITION
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KEYWORDS
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MMU276505
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TITLE
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AUTHORS
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JOURNAL
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Rattus norvegicus clone CH230-143P6, *** SEQUENCING IN PROGRESS
***, 63 unordered pieces.
AC126076.2 GI:21699142
HTG; HTGS_PHASE1.
Rattus norvegicus.
Rattus norvegicus
Eukarvota...
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                                                                                                                                                                                                                                            Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louls, MO 63108, USA
3 (bases 1 to 140819) McPherson,J.D. and Waterston,R.H.
                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                           Submitted (16-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA.
On Jul 16, 2002 this sequence version replaced gi:21040003.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Best Local Similarity 77.8%; Pred. No. 23;
Matches 35; Conservative 0; Mismatches
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                                                                                                   1 (bases 1 to 140819)
McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
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/organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                             2 (bases 1 to 140819)
McPherson, J. D. and Waterston, R.H.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WUGSC
                                                                                                                                                                                                                                                                                                                               Direct Submission
                       house mouse.
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                                                                                                                        AUTHORS
TITLE
                                                                                                                                                                               REFERENCE
AUTHORS
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JOURNAL
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AC126076
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47068. .47141,48531. .48627)
/gene="Tnfrhl"
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/gene="Tnfrhl"
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/protein_id="CAC_31352.1"
/db_xref="GI_12583597"
/db_xref="SPTREMBL:Q9ER63"
/db_xref="SPTREMBL:Q9ER63"
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KCHPGTFTGKDDGLHDCELCSTCDKDONWADCSATSDRKCECGIGLXYYDPKFPESC
RPCTKCPQGIPVLQBCNSTANTVCSSSVSNPRNWLPLIAMLIVFCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(67525. .67596,72244. .72334,73711. .7
77140. .77213,77826. .77868,78677. .78828)
/gene="¶nfrh2"
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77140. .77213,77826. .77868,78677. .78828)
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/gene="Tnfrh1"
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/gene="Tnfrhl"
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/gene="Tnfrh1"
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/gene="Infrh1"
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/gene="Tnfrh1"
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g of 1433 bp in length
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g of 1822 bp in length
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g of 1980 bp in length
f unknown length
g of 1518 bp in length
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Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hatt, M., Havlak, P., Hawes, A., Hamilton, K.,
Harnandez, O., Harris, K., Hatt, M., Holloway, C., Hollins, B.,
Hernandez, O., Hober, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, J., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.
Li, J., Lu, X., Lucler, A., Lucler, R., Luna, R., Marines, E.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Mansey, E., Mahhiney, E., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Miner, G., Mitchell, T., Mohabbat, R., Martinez, E.,
Moser, M., Nedl, D., Newtson, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oraquuye, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oraquuye, N., Stote, R., Pitmus, E., Pul, L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, I., Shooshrai, N., Sisson, I.,
Sodergren, E., Sontike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Tansor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Win, Y., Way, Y. F., Zhou, J., Zorrilla, S., Wallingron, S.,
Williams, G., Williamson, A., Wieczyk, R., Woden, S., Wallingron, S.,
Williams, G., Williams, C., Wallingron, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, 77 77030, USA.
On Jul 5, 2002 this sequence version replaced g1:21686820.
Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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1155: gap of unknown length
2165: contig of 1010 bp in length
2265: gap of unknown length
3314: contig of 1049 bp in length
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Center project name: GZTG
Center clone name: CH230-143P6
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Worley, K.C.
Direct Submission
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Jackson.L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowar,C., Kowar,C., Liu,M., Liu,Y., Liu,Y., London,P., Longacre,S., Lopez,J., Liu,J., Liu,M., Malhindarthe,M., Marhing,M., Marlin,R., Martinez,E., Manju,R., Manbehwar,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Manbehwar,M., Manladarthe,M., Martin,R., Martinez,E., Manju,R., Manju,R., Martin,R., Martinez,E., Manju,R., Martinez,E., Manju,P., Martin,R., Martinez,E., Mindias,E., Montemayor,J., Moore,S., Morgan,M., Morris,R., Mindias,M., Morris,S., Mundasa,M., Murphy,M. Nair,L., Nankeryis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuou,G., Okwuou,G., Olarpunasagoon,A., Perez,A., Pal,S., Parks,R., Pasterneh,S., Palndi,H., Perez,A., Perez,A., Pal,S., Parks,R., Pasterneh,S., Poindexter,A., Redier,M., Rogie,F., Rives,C., Rodkey,T., Rojas,A., Reuter,M., Richards,S., Shen,H., Shetly,J., Shvartsbeyn,A., Soort,G., Shatsman,R., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Shtatman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sanders,M., Walds,M., Wang,J., Zhou,J., Zhao,J., Chack,J., Ch
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NOTE: This is a 'working draft' sequence. It currently consists of 79 contigs. The true order of the pieces is not known and their order in this sequence record is
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On Aug 23, 2002 this sequence version replaced g1:21716685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 155645)
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Sequencing vector; plasmid;
Assembly program: Phrap; version 0.990329
Consensus quality; 96145 bases at least Q40
Consensus quality: 105750 bases at least Q40
Consensus quality: 11678 bases at least Q20
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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------ Project Information
Center project name: GBUZ
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Rat Genome Sequencing Consortium.
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Rattus norvegicus clone CH230-6L21, *** SEQUENCING IN PROGRESS ***,
79 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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899 bp DNA linear STS 14-MAY-2002 MARC 11245-11246:999628105:1 Sheep WBC Ovis aries STS genomic, sequence tagged site, G75185 G75185 G75185.1 G1:20563988 STS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 899)
Freking, B.A., Leymaster, K.A., Keele, J.W. and Smith, T.P.L. Identification of a mutation apparently causing the polar overdominance callipyge phenotype in sheep
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                DB 2; Length 155645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50-200 ng genomic DNA
each 20 pmoles
each 88 uM
0.25 units (Qiagen Hotstar)
                                                                                                                                                                                                                                                                                     17; Indels
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Commercially supplied Qiagen HotStar buffer
                                                                                                                                                          length
bp in length
                                                                                                                                                                                             length
           in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 degrees for 15 minutes
95 degrees for 30 seconds
54 - 60 degrees for 30 seconds
68 degrees for 2 minutes
32 to 45
                                   in length
                                             length
bp in length
                                                                              in length
                                                                                                     in length
                                                                                                                           in length
                                                                                                                                                  bp in length
                                                                                                                                                                                                                     in length
                                                                                                                                                                                                                                          contig of 1282 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
Fax: 402 762 4173
Email: freking@email.marc.usda.gov
Primer A: AGTCTCACCCTTCCTGAC
Primer B: TGGAGACCCACTGGAAACTT
PCR Profile:
                       Length
                                                                     length
                                                                                           length
                                                                                                                 length
                                                                                                                                       length
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unknown length
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                                                                  gap of unknown l
contig of 2099 b
gap of unknown l
 unknown of 2195 k
unknown of 1208 l
unknown of 1181 l
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of 2022
unknown
of 1327
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0; Mismatches
                                                                                                     of 1308
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                                                                                                                                                                                                                                                                Score 28.8;
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70640:
70740:
71803:
71903:
                                                                                                    64125:
64225:
65714:
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67836:
67936:
69263:
55734:
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59237:
59337:
60518:
60518:
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                                                                                                                                                                                                                                         73185:
                                                                                                                                                                                                                                                                          69.68;
                                                                                                                                                                                                                                                              Query Match 47.2
Best Local Similarity 69.6
Matches 39; Conservative
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Extension:
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Ovis aries
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60718
64126
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AUTHORS
TITLE
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G75185/c
                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
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KEYWORDS
SOURCE
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The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from POlyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of 20 or greater.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G74939 945 bp DNA linear STS 14-MAY-2002
MARC 11247-11248:1020442896:1 Sheep WBC Ovis aries STS genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                 /organism="Ovis aries"
/strain="Dorset, Romanov, and Dorset-Romanov crossbreds"
/db_xref="taxon:9940"
/clone_lib="Sheep WBC"
/dev_stage="adult"
/note="norgan: blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Caprinae; Ovis.
1 (bases 1 to 945)
Freking, B.A., Leymaster, K.A., Keele, J.W. and Smith, T.P.L.
Identification of a mutation apparently causing the polar
overdominance callipyge phenotype in sheep
                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                         Length 899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  units (Qiagen HotStar)
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15 degrees for 30 seconds
14 - 60 degrees for 30 seconds
8 degrees for 2 minutes
2 to 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
NO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
Fax: 402 762 4173
                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        each 20 pmoles
each 88 uM
                                                                                                                                                                                                                                                                                                                                ب
                                                                                                                                                                                                                                                                                                                                                                                       Score 28.6; 1
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: freking@email.marc.usda.gov
Primer A: ATCTGGCAGCTCCTCCTCTA
Primer B: GAACTTGCCCTTGGAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               each
0.25
                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hotstart: 95 d
Denature: 95 d
Anneal: 54 -
Extension: 68 d
Cycles: 32 t
                                                                                                                                                                                                                                                                                                                                                                                         46.9%;
67.8%;
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DEFINITION
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ORIGIN
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KEYWORDS
SOURCE
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sequence does not necessarily represent the entire amplicon. Sequence derived from Polyphred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of 20 or greater.
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Ovis aries chromosome 18 clone 229611; 359E3, WORKING DRAFT
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Submitted (22-FEB-2001) Department of Genetics, B43, University of
Liege, 20, Bd de Colonster, Liege 4000, Belgium
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Georges,M.

Human-ovine comparative sequencing of a 250-kb imprinted domain encompassing the callipyge (clpg) locus and identification of six imprinted transcripts: DLK1, DAT, GTL2, PEG11, antiPEG11, and MEG8 Genome Res. 11 (5), 850-862 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Boxidae; Caprinae; Ovis.

1 (bases 1 to 215046)
Charlier,C., Segers,K., Wagenaar,D., Karim,L., Berghmans,S., Jaillon,O., Shay,T., Weissenbach,J., Cockett,N., Gyapay,G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Dorset, Romanov, and Dorset-Romanov crossbreds" /db_xref="taxon:9940"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 215046)
Charlier,C., Segers,K., Wagenaar,D., Karim,L., Berghmans,S.,
Jaillon,O., Shay,T., Weissenbach,J., Cockett,N., Gyapay,G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 12054: contig of 12054 bp in length

* 12055 27941: contig of 1847 bp in length

* 27942 27941: gap of unknown length

* 27942 27941: gap of unknown length

* 27942 27941: gap of unknown length

* 27942 23846: contig of 1905 bp in length

* 28677 33482: contig of 3516 bp in length

* 33483 33502: gap of unknown length
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Pred. No. 59;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              219
                                                                                                                                                                                                                                                        /clone_lib="Sheep WBC"
/dev_stage="adult"
/note="Organ: blood"
                                                                                                                                                               1. .945
/organism="Ovis aries"
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Ovis aries.
                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           236 g
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AF354168.1 GI:13926066
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l Similarity 67.8%;
40; Conservative (
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                                                                                                                  or greater
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Best Local S
Matches 40
                                                                                                                                                                  Source
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AF354168/C
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REFERENCE
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SOURCE
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                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus norvegicus clone CH230-326J5, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces. AC128911.1 GI:21953455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 115726 bases at least Q40
Consensus quality: 144728 bases at least Q30
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: CH230-326J5
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Worley, K.C.
Direct Submission
                                                                                                                     HTG; HTGS_PHASE1.
Rattus norvegicus.
Rattus norvegicus
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         61: contig of 1605 bp in length
31: gap of unknown length
5: contig of 2854 bp in length
6: contig of 2854 bp in length
7: contig of 2899 bp in length
8: contig of 9899 bp in length
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contig of 1555 bp in length
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gap of unknown length
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contig of 3205 bp in length
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contig of 1746 bp in length
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1 Similarity 67.8%; Pred. No. 29;
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Rattus norvegicus clone CH230-195D20, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.
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                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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MANDRYD.M., Addms.C., Adio-Oduola.B., All-osman.F.R., Allen.C., Amaratumge, H.C., Are,J.R., Agele,M., Banks,T., Barbooks,S.L., Amaratumge,H.C., Are,J.R., Agele,M., Banks,T., Barbooks,S.L., Amaratumge,H.C., Are,J.R., Agele,M., Banks,T., Barbooks,S.L., Amaratumge,H.C., Brown,E., Borndin,D., Bouck,J., Burch,P., Burkett,C., Burchll.K.L., Byrd,N.C., Charez,D., Chen,G., Chen,Z., Chen,Z., Chowdhry,I., Christopoulos,C., Chen,S., Chen,Z., Chan,Z., Chowdhry,I., Christopoulos,C., Chen,S., Chen,Z., Chan,A., Douthorne,S.R., David,R.P., Devilam,H.H., Douthwaite,K.R., Delgado,O., Penn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dudana,R.C., Edgar.D., Edwards,C.C., Ellaj,C., Escotto,M., Farls,T.F., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabis,A., Ganrer,T., Gazza,N., Ganrer,T., Gazza,N., Ganrer,T., Gazza,N., Hernandez,O., Hedgson,A., Houe,S., Hame,J., Jackson,L.E., Jackson,E.K., Huber,J., Hule,S., Hame,J., Jackson,L.E., Jackson,E., Huber,J., Hule,S., Hame,J., Jackson,L.E., Jackson,E., Mawhiney,E., McLodd,M.P., Marling,R., Marting,R.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2002 this sequence version replaced gi:19525921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 164800)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 96892 bases at least Q40 consensus quality: 103381 bases at least Q30
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .---- Project Information
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 79 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T. R., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Coyle, M.D., Dathorne, S.R., David, R., J., Draper, H., Dugan Rocha, S., Dubbin, K.J., Barnhart, C., Bdgar, D., Edag, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gorrell, J.H., Gavards, C.C., Ellay, R., Harnandez, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Harnandez, C., Harris, R., Hart, M., Havlak, P., Hawes, A., Harnandez, C., Harris, R., Hart, M., Havlak, P., Hawes, A., Jackson, L.B., Jacobson, B., Jai, Y., Johnson, R., Holles, M., Hollews, M., Hollews, M., Harnandez, C., Harly, S., Khan, U., King, L., Kovah, J., Kovar, C., Karlsson, E., Kally, S., Khan, U., King, L., Kovah, J., Kovah, J., Kovah, J., Lid, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H., Massey, E., Marthiney, R., Martin, R., Machor, M., Morbak, M., Mayuen, M., Martin, R., Machon, M., Morgan, M., Morserson, P., Marthiney, R., Worledo, R., Park, D., L., Quiles, M., Rei, S., Kallson, H., Rolfe, M., Rulz, S., Savery, G., Scherr, S., Sonti, G., Shen, P., Primer, S., Panerisa, A., Tanerisa, A., Taneris, C., Wull, M., Welley, M., Wellington, S., Walliams, G.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contings. The true order of the pieces

* to not known and their order in this sequence record is
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Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2002 this sequence version replaced gi:18701729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 170476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 103990 bases at least Q40 Consensus quality: 112822 bases at least Q30 Consensus quality: 119677 bases at least Q20
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Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus clone CH230-26L15, *** SEQUENCING IN PROGRESS
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Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
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7	27.2	44.6	143899	24	AAL38336	Genomic sequence e
3	26	42.6	17761	22	AAK79415	Human immune/haema
4	26	42.6	17761	23	ABK42709	Genomic sequence #
c S	25.8	42.3	112414	24	ABL59091	Nucleotide sequenc
9	25.6	42.0	14070	22	AAK70465	Human immune/haema
c 2	25.2	41.3	989	22	AAH08414	Human cDNA clone (
ထ တ	25.2	41.3	1030	21	AAC77940	Human cancer assoc
٥ ٥	25.2	41.3	1105	22	AAF77880	Human ATFx coding

Human cDNA sequence # Human p53AIPI asso Gene #2926 used to CDNA encoding a but thin an escreted proDNA of App related Rat metastatic tum DNA encoding novel Human brast call Probe #4800 for ge Human brain express Human penome-deriv Human genome-deriv Human genome-deriv Human penome-deriv Human prain express Human brain express Human brain express Human brain express Human penome-deriv Human genome-deriv Human penome-deriv Human probe #14665 for general express Human brain express Human brain express	human bone marrow Probe #18146 used Human genome-deriv Human RD-interacti Human RIZ allele D Human RIZ allele D Human RIZ allele D Human RIZ allele D Human RIZ allele D Human RIZ allele D Human RIZ allele D Human Mutant RIZ a DNA sequence encod Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Human Genomic DNA Human Genomic DNA Human Doctal liver Probe #17409 for g Human bone marrow Probe #16156 for g	nmma 3 subunit; PRKAG3; variant; substitution; ds. intron 4"
AAH18673 ABK42266 ABI54634 AAB154634 AAA14998 AAX337383 AAX337383 AAX337383 AAX337383 AAX64847 AAX30374 AAX130374 AAX130374 AAX303774 AAX30374 AAX30374 AAX30374 AAX	AAA49460 ABS17483 ABS17483 ABS17483 AABS17483 AAA60123 AAA50124 AAA518781 AAA16646 AAT16646 AAT16646 AAT16646 AAT16646 AAT16646 AAT16646 AAT16646 AAT1764 AAX22202 AAK8368 AAI26223	nase ga esity; iers on 4" ion of 5" 5" 6"
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225 255.2 265.2 27	* * * * * * * * * * * * * * * * * * * 	standar; i 002 (fi ntron 4 mP-activ c diseas iens.
000 0 01122401111122222222222222222222222222	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 AAH43683 ID AAH43683 XX AC AAH43683 XX DE PRKAG3 i XX Human; A KW Human; A KW MC MC Sap XX COS HOMO Sap XX FT intron FT FT EXON FT FT FT FT FT FT FT FT FT FT FT FT FT F

AAL38336 standard; DNA; 143899 BP.

RESULT 2 AAL38336

(first entry)

15-AUG-2002

AAL38336;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PKRAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A, in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of A T for a C at nucleotide 1037, resulting in the amino acid substitution R340M. There may also be nucleotide variation
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Pred. No. 5.1e-10;
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                                                              "Intron 7"
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                       "Exon 7"
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The invention relates to a Nogo receptor homologue polypeptide, NGR2 or NGR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT sequence, or a 420, 461 or 392 amino acid sequence, all given in the sequence. The NGR3 protein or its binding antibody is useful for specification. The NGR3 protein or its binding antibody is useful for decreasing inhibition of axonal growth of a central nervous system (CNS) neuron, by contacting the neuron NGR3 or a vector comprising NGR3 is cuseful for treating cerebral injury, Spinal cord injury, stroke, demyelinating disease, e.g. multiple Sclerosis, monophasic cemyelinating disease. e.g. multiple Sclerosis, monophasic cemyelinating disease. e.g. multiple Sclerosis, monophasic cemyelinating disease. Canavan's disease, Spongy degeneration, alexander's disease. NGR3 is useful for inducing an immune response in a mammal against NGR3, as a bait protein in a two-hybrid or three-hybrid assay, and as a research tool for identification, characterisation and purification of interacting, regulatory proteins. The notedated vich certain disorders, for genetic mapping, and for spee therapy. The vector containing NGR3 is useful for producing non-human transgenic annimals. The NGR3 binding antibody is useful for isolating entifying annimals.
                                                                                                                                                   Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue; NGR2; NGR3; axonal growth; central nervous system; CMS: cerebral injury; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasic demyelinatio; encephalomyelitis; Marchiatava Bugnami disease; multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; canavan's disease; metachromatic leukodystrophy; Krabbe's disease; immune; bait protein; genetic mapping; gene therapy; transgenic animal; unrequlated cellular growth; cancer; tumour; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Nogo receptor homolog polypeptide, NGR2 or NGR3, useful for treating central nervous system disorder, cerebral injury, spinal cord
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                                                                                                            Genomic sequence encoding a human NgR2 protein.
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(BIOJ ) BIOGEN INC.
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Sequence 143899 BP; 36346 A; 35277 C; 35318 G; 35657 T; 1301 other;

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08-SEP-2000; 20000S-0231243.
08-SEP-2000; 20000S-0231244.
08-SEP-2000; 20000S-0231244.
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08-SEP-2000; 20000S-0231244.
08-SEP-2000; 20000S-02312413.
08-SEP-2000; 20000S-0231268.
14-SEP-2000; 20000S-023239.
14-SEP-2000; 20000S-0233365.
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14-SEP-2000; 20000S-0233365.
14-SEP-2000; 20000S-023339.
14-SEP-2000; 20000S-023439.
12-SEP-2000; 20000S-023439.
12-SEP-2000; 20000S-0244617.
08-NOV-2000; 20000S-0244617.
08-NOV-2000; 20000S-0246619.
08-NOV-2000; 20000S-0246619.
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2000US-0249217.
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                                                                                                  Human, immune; haematopoletic; immune/haematopoletic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                             0; Gaps
                                                                                                                                                                                                                                                                                               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34227
               Length 143899;
                                              Indels
               DB 24;
          Score 27.2; DB; Pred. No. 25; 0; Mismatches
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2000US-0217487.
2000US-0217496.
            Query Match 44.6%;
Best Local Similarity 67.9%;
Matches 38; Conservative (
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Human; connective tissue related disorder; cancer; gene therapy; cytostatic; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
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The present invention relates to the isolation of novel human connective tissue related polypeptides (AAUB6435-AAUB6923) and the polynucleotide (CDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK43105-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of Bhime-1 strain of Red sea bream iridoviris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A DNA encoding a protein related to neutralization and infection
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65.5%; Pred. No. 50;
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                                                                                                                                                                                                                Disclosure; SEQ ID No 1596; 673pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 13-51; 65pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL59091 standard; DNA; 112414 BP
                                                                       SM;
                                     (HUMA-) HUMAN GENOME SCI INC.
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05-JAN-2001; 2001US-0259678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Conservative
                                                                       Rosen CA, Barash SC,
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                                                                                                        WPI; 2001-565190/63.
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20000S-024617
20000S-0246474
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20000S-0246477
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2000US-0232081
2000US-0231968
2000US-023339
2000US-023339
2000US-0232400
2000US-0232400
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2000US-0234274.
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2000US-0233064.
2000US-0233065.
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12-SEP-2000;
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13-0CT-2000;
13-0CT-2000;
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20-0C
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25-SEP-2000;
26-SEP-2000;
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nucleotide sequence of the Ehime-1 strain of Red sea bream iridoviris
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                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25277
                                                                                       DB 24; Length 112414;
                                                    Sequence 112414 BP; 26205 A; 29684 C; 30351 G; 26174 T; 0 other;
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                                                                                                                                                       Indels
                                                                                     Score 25.8; DB 24;
Pred. No. 67;
0; Mismatches 12;
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20000US-0184664.
2000US-0184664.
2000US-018974.
2000US-0199174.
2000US-020515.
2000US-020515.
2000US-020515.
2000US-020515.
2000US-0216464.
2000US-021680.
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2000US-021680.
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2000US-0217487.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-022526.
2000US-022526.
2000US-022526.
2000US-0225270.
2000US-0225447.
2000US-0225757.
                                                                                   Query Match 42.3%;
Best Local Similarity 73.3%;
Matches 33; Conservative
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2000US-0228924.
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2000US-0226681
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01-SEP-2000;
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                    (RSIV).
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                       Human cDNA clone (5'-primer) SEQ ID NO:5249.
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAX-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-02418999.
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                                                                                                                                                                                      Homo sapiens.
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amino acid sequences given in AMM2170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/Amematopoietic-feried cells. AAK4703 cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
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0; Mismatches 19; Indels
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37; Conservative
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2000US-0251990.
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2001US-0259678.
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                                             17 - NOV - 2000;
17 - NOV - 2000;
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Yamamoto J;

Hayashi K, Saito K, Ya A, Nagai K, Otsuki T;

Sugiyama T, Wakamatsu Isogai T, Nishikawa T,

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The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-d' primer and an oligonocleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonocleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonocleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 1'-end sequence complementary to the
complementary strand of a polynucleotide which comprises at 1-enset 16 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
complementary The primer sets can be used in antisense therapy and
in gene therapy. The primer sets can be used in antisense set therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
condition and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
condition of the protein of the condition of the condition of the condition and the condition of the condition of the condition of the condition of the condition and the condition of the condition of the condition of the condition of the condition and the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condit of the condition of the condition of the condition of the condi
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.3%; Score 25.2; DB 22; Length 686; 66.7%; Pred. No. 70;
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                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 5249; 2537pp + CD ROM; English.
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AAC77940/c
ID AAC77940 standard; cDNA; 1030
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Matches 36; Conserv
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5618 GIGGGGGTGGGGCTGGTGTGTGAACCCTGGGGGTGGGGCTGGGGGTG 5673

AAH08414 standard; cDNA; 686 BP.

AAH08414/c

RESULT

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AAH08414;

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AAF77880 standard; cDNA; 1105 BP.

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antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antialabetic; antiasthmatic; antirheumatic; antiarthritic; antiasthmatic; antirheumatic; antiarthritic; antiasthmatic; antirheumatic; antiarthritic; antinflammatory; antithrective; cardiant; thrombolytic; cagulant; dermatological; neuroprotective; cardiant; thrombolytic; cagulant; nootropic; vasotropic; antipsocitatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of thematopoictic cells, autoimmune colls, interest incompositic cativity, modulate rejection, modulate haemostatic or thrombolytic activity, modulate infections. The peptides, neurological disease and cagination cancers, cardiovascular disorders, neurological disease and antagonists may be also be used in drug screens. AAC78449 to AAC78451 in the exemplification of
                                                                                                                                                                                                                                                diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidabentic; antiasthmatic; antiantheumatic; antiathritic; antiviral; antiinflammatory; antithyroid; antiallargic; antibacterial; cardiant; dermatological; neuroprofective; thrombolytic; coagulant; nootropic; avastropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; hematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acids comprising sequences encoding peptides
                                                                                                                                                                                                     cancer associated gene; cancer antigen; detection; cancer;
                                                                                                Human cancer associated gene sequence SEQ ID NO:334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for treating or diagnosing e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological disease; drug screening; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0124270.
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-587533/55.
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                        DB 21; Length 1030;
                                                 Indels
Sequence 1030 BP; 175 A; 362 C; 287 G; 195 T; 11 other;
                                                Mismatches
                       Score 25.2; |
Pred. No. 72;
                                                ó
                        41.3%;
66.7%;
                                                36; Conservative
                                   Local Similarity
                        Query Match
                                                Matches
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Homo sapiens.
                                              418 AGGCTCCCCCAAGGACCTCATAGGGAGCCAGGGGGCAGGGGCCGGGGGGAGT 365
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RESULT 9 AAF77880/c

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The present invention relates to a method for identifying a modulator of gamma aninobutyric acid_B (GABA_B) receptor-mediated activity, by monitoring the interaction between a CRED/ATF transcription factor capable of binding to GABA_B receptor. The present sequence is the coding sequence for human ATFX, which was used in the method of the present invention. ATFX is a member of the CRED/ATF family of transcription factors. ATFX contains a DZIP domain, by which it interacts with the coiled coil domain of GABA_B receptor. Wodulators of GABA_B receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying modulators of gamma aminobutyric acid(GABA)-B receptor mediated activity by monitoring the interaction between GABAB receptor and the CREB/ATF transcription factors in the presence of a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nervous system disorders. The present sequence encodes an ATFx protein with a N-terminal extension (compared to AAB80892).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity are useful for treating central nervous system or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1105 BP; 198 A; 399 C; 308 G; 200 T; 0 other;
                                                                                      Human ATFx coding sequence with 5' extension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25.2;
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA sequence SEQ ID NO:18921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH18673 standard; cDNA; 1374 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Fig 9; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.3%;
                                                                                                                                                                                                                                                     31-AUG-2000; 2000WO-GB03361.
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                                                      30-MAY-2001 (first entry)
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                                                                                                                                 transcription factor; ss
                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD
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Best Local Similarity
                                                                                                                     gamma
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                                                                                                                                                                                          WO200116596-A2.
                                                                                                                                                               Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substance
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                            AAE77880;
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WO200155343-A1
    Homo sapiens
                                                          02-AUG-2001
    The present invention describes primer sets for synthesising 5602

(ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprising a sequence complementary to the
an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 1'-end sequence complementary to a
coligonucleotide which comprises a 1'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
chall-length cDNAs. The primers allow obstanting of the full-length
chall-length cDNAs. The primers allow obstanting of the full-length
chall-length cDNAs. The primers allow obstanting of the full-length
chall comprised and machiners allow obstanting of the full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13632 represent human cDNA sequences; AAB9246 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNas defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; connective tissue related disorder; cancer; gene therapy; cytostatic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.3%; Score 25.2; DB 22; Length 1374; 66.7%; Pred. No. 73;
tive 0; Mismatches 18; Indels 0;
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                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID 18921; 2537pp + CD ROM; English.
                                                                                                                                                                                                   Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK42266 standard; DNA; 5938 BP
                                                                                                 27-Aug-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                       28-JUL-2000; 2000EP-0116126
                                                                                     99JP-0248036
                                                                                                                              02-MAY-2000; 2000JP-0183767 09-JUN-2000; 2000JP-0241899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention.
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                                                                                                                                                                       (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                               full-length cDNAs
EP1074617-A2
                                                                                     29-JUL-1999;
                             07-FEB-2001
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22 AUG 2000; 2000US -0226681.
22 AUG 2000; 2000US -0226688.
22 AUG 2000; 2000US -022182.
33 AUG 2000; 2000US -0227824.
01 SEP 2000; 2000US -0229874.
                                                                                                           02-MAR-2000; 2000US-0186350.
16-MAR-2000; 2000US-0189874.
17-MAR-2000; 2000US-0199874.
18-APR-2000; 2000US-0198123.
19-MAY-2000; 2000US-0205515.
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07-JUL-2000; 2000US-021647.
07-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217496.
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08-SEP-2000; 2000US-0231413.

08-SEP-2000; 2000US-0231414.

08-SEP-2000; 2000US-0232080.

08-SEP-2000; 2000US-0232081.

12-SEP-2000; 2000US-0231968.

14-SEP-2000; 2000US-0231968.
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2000US-0229345.
2000US-0229509.
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14-AUG-2000; 2000US-0224518.
14-AUG-2000; 2000US-0224519.
14-AUG-2000; 2000US-025513.
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14-AUG-2000; 2000US-0225266.
14-AUG-2000; 2000US-0225267.
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14-AUG-2000; 2000US-0225270.
14-AUG-2000; 2000US-0225447.
14-AUG-2000; 2000US-0225757.
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14-AUG-2000; 2000US-0225759.
18-AUG-2000; 2000US-0226279.
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06-SEP-2000; 2000US-0230437.
06-SEP-2000; 2000US-0231243.
08-SEP-2000; 2000US-0231243.
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28-JUN-2000; 2000US-0214886.
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2000US-0220963.
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14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232400.
17-JAN-2001; 2001WO-US01322
                                                                                        2000US-0184664
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01-SEP-2000; 2
05-SEP-2000; 2
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25-SEP-2000;
26-SEP-2000;
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26-JUL-2000;
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01-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251479.
06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
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02-OCT-2000;
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(HUMA-) HUMAN GENOME SCI INC

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tissue related polypeptides (AAUB6435-AAUB6923) and the polynucieotide (cDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                    present invention relates to the isolation of novel human connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53-dependent apoptosis-associated protein and its encoding gene p53ALPI, used for screening apoptosis mediated remedies for cancer and as controllers of apoptosis induction
                                                                             Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human p53-dependent apoptosis-associated protein, P53AIPI comprising fully defined 806, 777, 2659 nucleotide sequences (ABL54631-ABL54633 respectively) given in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; p53; p53AIPI; p53-dependent apoptosis-associated; apoptosis;
cytostatic; cancer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23; Length 5938;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5938 BP; 1295 A; 1601 C; 1751 G; 1291 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        41.3%; Score 25.2; D
66.7%; Pred. No. 82;
tive 0; Mismatches
                                                                                                                                                 Disclosure; SEQ ID No 1153; 673pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human p53AIPI associated DNA SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 92-104; 121pp; Japanese.
              Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL54634 standard; DNA; 9305 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYTY ) UNIV TOKYO.
(ONCO-) ONCOTHERAPY SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 66.7
hes 36; Conservative
              Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura Y, Arakawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-217192/27.
                                             WPI; 2001-565190/63.
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              CA,
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                Rosen
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RESULT 14
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                                   86 and 108 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for diagnosing and detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene, liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                            apoptosis-associated proteins having fully defined 124, 86 and 108 ami acid sequences (ABB08837-ABB08839 respectively) given in the specification. The protein and encoded gene have cytostatic activity, useful in screening for regulators of apoptosis for subsequent use as cancer treatments. The present sequence is that of the Human p53AIPI associated DNA, useful to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in
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                                                                                                                                                                                                                                                                                                                                               Length 9305;
                                                                                                                                                                                                                                                                    Sequence 9305 BP; 2133 A; 2438 C; 2570 G; 2164 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
and the three respectively encoded human p53-dependent
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                                                                                                                                                                                                                                                                                                                                            41.3%; Score 25.2; DB 24;
66.7%; Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene #2926 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peres Da Silva S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 2926; 298pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN96428 standard; DNA; 275 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                   36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horne D, Alvares C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liver tissue sample
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related protein (PROAP). The polypeptides and polynucleotides can be used for the diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders Disorders associated with decreased expression or activity of include arteriosclerosis, cirrhosis, hepatitis, psoriasis, melanoma, lymphoma and cancers of the breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human proliferation and apoptosis related protein polypeptides used for diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders -
                                                                                                                                                                                                                                                                                                                          Human; proliferation and apoptosis related protein; PROAP; psoriasis; cell proliferative disorder; immunological disorder; hepatitis; reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphoma; cancer; acquired immune deficiency syndrome; AIDS; allergy; anaemia; asthma; diabetes mellitus; osteoarthritis; endometriosis; uterine fibroid; menstrual cycle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "proliferation and apoptosis related protein"
                                         Gaps
                                                                                                                                                                                                                                                                                             cDNA encoding a human proliferation and apoptosis related protein.
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Score 25; DB 24; Length 275;
Pred. No. 75;
0; Mismatches 10; Indels
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Shih LL;
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                                                                                            57
                                                                       17 GAATCTTATGGGCACCCAGAGGGGGGGGGGGGGGGGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
82..303
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n MR, Yang J,
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        41.0%;
75.6%;
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99US-0118559.
99US-0172229.
99US-0154336.
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                                                                                                                                                                                                                                                           (first entry)
      Query Match 41.0
Best Local Similarity 75.6
Matches 31; Conservative
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11-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or amount of expression of the new polypeptides in a sample or by determining the presence or absence of mutations in the new polypucleotides. Specific uses are
                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; prevention; treatment; protein therapy;
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                                                           Score 25, DB 21; Length 303;
Pred. No. 75;
0; Mismatches 20; Indels
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Lafleur DW;
Shi Y, Sopp
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein cDNA fragment containing gene 15.
                  Sequence 303 BP; 67 A; 85 C; 110 G; 41 T; 0 other;
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C, Florence KA, Komatsoulis GA,
Olsen HS, Rosen CA, Ruben SM,
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                                                                                                                                                                                                                                                                                                   AAX37383 standard; cDNA; 541 BP.
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9705-0056369.
9705-0056339.
9705-0056535.
9705-0056556.
9705-0056629.
9705-0056629.
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                                                           Match 41.0%;
Local Similarity 64.9%;
es 37; Conservative
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P-PSDB; AAY07758.
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19-AUG-1997;
19-AUG-1997;
19-AUG-1997;
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19-AUG-1997;
19-AUG-1997;
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Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            foung PE;
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                                                                Query Match
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described for each of the 70 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, asthma, sepsis, diabetes, Alzheimer's and cognitive disorders, schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine disorders, infections and AIDS. The human secreted proteins of the invention are represented in AAX37369-X3744.V77850 and the encoding nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 541 BP; 118 A; 135 C; 131 G; 155 T; 2 other;
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Best Local Similarity
Matches 34; Conserv
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June 13, 2003, 02:37:44; Search time 151.839 Seconds (without alignments) 6506.409 Million cell updates/sec
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61
1 gtgaggagtgggclgggaat......999ggcggaggggagtcctc 61
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                OM nucleic - nucleic search, using sw model
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em_gss_pro:*
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BG309093 HVSNECOOD BM909483 AGENCOURT BQ521472 NISC_n111 BQ038856 pgn1c_pk0 AG122806 Pan trog1 AG090162 Pan trog1 BG44867 AGENCOURT BH756447 SALK_0536 BH756447 SALK_0536 BH756447 SALK_0536 BH756447 SALK_0536 BH756447 SALK_0536 BH756447 SALK_0536 BH756447 SALK_0536 BH756447 SALK_0536 BH75647 SALK_0536 BH75647 SALK_055 BH7565498 G01657281 AG200974 SP_0055_A BE63498 G01657281 AG2187770 ENTDA487TF BF7272077 GA_BD011 B1553428 HVSNEMMO11	BG191779 RST10875 BBG90765 601431204 BD675584 AGENCOURT ALG67198 DIOSOPALI BM464195 AGENCOURT BM579140 BB379140 BM116323 L0834C09- BE559614 601347308 BF215427 601880953 BQ06668 AGENCOURT AA872225 ch71h02.3 BB858755 BB858755 BB858755 BB858755 BB734657 60157506 BD978976 AGENCOURT BM923470 AGENCOURT BM923470 AGENCOURT BM923470 AGENCOURT BM928475 BB138623 AWW81866 xb56c05.x B1954751 HVSNEM001	4 bp mRNA linear EST 09-MAR-2000 fomo sapiens cDNA clone IMAGE:2529345 3/ MSR1 repetitive element; mRNA mRNA craniata; Vertebrata; Euteleostomi; ss; Catarrhin; Hominidae; Homo. Hobi.nlm.nih.gov/ncicgap. "National Institute of Neurological of Tumor Genome Anatomy Project dex. Ph.D. Ph.D. "Louis, M.D., Myrna R. Rosenfeld M.D., W. Bento Soares, Ph.D., M. Fatima	Greg Lennon, Ph.D. quon vilversity Genome Sequencing Center SAP clone distribution information can be E. Consortium/LLNL at:
BG309093 BM909483 BM909483 BQ521472 BQ038856 AG122806 AG122806 BH756447 BH756447 BH756447 BH756447 BH756447 BH756901 BH9155902 BF963498 AU256222 AG180340 AG256222 AG180340 AG256222	BEG191779 BEG191779 BEG19179 BEG191525 BMG1525 BMG1525 BMG195 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140 BMG195140	3 nn23 emen corde ilmatinatinatinatinatinatinatinatinatinatin	Library Arrayed by: Greg Lenne Sequencing by: Washington Unive e distribution: NCI-CGAP clone through the I.M.A.G.E. Consor
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AGENCOURT_6419113 NIH_MGC_71 Homo sapiens cDNA clone LWAGE:5534991 BM800472
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MSH MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Braal: gapubs-rémail.infh.gov

Tissue Procurement: ARCC

CDN Library Preparation: Life Technologies, Inc.

CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution Information can be
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                                              Length 1208;
                                                                                   Indels
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http://image.llnl.gov
Plate: LLAMI222 row: f column: 16
High quality sequence stop: 635.
Location/Qualiflers
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Pred. No. 69;
0; Mismatches 16;
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/clone_lib="NIH_MGC_71"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
129 g 360 t lothers
                                                                                                                                                                                                                                        1208 bp mRNA linear EST 24-MAY-2002 AGENCOURT_7751176 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6062177
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Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC/CTCTCTOTOTO

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Riage: LLAM1333 row: column: 18

High quality sequence stop: 135.

Location/Qualifiers

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NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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www-bio.llnl.gov/bbrp/image/image.html
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High quality sequence stop: 338.
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Best Local Similarity 74.1%;
Matches 40; Conservative (
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MIH-MGC http://mgc.nci.ni.nh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2472 rown column: 07
High quality sequence stop: 415.
Location/Qualifiers
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                                                                                           Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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1 (bases 1 to 688)
Li,W.B., Gruber.C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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99 c 163 g 145 t 8C
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Tissue Procurement: Dr. Mark Watson
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/db_xref="taxon:9606"
/clone="IMAGE:6280902"
                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIH_MGC_113"
//lab_host="DH/DB (phage=resistant)"
//lab_host="DH/DB (phage=resistant)"
//note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGA(GG). Library constructed by Ling Mong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: brain; Vector: pcNVSPORT 6; 1st strand cDNA was primed with a Notr-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcNVSPORT 6 Vector. Library was normalized. Library was constructed by Life Technologies. Contact: Reng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                          y Match 47.2%; Score 28.8; DB 14; Length 1084; Local Similarity 69.6%; Pred. No. 1.9e+02; hes 39; Conservative 0; Mismatches 17; Indels 0;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/lab_host="DH10B"
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189 c 337 g 38 t 11
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/db_xref="taxon:9606"
/clone="CSODD007Y022"
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/note="Organ: lymph; Vector: poTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using APP-cDNA synthesis kit (Strategene) and Superscript Library."
                                                                                                                                                                            AGENCOURT_6640847 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5434071
BM999483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1910 row: i column: 16
High quality sequence stop: 136.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Prlmates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                            1 (bases 1 to 1729)
NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
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BQ521472.1 GI:21380341
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BQ521472/c
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/organism="Hordeum vulgare"
/db_xref="Laxon:4513"
/dlone="HVSWEC002216f"
/clone=lib="Hordeum vulgare seedling shoot EST library
HVSDNA0003 (Etiolated and unstressed)"
/tissue_type="Seedling shoot"
/tissue_type="Seedling shoot"
/lab_host="TuTill and celling shoot"
/lab_host="TuTill and celling shoot"
/seeds were surface sterilized then genminated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling shoots were then harvested, total RNA was prepared, poly(A) RNA was putified, one primary unamplified cDNA library was made, and I million plu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California,
Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University of California,
Riverside (Choi, Close, Fenton). Phagemids were performed and preparations, DNA sequencing and sequence analysis were performed at CUGI (Milmy Yu, Frisch, Henry, Simmons, Oates Pambo, Main). The sequence analysis were
                                                                                                                                                                                                                                                      Hordeum vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

Triticeae; Hordeum.

1 (bases 1 to 735)

Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library
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                                                         EST 22-0CT-2001
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this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                                      HVSMEC0002B16f Hordeum vulgare seedling shoot EST library HVCDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEC0002B16f, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
156 c 264 g 116 t 10 others
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On Feb 22, 2001 this sequence version replaced gi:13109940.
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68.4%; Pred. No. 2.7e+02;
Live 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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High quality sequence stop: 718.
Location/Qualifiers
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                                                                                                                                                         BG309093
BG309093.2 GI:16313793
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Best Local Similarity 68.4'
Matches 39; Conservative
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RESULT 7
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                                                                                                                                                                                  Email: cgapbs-remail.nih.gov

CDNA Library Preparation:

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pgnlc.pk0l0.k15 normalized chicken lymphoid cDNA lihear EST 01-MAY-2002 gallus connected chicken lymphoid cDNA liheary Gallus gallus chone pgnlc.pk0l0.k15 5' similar to no significant hits BQ038856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /close_lib="MICHED_XGC_EMb7"
/tissue_type="tailbud"
/tissue_type="tailbud"
/dev_atage="embryo, stages 20-27"
/dev_atage="embryo, stages 20-27"
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ECORV; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
                     Xehopodinae; Silurana.

1 (bases 1 to 403)

NIH-XCG http://image.llnl.gov/image/html/xehopuslib_info.shtml.

NIH-XCG http://image.llnl.gov/image/html/xehopuslib_info.shtml.

National Institute of Child Health and Human Development, National Cancer Insitute, Xenopus Gene Collection

Unpublished (2002)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves; Neognathae, Galliformes, Phasianidae, Phasianinae, Gallus.

f Jases I to 530)

Morgan, R.W. and Burnside, J.

Chicken lymphold ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
On Mar 27, 2002 this sequence version replaced gi:19772396.
Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 14; Length 403; Pred. No. 2.9e+02;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 403
//Organism="Silurana tropicalis"
//db_xref="taxon:8364"
//clone="IMAGE:5336064"
                                                                                                                                                                                                                                                                                                                                              info@image.llnl.gov
Plate: LLAMI1853 row: F column: 1
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
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Tel: 302 831-1345
Fax: 302-831-3411
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/db_xref="taxon:9031"
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BQ038856
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Lydyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission.

Direct Submission.

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suchiro-chou, Faurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:B1-45-503-9111, Fax:B1-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end clone tracking errors.
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Pan troglodytes
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Pan Froglodytes DNA, clone: PTB-132E07.R, genomic survey sequence.
AG122806
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                             /tissue_type="thymus, bursa, spleen, PBL, bone marrow"
/lab_host="E.coli EMDH10B"
/clone="pgnlc.pk0l0.k15"
/clone_lib="normalized chicken lymphoid cDNA library"
/sex="Male and Female"
                                                                                                                                                                                                                                     Gaps
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/clone_lib="PTB Chimpansee Wale BAC Library"
258 c 92 q 171+
                                                                                                                                                                                     Query Match 45.9%; Score 28; DB 14; Length 530; Best Local Similarity 66.7%; Pred. No. 2.9e+02; Matches 40; Conservative 0; Mismatches 20; Indels
                                                                                                                              33 others
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                                                                                                                          126 t
                                                                                                    /note="Vector: pCMVSPORT 6"
149 c 142 g 126 t
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/db_xref="taxon:9598"
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R.Site 1 : SacI
R.Site 2 : SacI.
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lissue Procurement: CGAP (Stanford)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .ch 45.6%;
.l Similarity 69.1%;
38; Conservative (
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• 552 c
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BQ648687  
BQ648687.1 GI:21772859  
EST.
                                                                                                                                                                                                                                                                                                                    Totoki,Y., Watanabe,H. and Sakaki,Y. Taylor,T.D., Yada,T.,
Pujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Pujiyama,A., Hattori,M. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Yaurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URI:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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                                                                                                                              Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-089K05.R.
Pan troglodytes
                                    GSS 03-NOV-2001
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                                      00162 712 bp DNA linear GSS 03-NOV-200 troglodytes DNA, clone: PTB-089K05.R, genomic survey sequence.
                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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BAC end sequences of Library PTB
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
230 c 205 g 150 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 45.6%; Score 27.8; DB 17; Best Local Similarity 69.1%; Pred. No. 3.5e+02; Matches 38; Conservative 0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pan troglodytes"/db_xref="taxon:9598"
/clone="PTB-089K05.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vector : pKS145
R.Site 1 : Saci
R.Site 2 : Saci.
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                                                                                          AG090162.1 GI:16641964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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                                      AG090162
                                                                        AG090162
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ORIGIN
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RESULT 12
AG090162/c
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TITLE
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JOURNAL
                                                                                                                                                                                                                                                                                                        JOURNAL
REFERENCE
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KEYWORDS
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SOURCE
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BH756447 452.05.n Arabidopsis thaliana TDNA insertion lines Arabidopsis clone SALK_053697.52.05.n, DNA Arabidopsis thaliana genomic clone SALK_053697.52.05.n, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="hepatocellular carcinoma, cell line"
/lab_host="hepatocellular carcinoma, cell line"
/lab_host="bhild (phage-resistant)"
/note="Gram = liver; Vector: poTB7; Site_1: XhoI: Site_2:
ECORI; CDNA made by oligo-dr priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACAGG(G). Size selected >500pp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 493)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jaske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Limmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thale cress.
Arabidopsis thaliana
Enkaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is single pass sequence recovered from the left border of IDNA.
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2444 row: j column: 15
High quality sequence stop: 438.
Location/Qualifiers
1. 1434
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1/52
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27.8; DB 14;
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_MGC_100"
                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:6270062"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/olone="INAGE: 5191807"
/clone=lib="NIH_MGC_114"
/lab_host="DHIOB"
/lab_host="DHIOB"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biab9045 1242 bp mRNA linear EST 28-AUG-2001
603021030R1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5191807 3',
mRNA sequence.
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0
/db_xref="taxon:3702"
/clone="Xalx_038697.52.05.n"
/clone="Xalx_038697.52.05.n"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
a 160 c 112 g 106 t 12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1242)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapberfemail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Phitp://image.llnl.gov
Plate: LLAM11479 row: k column: 08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 45.2%; Score 27.6; DB 17; Length 493; Best Local Similarity 67.2%; Pred. No. 3.8e+02; Matches 39; Conservative 0; Mismatches 19; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 others
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436 c 297 g 187 t
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Location/Qualifiers
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BI489045.1 GI:15328273
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Matches 36; Conserva
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
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Db 754 TGGGCGGGGAGTTTATGGTTATCCTGCGGCGGGGGGCGGTGAT 705
Search completed: June 13, 2003, 05:58:15
Job time: 156.839 secs
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Sequence 3, Appli
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Sequence 1, Appli
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Sequence 136, Appl
Sequence 136, Appl
Sequence 26, Appli
Sequence 27, Appli
Sequence 2, Appli
Sequence 218, Appli
Sequence 11, Appli
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Sequence 11, Appli
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                                                                                                                                                 (without alignments) 4027.262 Million cell updates/sec
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Sequence 11,
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                                                                                                                                                                                                                                           Description
                                                                                                                             June 13, 2003, 02:39:09; Search time 4.64516 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-516-859A-3
US-09-586-472-3
US-09-528-706-3
US-08-290-665A-139
US-08-290-665A-140
PCT-US95-10398-140
US-08-836-075A-17
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US-09-103-840A-1

US-08-23-443B-1

US-08-658-136-2

US-08-658-136-2

US-08-658-131-36

US-08-943-731-136

US-08-943-731-136

US-09-188-930-26

US-09-386-536-74

US-09-188-930-218

US-09-386-536-2

US-09-386-536-1

US-09-386-536-1

US-09-386-536-1

US-09-386-536-1

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US-09-073-663-11
US-09-264-737-3
                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                     441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                  US-09-826-581-3_COPY_612_672
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                            - nucleic search, using sw model
                                                                                                                                                                                                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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4411529
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4 1015
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4 1347
4 2543
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Sequence 135, App
Sequence 136, App
Sequence 137, App
Sequence 144, App
Sequence 135, App
Sequence 135, App
Sequence 136, App
Sequence 136, App
Sequence 137, App
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              Sequence 1
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Sequence 1
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Sequence 3
Sequence 8
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Sequence B
Sequence B
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                                                                                                                                                                                                                                                                                                                            18-08-459-568-3/c
Sequence 3, Application US/08459568
Fatent No. 5811304
Fatent No. 5811304
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Ainc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,568
FILING DATE: US-JUNN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
           PCT-US91-00399-1

US-08-290-665A-135

US-08-290-665A-137

US-08-290-665A-134

US-08-290-665A-144

PCT-US95-10398-135

PCT-US95-10398-136

PCT-US95-10398-136

PCT-US95-10398-134

US-08-123-936-85

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 5183 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 40.7
Best Local Similarity 67.3
Matches 35; Conservative
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STREET: 43/v ...
CIIY: San Diego
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US-08-459-568-3
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CDS
121..5278
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-586-472-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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US-08-516-859A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                        APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
STREET: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTONEYAGENET INCORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET UNBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08516859A Patent No. 6069231
                                                                                                                     Sequence 3, Application US/08399411 Patent No. 5831008 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.7%;
                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 5183 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 67.3
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                      ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                     San Diego
California
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US-08-516-859A-3/c
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                                                                                                     JS-08-399-411-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-08-399-411-3
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R.H.
NUCLECTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                               DB 4; Length 5868;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.3%; Score 24.6; DE 70.2%; Pred. No. 11; ive 0; Mismatches
                                                                                                                                   40.7%; Score 24.8; D. ilarity 67.3%; Pred. No. 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/290,665A
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                                                                                                                                                                                                                                                                                                                            US-08-290-665A-139/c
; Sequence 139, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATORNEY, AGRNT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: homosapiens INDIVIDUAL ISOLATE: Z4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 70.2 Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUCL
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQ
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                           CDS
121..5278
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BUKH, J., APPLICANT: PURCELL, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                         linear
                                                                                                                       Query Match
Best Local Similarity
 STRANDEDNESS:
TOPOLOGY: 11n
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US-09-528-706-3
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                                                           NAME/KEY:
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                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09528706
Patent No. 6468985
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: 2 inc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,706
                                                 ATTORINEY CACHT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION KUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 535-9001
TELEPRA: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24.8; DB; Pred. No. 13; 0; Mismatches
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-900-1994
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKEY NUMBER: P-LJ 1776
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                            LOCATION: 121..5278
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/516,859
                                                                                                                                                                                                                             LENGTH: 5868 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (619) 535-9001
IELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5868 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.7%;
Best Local Similarity 67.3%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 43, CCITY: San Diego STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                          FEATURE
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEAPATTIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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Sequence 140, Application PC/TUS9510398

GENERAL INFORMATION:

APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.

TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED

TITLE OF INVENTION: AMINO ACID SEQUENCES OF TH

TITLE OF INVENTION: AMINO ACID SEQUENCES OF TH

TITLE OF INVENTION: AND THE USE OF REAGENTS OF

TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC ME

TITLE OF INVENTION: 2603

TOTALE OF INVENTION: 2603

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION NUMBER: 08/290/665
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECHOMBICATION INFORMATION:
TELECHOMBICATION INFORMATION:
TELECHOMBICATION INFORMATION:
TELECHOM (212) 751-6849
TELEFAX: (212) 751-6849
TELEFAX: 42192
TELEFAX: 42192
TELEFAX: 42192
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
STRANDENDESS: SINGLE
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COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 15-AUG-1995
                                                                                                                                                                                                    NUMBER: PCT/US95/10398
15-AUG-1995
                                                                                                                                            SYSTEM: PC-DOS/MS-DOS WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                      IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.3%;
70.2%;
                                                                                               FLOPPY DISK
                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 15-AUG-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: Z4
PCT-US95-10398-139
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Best Local Similarity 70.2
Matches 33; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                      COMPUTER: IBM PC OPERATING SYSTEM:
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STATE: NEW YORK
                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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ORIGINAL SOURCE:
                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION:
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION:
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION:
AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION:
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                       AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLARES OF HEAPATITIS C VIEUS AND THE USE OF REAGENYS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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APPLICANT: BUKCELL, R.H.
APPLICANT: PURCELL, R.H.
TANTENTION: NUCLECTIDE AND DEDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-194
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RIGHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERNEX/POCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 756-4800
FELEPHONE: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
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                         US-08-290-665A-140/c
; Sequence 140, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                         MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 421792
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 Dase pairs
TYPE: nucleic acid
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70.2%;
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CITY: NEW YORK
                                                                                                                                                                                                                                                                                         263
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TITLE OF INVENTION: AMIN
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQU
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-290-665A-140
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APPLICANT: FLEISCHMAN, Robert D.
REFERENCE/DOCKET NUMBER: I:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                         LENGTH: 957 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 37; Conservative
                                                                                                                                                                                                                                                                  Best Local Similarity 68.0 Matches 34; Conservative
                                                                                                                            linear
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                                                                                                                         TOPOLOGY: lin
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LENGTH: 4403765
                                                                                                                                                                HYPOTHETICAL:
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                                                                                                                                                                                                                                               Query Match
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AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MIGCROSOft Word 6.0 / ASCII text output
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION NUMBER: PCT/FP95/04155
FILING DATE: 23 Oct 1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
40.3%; Score 24.6; D
Best Local Similarity 70.2%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches
                                                                                                                                                              NAME: RICHARD W BORK
REGISTRATION NUMBER: 36,459
REPERBUCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433
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FILING DATE: 21 Oct 1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: EP 95870076.7
                 PRIOR APPLICATION DATA:
APPLICATION NOMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
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; Sequence 17, Application US/08836075A
; Patent No. 6180768
                                                                                                                                                                                                                                                            TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR EXD ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: KAMMERER, PATRICIA A. REGISTRATION NUMBER: 29,775
                                                                                                                                                                                                                                           (212) 758-4800
(212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MAERTENS, GEERT APPLICANT: STUYVER, LIEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NEW SET TITLE OF INVENTION: AND THE TITLE OF INVENTION: AGENTS NUMBER OF SEQUENCES: 207 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: Z8
PCT-US95-10398-140
                                                                                                                                                                                                                                                                                                                                                                                                             linear
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: TEXAS
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3958304 GAAGGGTGGTCGACGACGAAGTTTGTGGGCGCCCAGATCGGTGCGGACGCGATGGACGACCCT 3958247
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                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09103840A
Fatent No. 6204328
Batent No. 6204328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
TILE OF INVENTION: UPBRCUIOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
SOSTWARE: PALENTING DAIE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOSTWARE: PALENTIN VEY: 2.1
                                                           Gaps
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Live 0; Mismatches 21; Indels 0;
                                                                                                                                             343 TGTGCCGGGGGTCGTTTGGGCCCCACGAGGGGCGAGAGCCCCGGGGGGGAC 294
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                                                                                                           40.0%; Score 24.4; DB 4; Length 957; 68.0%; Pred. No. 14; ive 0; Mismatches 16; Indels
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single
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ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                              GENERAL INFORMATION:
                                              16496 C 16496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 C 61
               61 C 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
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                                                                                                              US-08-658-136-2
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                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                              0; Gaps
                                                                                            Score 24.4; DB 4; Length 4411529; Pred. No. 30;
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                                                                                                                              21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUBBER: US/08/323,443B
FILLING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0372/08462
TELECHONICATION INFORMATION:
TELECHONE: (212) 527-7700
TELECHONE: (212) 527-7700
TELECHONE: (212) 527-7700
TELECHONE: (212) 53-633
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CRARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                              0; Mismatches
           TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                      APPLICANT: KLINGER, KATHERINE W.
APPLICANT: LANDES, GREGORY M.
APPLICANT: BURN, TIMOTHY C.
APPLICANT: CONNONS, TIMOTHY D.
APPLICANT: DACKOWSKI, WILLIAM R.
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                         Sequence 1, Application US/08323443B Patent No. 5654170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Darby & Darby PC STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                             40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
                                                                                                           Sest Local Similarity 63.8 Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                           US-09-103-840A-1
                                                                                                                                                                                                                                                          US-08-323-443B-1
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                                                                                            Query Match
                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Indels
                                                                   APPLICANT: KINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: CAKNOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GIRMINO, GREGORY
APPLICANT: GIRMINO, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PartentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                E: GENZYME CORPORATION ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGIGTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4
TELECOMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SECIED NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
; Sequence 2, Application US/08658136 ; Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/08658136
; Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 53526 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pai.
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Sequence 1, Appli
Sequence 1596, Ap
Sequence 134, App
Sequence 1153, Ap
Sequence 2153, Ap
Sequence 225, Appl
Sequence 20, Appl
Sequence 30, Appl
Sequence 4800, Ap
Sequence 1539, Appl
Sequence 1539, Appl
Sequence 1539, Appl
Sequence 163, Appl
Sequence 164, Appl
                                                                              June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds (Without alignments) 4579.068 Million cell updates/sec
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                                                                                                                                         US-09-826-581-3_COPY_612_672
61
1 9tgaggagtgggctgggaat.........99999cggagggagtcctc
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1. /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/PSO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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9 US-10-092-154-1596

10 US-09-925-301-334

1 US-09-925-301-334

1 US-09-925-301-334

1 US-09-96-154-1153

1 US-09-764-847-1153

1 US-09-764-847-1153

1 US-09-96-107-2925

1 US-09-96-30

1 US-09-864-761-2139

1 US-09-864-761-2139

1 US-09-864-761-2139

1 US-09-89-046-13

1 US-09-89-046-13

1 US-09-89-046-13

1 US-09-89-4761-2139

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1 US-09-89-4761-3

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1 US-09-89-1761-193

1 US-09-864-761-193

1 US-09-864-761-193

1 US-09-864-761-193

1 US-09-864-761-183

1 US-09-864-761-183

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1 US-09-864-761-183
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                1029858 seqs, 724030393 residues
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                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                     IDENTITY_NUC Gapox 1.0
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Maximum DB seq length: 200000000
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Query
Match Length DB
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25.2
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25
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Perfect score:
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367 9 US-10-223-085-33 Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sed Sequence 400, Appl Sec Sequence 1, Appl Sequence 2,	ALIGNMENTS n US/09826581 Leif L. Holger Stefan Stefan -0.07001 UMBER: US/09/826,581 2001-04-05 14-07 Windows Version 4.0	Query Match 100.0%; Score 61; DB 10; Length 1722; Best Local Similarity 100.0%; Pred. No. 1.8e-12; Indels 0; Gaps 0; Matches 61; Conservative 0, Mismatches 0; Indels 0; Gaps 0; QY 1 GTGAGGAGTGGGCTGGGAATCTTATGGGCACCCAGAGGGGGGGG
40.0 3367 40.0 3367 40.0 3367 40.0 3367 40.0 174566 39.7 13862 39.3 13862 39.0 1046 39.0 1046 39.0 1046 38.7 4711 38.7 4711 38.7 22452 38.4 1001 38.4 1001 38.4 1001	pplication US, 20020142310A1 MATION: ndersson, Leifuthman, L. HG Marklund, Stef Marklund, Stef ENTION: VARIA ENTION: VARIA CCE: 11145-007 ICATION NUMBER: 2001 ATION NUMBER: LATION NUMBER: LATION NUMBER: 2000-00 ID NOS: 14 stSRQ for Wind como sapiens	100 61; Conservative 61; Conservative 1 GrGAGGAGTGGGCTG 1 [
22 22 22 22 22 22 22 22 22 22 22 22 22	1 926-5 916-5 916-5 917-	Ouery Match Best Local Similarity Matches 61; Conseived 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAG7 1 GTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
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                                                                                                                                                                                                                                 Score 25.2; DB 10; Length 1030;
Pred. No. 5.3;
0; Mismatches 18; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-10-092-154-1153/c
; Sequence 1153, Application US/10092154
; Publication No. US2030054375A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.;
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies;
; FILE REFERENCE: PC009G1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF ESQ ID NOS: 2003
; PRIOR APPLICATION TEMOVED - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.3%; Score 25.2; DB 9; Length 5938;
66.7%; Pred. No. 4.7;
tive 0; Mismatches 18; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1153, Application US/09764847

Petent No. US20020132767A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper: NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; DB 10;
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66.7%; Pred. No. 4.7;
Live 0; Mismatches 18;
                       LOCATION: (989)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1006)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1023)
                                                                                                                                                                ) OTHER INFORMATION: n equals a,t,g, or c US-09-925-301-334
                                                                                                                                                                                                                                     41.3%;
66.7%;
                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7<sup>5</sup>
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 66.7
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
US-10-092-154-1153
        NAME/KEY: misc_feature
LOCATION: (989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-09-764-847-1153/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-764-847-1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                            1563 GTGAGGTGTGGGGTATTGTCTGGGGTTCCAGAAAGCCTGTGCGGTGCTGGAGTC 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1563 GTGAGGTGGGCGTGGGTATTGTCTGGGGTTCCAGAAAGCCTGTGCCGTGCTGGAGTC 1620
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.6%; Score 26; DB 10; Length 17761; 65.5%; Pred. No. 2.3;
                                                                                                                                                                                                                                                  Query Match 42.6%; Score 26; DB 9; Length 17761; Best Local Similarity 65.5%; Pred. No. 2.3; Matches 38; Conservative 0; Mismatches 20; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION TROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILLE REPERENCE: PAIGE
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SEQ ID NO 334
LENGTH: 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENY APPLICATION NUMBER: US/09/764,847
CURRENY FILING DATE: 2001-01-17
FILE PALE ALD NOS: 2003
SOFTWARE: PALENT OF NOSE 1003
FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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LOCATION: (59)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1596, Application US/09764847 Patent No. US20020132767A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 334, Application US/09925301 Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 65.5
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-764-847-1596
                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-092-154-1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                              LENGTH: 17761
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LENGTH: 17761
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APPLICANT: Olga Bandhan
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOSTWARE: PERL PROGram
SEQ ID NO 338
                                                                                                                                                                                                                Sequence 30, Application US/09964899
Fatent No. US20020174446a1
GENERAL INFORMATION:
I TITLE OF INVENTION: Identification of Genes Involved in
ITILE OF INVENTION: Alzhaimer's Disease Using Drosophila Melanogaster
FILE REFERENCE: 4-31512 A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/236,893
PRIOR RILING DATE: 2000-09-29
PRIOR RILING DATE: 2000-06-29
PRIOR RILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                   Query Match 41.0%; Score 25; DB 12; Length 1847; Best Local Similarity 64.9%; Pred. No. 6; Matches 37; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 9; Length 1351;
Pred. No. 6.2;
0; Mismatches 20; Indels
                         Indels
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) OTHER INFORMATION: Incyte ID No. US20020137081A1 344297.3
US-10-044-090-338
  Best Local Similarity 69.4%; Pred. No. 6.6;
Matches 34; Conservative 0; Mismatches
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; Patent No. US20020137081A1
; GENERAL INFORMATION:
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Best Local Similarity 64.9%;
Matches 37; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo Sapien
US-09-964-899-30
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US-09-864-761-4800
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                                                                                                                                                                              RESULT 9
US-09-964-899-30
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LENGTH: 1351
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1855 GAGGGGACAGAGCTAGGAGAAGGGAGGGCAGCCAGAAGGGCAGGGGTGCAGGGG 1802
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GENERAL INCORMATION:
APPLICANT: Horne, Joseph G.
APPLICANT: Scherf, Use
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028 WO.
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR PILLING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2925
LENTH: 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Genbank Accession No. US20020142981A1 R62519
NAME/KEY: unsure
LOCATION: (1).(275)
COTHER INFORMATION: n = a or c or g or t
US-09-880-107-2925
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Publication No. US20030069405a1
GENERAL INFORMATION:
ITILE OF INVENTION:
FILE REFERENCE: PZ014P1
CURRENT APPLICATION UNDBER: US/10/144,929
CURRENT APPLICATION NUMBER: US/10/144,929
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: US/09/251,329
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: PZ-17
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                                                                                                          ; Sequence 2925, Application US/09880107
; Patent No. US20020142981A1
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; OTHER INFORMATION: n equals a,t,g,
US-10-144-929-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: n equals a, t,g,
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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LENGTH: 541
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GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Honen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REPREMENT. ACOUNTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23
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N: EXPRESSED IN BT474, SIGNAL - 1.4
N: EXPRESSED IN BONE MARROW, SIGNAL - 1.1
SEAPRESSED IN LUNG, SIGNAL - 2.6
N: EXPRESSED IN PLACENTA, SIGNAL - 1.8
N: EXPRESSED IN PLACENTA, SIGNAL - 0.98
N: NT HIT: 9111423021, EVALUE 0.00e+00
N: NT HIT: 961116, EVALUE 1.00e-09
N: EST_HUMAN HIT: BE885438.1, EVALUE 0.00e+00
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
LENGTH: 2837
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Pred. No. 6.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR PLEATURY NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-08-03
PRIOR PLILING DATE: 2000-08-03
PRIOR PLILING DATE: 2000-09-04
PRIOR PLILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-07
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
                                     Sequence 21539, Application US/09864761
Patent No. US20020048763A1
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67.3%;
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Best Local Similarity 67.3:
Matches 35; Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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                                                                                                                                                                        TITLE OF INVENTION: GIANG GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITITLE OF INVENTION: GIANG GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITITLE OF INVENTION: GIANG GENOME ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica X. I Acomica X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 17; Indels
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BR474, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
US-09-864-761-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 4800
                                                         APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 49117
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Patent No. US20020048763A1
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ORGANISM: Homo sapiens
                                                                                                                                                                 APPLICANT:
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RESULT 12

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Sequence 193, Application US/09878281

Publication No. US20030032005A1

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.

NUMBER OF SEQUENCES: 270

COMPUTER READABLE FORM:

MEDIUM TYPE: IBW PC compatible

COMPUTER: IBW PC compatible
                                                                                                                                 ;
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                                                              40.3%; Score 24.6; DB 9; Length 498; 70.2%; Pred. No. 9.1; tive 0; Mismatches 14; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/878,281
FILING DATE:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/362,455
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70.2%;
                                                           Query Match
Best Local Similarity 70.2%
Matches 33; Conservative
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MOLECULE TYPE: C
HYPOTHETICAL: NO
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US-09-878-281-193/c
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LOCATION:
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US-09-878-281-193
      US-09-899-046-193
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                                                                                                           RESULT 13
US-10-024-450-3/C

Sequence 3, Aplication US/10024450

Publication No. US2003092606A1

GENERAL INFORMATION:
APPLICANT: Huang, SM.
TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ

TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ

FILE REFERENCE: P-LJ 5101

CURRENT FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: US 60/256,582

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0
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Score 24.8; DB 9; Length 5868;
Pred. No. 6.5;
0; Mismatches 17; Indels 0
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APPLICATION NUMBER: US/09/899,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: New sequences of TITLE OF INVENTION: genotypes for di NUMBER OF SEQUENCES: 270 COMPUTER READABLE FORM: MEDIUM TYPE: Flospy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-POS/MS-DOS
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Publication No. US20030008274A1
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
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Best Local Similarity 67.3%;
Matches 35; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 498 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
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; LOCATION: (121)...(5277)
US-10-024-450-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapien
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FEATURE:
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LENGTH: 5868
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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June 13, 2003, 01:49:14 ; Search time 5200.55 Seconds (without alignments) 9216.782 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
OM nucleic - nucleic search, using sw model
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2: 9b_htg:*

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Perfect score:
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is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AX281582 Sequence AJ249977 Homo sapi AX099802 Sequence AX099803 Sequence AX099804 Sequence AX398335 Sequence AX398335 Sequence AX398335 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX099774 Sequence AX099774 Sequence AX09974 Homo sapi AX000358 Homo sapi AX364014 Sequence AE015280 Homo sapi AX364014 Sequence AE025580 Homo sapi AX364014 Sequence AX364014 Sequence AE025580 Homo sapi AX364014 Sequence AX364018 Forosophil AX364014 Sequence AX364018 Drosophil AX482695 Sequence AX064138 Drosophil AX28181 Sequence AX28181 Sequence AX28181 Sequence AX28181 Sequence AX28181 Sequence AX28181 Sequence AX28181 Sequence AX28180 Sequence	NA linear PAT 02-NOV-2001 tta; Vertebrata; Euteleostomi; hini; Hominidae; Homo. d,S.
SUMMARIES	AX281582 HSA249977 AX299802 AX099804 AX099804 AX099804 AX099804 AX099800 AX398333 AX099800 AX398331 AX398331 AX398331 AX398339 AX398339 AX398339 AX398339 AX398339 AX381579 AX381579 AX009974 HSG42412 AX009974 HSG42412 AX001887 AX001887 AX001887 AX001887 AX001887 AX001887 AX001887 AX001887 AX001887 AX001887 AX01581 AX217107 AC127107 AC127107 AC127107 AC127107 AC127107 AC127107	ALIGNMENTS 1647 bp
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2290 bp mRNA linear PRI 07-APR-2000 for AMP-activated protein kinase gamma 3 subunit
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/db_xref="taxon:9606"
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                                                               Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
      AMPK gamma 3 gene; gamma 3 subunit.
                                                                                               1 (bases 1 to 2290)
Cheung, P.C., Salt,I.P., Davies,S.P., Hardie,D.G. and Carling,D. Characterization of Amp-activated protein kinase gamma-subunit isoforms and their role in AmP binding Biochem. J. 346 Pt 3, 659-669 (2000)
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Submitted (12-OCT-1999) Carling D., Cellular Stress Gro
Clinical Sciences Centre, Hammersmith Hospital, DuCane
London, W12 ONN, UNITED KINGDOM
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/gene="AMPK gamma 3"
/function="AMP-activated protein kinase
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/protein_id-"CAB65117.1"
/db_xref="G1:6688201"
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                               Chordata;
Primates;
-activated protein kinase; sapiens.
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                      Score 1453;
Pred. No. 0;
                  Query Match 88.2%;
Best Local Similarity 97.3%;
Matches 1501; Conservative
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RFWQEHTCYDAMATSSKLVIFOTMLEIKKAFFALVANGVRAAPLWDSKKOSFVGMLTI
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Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
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KNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
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GEALRORTLCLEGVLSCOPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
                  GGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATCGAT 1380
                                                                                                                                               1440 CAATGAAGGAATTGAGA-----ACAGCTTCATTTCCCCAACCCCAATTTGCTGGTTCAG 1493
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597, Uppsala 751 24,
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
Kalm. E., Le Roy, P., Chardon, P. and Andersson, L.
Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedi
                                              1535 CAATGAAGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCCACCCCCATTTGCTGGTTCAG
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Science 288 (5469), 1248-1251 (2000)
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ORIGIN Query Match Best Local Similarity 97.3%; Score 1447; DB 6; Length 2109; Best Local Similarity 97.3%; Pred. No. 0; Matches 1495; Conservative 0; Mismatches 35; Indels 7; Gaps 2; QY 101 TTCCTAGAGCAAAACAGGGCTAGGCCATCACAGGCTGTGACCAGCAGCTCAGAA 160			1	QY 521 CCCAAGCTGGGATGACGAACCGGGAACCCGGCGCCCAGATCTACATGCGCTTC 580	QY 641 ACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGCGGCCAGCC 1	761 CTGGTGCTGCATCGCTACTACAGGTCCCCCTGGTCCAGATCTATGAGATTGAACAACAT 	QY 821 AAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTCCATC 880	941 CTGCCTGTTCTTGACCCGGTGTCAGCAACGTACTCCACACTCACACACA
09 1115 GCACCCATCCTGACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTG 1174 1111	Qy 1295 CTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCACGAGAGCTTGGGGGAAGTGATCGAC 1354 Db 1201 CTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCACGAGAGCTTGGGGGAAGTGATCGAC 1260 Qy 1355 AGGATTGCTGGAGGACACACAGGCTGGTGCTGAGTGGACGAGACCCAGCATCTTG 1414 Db 1261 AGGATTGCTCGGGAGCAGACACAGGCTGGTGCTACTGGACGACACCAGCATCTTTG 1320	13	1535 CAATGAAGGAACTGGAGAACTCAGCTTCATCTCCCCACCCCATTGCTGGTTCAG 159 1111111111111111111111111111111111	4	VERSION AX099776.1 GI:13538810 KEYWORDS . SOURCE human. ORGANISM HOMO sapiens Charyota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. AllTHORS Anderson I. Locito; AllTHORS Anderson I. Locito; AllTHORS Anderson I. Locito;		JOURNAL PATENT: WO 0120003-A 3 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR); Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE) FEATURES Location/Qualifiers 12109 /organism="Homo sapiens" /db_xref="taxon:9606"	CDS 4721389 /note="unnamed protein product" /codon_start=1 /codon_start=1 /protein_id="CA035799_1" /do_xref="G1:1353881" /translation="MREMOEHTCVDAMATSSKLVIFDEMLEIKKAFFALVANGVRAAP LWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLGGCFKPLVS ISPNDASIERANTIKKHIHALLOLDIYONYRILFGELLEPSEL YRTIQDLGJGTFRDLAVLETAPILTADLFVDRYSALPVNRCGGVVGITSREVI HLAAQQTYNHLDMSVGEALRQRILCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDE TQHILGVVSLSDILQALVLSPAGIDALGA TQHILGVSLSDILQALVLSPAGIDALGA TQHILGVSLSDILQALVLSDILQALVLSPAGIDALGA TQHILGVSLSDILQALVGSLSDILQALVLSDILGALVGSLSDILGALGA TQHILGVSLSDILQALVGSLSDILQALVGSLSDILGALGA TQHILGVSLSDILQALVGSLSDILQALVGSLSDILGALGALGALGALGALGALGALGALGALGALGALGALGAL

113 GAAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCTCAGAAAGAA	173 AAACGGAGGCCAAAGCCTTGAGATGGACAAAGGCAGAAGTCGGTGGAGGAAGGGGGGGCA 232 	233 CCAGGTCAGGGGAAGGTCCCCGGTCCAGGCTAGTGATGCTCACCGGGCTGGAGGCC 292		350 CCAACAGGGTGGGACTGCCCTCCTGACTGTACAGCCTCAGGCTGCAGGCTCCAGCACA 409 [410 GATGATGTGGAGCTGGCCACGGAGTTCCCAGCCACAGAGGCCTGGGAGTGTGAGAA 469 		530 GGCIGGGAIGACGAACTGCGGAAACCCGGCGCCCAGAICTACAIGCGCITCAIGCAGGAG 589 	590 CACACCTGCTACGATGCCATGGCAACTACCTCAAGCTAGTCATCTTCGACACCATGCTG 649	650 GAGATCAAGAAGECCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGG 709	710 GACAGCAAGAAGCTGTGTGGGGATGCTGACCATCACTGACTTCATCCTGGTGCTG 769 	770 CATCGCTACTACAGGTCCCCCTGGTCCAGATCTATGAGATTGAACAACATAGAG 829	830 ACCIGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTCTCCATCTCTCCTAAT 889	890 GATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGCCTGCTTT 949	950 CITGACCCGGTGICAGGCAACGIACTCCACATCCTCACACAAAGGCCTGGTCAAGTIC 1009 	1010 CTGCACATCTTTGGTTCCCTGCTGCCCGCCCTCCTTCCTACCGCACTATCCAAGAT 1069 	1070 TIGGGCATCGGCACATICCGAGACTIGGCTGTGGTGCTGGACACACCCCCTCTGACT 1129 	1130 GCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGGTCAACGAATGTGGT 1189	1190 CAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCCAGCAAACCTAC 1249
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	srggargagaccagcacctrctgggg srgctcagccctgctgcatcgatgcc 		Eukaryota: Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1 AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G. TITLE Rovel prkagi alleles and use of the same as genetic markers for reproductive and meat quality traits. JOURNAL Patent: WO 0220850-A 3 14 *MAR-2002; Iowa State University Research Foundation, Inc. (US) FEATURES 11873 COS 11873 CODS **Inamed protein product" / Codom_State = "unnamed protein product" / Codom_State = "unnamed protein product" / Protein id="CAD32626.1"	// AGE_XTEF="GI:2126H109" // AGE_XTEF="GI:2126H109" // AGE_XTEF="GI:2126H109" // AGE_XTEF="GI:2126H109" // AGE_XTEF="GI:2126H109" // AGE_XTEF="GI:2126H109" // AGE_XTEF="GI:2126H109" // AGE_XTEF=TOWN OF THE TOWN

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0; Mismatches 211; Indels 8;
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                                     GTGGTCAACGAAACTGGACAGGTAGTGGGCCTCTACTCTCGCTTTGATGTGATCCACCTG 1137
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1 (bases 1 to 1873)
Milan,D. Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Lannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
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Milan,D., Jeon,J.T., Looft,C., Amarger.W., Robic,A.,
Rogel-Gallard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.
Kalan,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/chromosome="15"
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GPPGFPEGPGSRPVAESTGQEAFPFRATPLAQAAPLAEVDNPPTERDILESDCABSAS
DSNPDHLDGIIEFSABAGGDELGLVEEKPAPCPSPEVLLPRLGWDDELQRFGAQVYM
HPMQEHTCVDAMAYSSKLVIFDPMLEIKKAFPALVARGVRAAPLMOSKROSFVSHAFI
                                                                                                                                                                                        TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLGGCFRPLVSISPNDSLFEAVYALI
KNRAHRLPVLDPVSRAVLHILTRKLLKEHTFGTLLPRPSFLKRITGOLGIGTREDA
AVVLERAPITAALDIEVDRYSALPVNREGGOVOGLYSREDYIHLAAQQIYNHLDMV
GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVTVDETQHLLGVVSLSDILQ
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Pred. No. 2.8e-252;
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                                                                                                            /protein_id="CAC35800.1"
/db_xref="GI:13538835"
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

    (bases 1 to 1873)

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Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
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Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P.
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JOURNAL Patent: WO 0220850-A 1 14-MAR-2002; IOWA State University Research Foundation, Inc. (US) FEATURES Location/Qualifiers Source 1.1873	GPEGPRESPECTATION AND LOGGEN TO ANY TOTAL TREAD VERSE AND AND LOGGEN TO ANY TOTAL TREAD VERSE AND AND AND AND AND AND AND AND AND AND	Duery Match 69.2%; Score 1140.4; DB 6; Length 1873; Best Local Similarity 85.7%; Pred. No. 2.8e-252; Matches 1315; Conservative 0; Mismatches 211; Indels 8; Gaps 95 ATGAGGTTCCTAGAGGAAGAAACAGCAGCTCATGGCCATCACCAGGTGGCACCAGCCAG	Db 61 TCAGAAAGAAGCCATGGGGAACAAGGCCTCTAGATGGACAAGGCAGGAGGAT 120 Qy	241 GCCGAGGTGGACACCCCCAACAGGGGGACATCCTCCCCTCTGACTGCTCTCTCT	1
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TITLE Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits JOURNAL Patent: WO 0220850-A 7 14-MAR-2002; IOWA State University Research Foundation, Inc. (US) FEATURES 1. 1873 CDS Adb_aref="taxon:9823" CDS Anote="unnamed protein product" Abortein id="Contain" CTARGET LOIN-RAY-LEGUESCANDESCRAPLAGGARASKWIYERDENGYRASKYNYERDENGYEEG GPPGFPEGPGSRPAGSTGEAFFRATPLAGAAFLAEVDNPPPERDILPSDCAAGAS DSNTDHLDLGIEFSASAASGDELGIVEEKPAPCPSPEVLLPRLGWDBLQKPCAQVYM HEMQEHPTODAMATSSKUTVIDDNGIEKRAPFATNAGIRABAPTBDSKGSPUGMJTI TDFILVLHRYTSPOLOYTYEIEBHKIETKRAFFATNAGIRABAPTBDSKGSPUGMJTI KNRIHALPVLDPYGYYYEIEBHKIETWRELYLGGCFFPLVSISPDSLFBAVALI KNRIHALPVLLEGOLFVORYSALLFKRLAFRGTLLRFSFIXRTIODLGGTGFFRDL AVVLETARITALDIFVORRYSALPVNNETGQVVGIYSRFDVHILAAQQTXHHLDNNV GEALRQRILCLEGVLSCOPHETLGEVIDRIVREVLVDETQHLLGVVSLSDILD	DASE COUNT 383 a 580 c 534 g 376 t ORIGIN Query Match 69.1%; Score 1138.8; DB 6; Length 1873; Best Local Similarity 85.7%; Pred. No. 6.6e-252; Matches 1314; Conservative 0; Mismatches 212; Indels 8; Gaps 4; OV 95 ATGACCTTCCTAGAGAAAAACAGCAGCAACCAACAACAACAACAACAACAA		215 GTGGAGGAGGGAGCCACGAGGGAAGGTCCCGGTCCAGGCAGG	181 TCCACGGGCAGGCCACATCCCCAAGCCACCTTGGCCAAGCCGCTCCCTTG 10 1 1 1 1 1 1 1 1		QY 512 GCCCATTICCCAAGCTGGGCTGGGATGACGAACTGCGGAAACCGGGCGCCCAGATCTAC 571		Qy 692 CGGCCACCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGATGCTGACCATCACT 751	
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AUTHORS Rothschild, M.F., Clobanu, D.C., Malek, M. and Plastow, G. TITLE Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits JOURNAL Patent: WO 0220850-A 9 14-MAR-2002; IOWA State University Research Foundation, Inc. (US) FEATURES 11873 /Organism="Sus scrofa" /Organism="Sus scrofa" /Organism="Sus scrofa" /Organism="Sus scrofa" /Organism="Sus scrofa" /Octanism= Sus scrofa" /Oct	/dbreald="chijac29.1" /db_xref="G1:21261115" /translation="MSFLEQGESRSMPSRAVTISSERSHGDQGNKASRWTROEDVEEG /translation="MSFLEQGESRSWPSRAVTISSERSHGDQGNKASRWTROEDVEEG GPGPREGPGSRPVAESTGQEATFPRATPLAQAAPLAEVDNPPTERDILPSDCAASAS DSNTDHILDGIEFGASASGDEIGIVERKAPROESPEVLIPRIGWDDELQRFGAQYYM HFWQEHTCYDAMATSKLV1FDTMLEIKKAFFALVANGVQAAPLWDSKRQSFVGMLT TDFILIVLHRYTREBLVQIYEIEEHKIETWREITLQGCRFRLV3ISPNDSLEAVYALI KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRESFLYRTJODIGIGTFRDIL	AVVLETAPILTA GEALRORTCLEK GEALRORTCLEK ALVLSPAGIDALK 383 a 580 c 580 c	Matches 1314; Conservative 0; Mismatches 212; Indels 8; Gaps 4; Qy 95 ATGAGCTTCCTAGAGCAAAAAACAGCTCATGACCATCACCAGCTGTGACCAGCAGC 154		Db 121 GTAGAGGAGGGGCCTCCGGGGCAAGGGAAGGTCCCCAGTCCAGGCCAGTTGCTGAG 180 QY		QY 452 TGGGAGTGTGAGCTAGCAAGAGCCTGGAAGAGGCCTGCCCTGTCCCCGCAG 511 Db 1 1 1 1 1 1 1 1 1 1	ATGCGCTTCATGCAGGAGCACACCTGCTACGATGGCAACTAGCTCCAAGGTAGTC	Qy 692 CGGGCAGCCCTCTATGGGACAGCAAGAGCTTGTGGGGATGCTGACCATCACT 751
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/db_xref-"SWISS-PROT:P80385"
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WTXITLHTHRALLKFRLKFTEFPREPERSELEBLGIGTVANIAWWFTTPVYVRALGIFVORDPESG
FVQHRVSALPVVDBKGRVPTTSKFPDVINLAABKTYNLDVSYTKALQHRSHYBGVL
KCYLHFILEALINRLVBARVHRLVVVDEHDVVKGIVSLDLLQALLQALGGGRKRP"
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 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                         Submitted (07-FEB-1996) D. Carling, MRC Clinical Sciences Centre, Department of Molecular Medicine, RPMS, Hammersmith Hospital, DuCane Road, London, W12 ONN, UK
                                                                                    gamma
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                                                                                                                                                                                                                                                                                                                 /function="binds to alpha and beta subunits of AMPK forming a heterotrimer"
                                                                                subunits. Assembly of the heterotrimeric complex in vitro J. Biol. Chem. 271 (17), 10282-10290 (1996)
                                                        Scott, J.
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                                                   Woods,A., Cheung,P.C., Smith,F.C., Davison,M.D., Beri,R.K. and Carling,D. Characterization of AMP-activated protein kinase
                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAA64831.1"
/db_xref="G1185271"
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                                                                                                                                                                                                                                                                      /strain="Wistar"
/db_xref="taxon:10116"
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                                                                                                                                                 2 (bases 1 to 1328)
Carling, D.
                                         (bases 1 to 1328)
              Mammalia; Eutheria;
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GCACCTTTGTGGGACAGCAAGAAGCAGAGCTTCGTGGGGATGCTGACCATCACAGACTTC
                                                                                 CATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTCTCC
                                                                                                CGCCTGCCGGTCCTGGACCCTGTCTCCGGGGCTGTGCTCCACATCCTCACACATAAGCGG
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                           ATCCTGGTGCTGCATCGCTACTACAGGTCCCCCTGGTCCAGATCTATGAGATTGAACAA
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AMP-activated protein kinase; gamma subunit..
Fattus norvegicus.
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Search completed: June 13, 2003, 04:39:40 Job time: 5204.55 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pig PRRAG3 polymor Pig AMPK gamma sub Human AMP-activate PRRAG3 intron 2 - Human cDNA differe Human pencreatic c Mammalian AMPK-gam Human NS cDNA sequence Brosophila melanog	Human immune/haema Human immune/haema Human immune/haema DNA encoding novel Human colon cancer Human colon cancer PRKAG3 intron 4 - DNA encoding novel Bovine embryonic g Human polyunciecti Drosophila melanog CDNA sequence #559	Pig PRRAG3 gene 5' Pig PRRAG3 gene 5' Human prostate exp Human prostate exp Human breast cell Human foetal liver Probe #3373 for ge Human brain expres Human bone marrow Probe #3398 for ge Probe #3398 for ge Probe #335 used t		subunit; PRRAG3; variant; itution; ss.	
22222222222222222222222222222222222222	466666666666666666666666666666666666666	1095 24 AAD36461 808 24 AAD36462 539 23 ABV09172 615 23 ABV39323 378 22 ABA4706 378 22 ABA5162 378 22 AAX28974 378 22 AAX13465 378 22 AAX13465 378 22 AAX13465 378 22 AAX13465 378 22 AAX13465	ALIGNMENTS DNA, 1647 BP.	protein kinase gamma 3 labetes; obesity; subst ion/Qualifiers	/*tag= a /*tag= a /*tag= b /*tag= b //tabel= "c230g" /*tag= c /*tag= c /*tag= c //tabel= "T559c" //tabel= "T559c" //tabel= "1559c" //tabel= "1559c" //tabel= "1559c" //tabel= "1559c" //tabel= "1559c" //tag= c /*tag= c /*tag= c /*tag= c /*tag= c /*tag= c //tag= c //
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us-09-826-581-5.rng

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This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nuclectide 320, resulting in the amino acid substitution p71A; in exon 4 variation may be a substitution of a T for a C at nuclectide 550; and in exon 10 variation may be a substitution of a T for a C at nuclectide 1037, resulting in the amino acid substitution R340M. There may also be conclected variation in infrom 6. The numbering of these variations is based on the full length cDNA as given, rather than on the proper reading frame.
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                                                                                                                                                                                  New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
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P-PSDB; QQB47679.
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WO200177305-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preferably a carbohydrate metabolism disorder. Frimers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PKKAG3. Transgenic animal and host cell transformed with PKKAG3 a
                                                                                                                                                                                                                                                     Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                              Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder,
                                                                                                                                                                                                                                                                                               cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                          "Human complete Prkag3 protein"
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Gellin J, Le Roy P,
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1..1395
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heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PKKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PKKAG3 and is useful in gene therapy.
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                                                                                                                                         88.2%; Score 1453; 97.3%; Pred. No. 0;
                                                                                                                                                                         Matches 1501; Conservative
                                                                                                                                                           Local Similarity
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2001-244810/25
                                                                (LOOF/) LOOFT C. (KALM/) KALM E.
                                                                                                                          P-PSDB; AAE00221
                                                                                         Andersson L, Lo
Iannuccelli N,
      11-SEP-2000;
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                                                                1355 AGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTCTTG 1414
                                                                                                                                                                                                                            1415 GGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATCGAT 1474
                                                                                                                                                                                                                                             1321 GGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATCGAT 1380
                                                                                                                                                                                                                                                              1475 GCCCTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCACCTGCACACCTGGAAGC 1534
                                                                                                                                                                                                                                                                                               1535 CAATGAAGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCCACCCCCATTTGCTGGTTCAG 1594
                                                       1115 GCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCCACTGCCTGTG 1174
                                                                                        GTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGGTTTGATGTGATTCACCTGGCT 1234
                                                                                                                          1295 CTATGICIGGAGGGAGICCTIICCIGCCAGCCCCACGAGAGCIIGGGGGAAGIGAICGAC 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; strKRG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbolydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                      CGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                         1595 CTATGATTCAGGTAGGCTCTGCCCTGGGCCATGACACCAGCCT 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human Prkag3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                         AAD03296 standard; DNA; 2109 BP.
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/*tag= c
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The present sequence is a cDNA encoding human adenosine monophosphate (AMP) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders associated with muscle metabolism as diabetes, obesity, and disorders associated with muscle metabolism cuch as myopathy and cardiovascular disease, to modulate AMPK cartivity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a chetectrimenic AMPK consisting of PRKAG3 or its mutant, are useful for encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                     Robic A, Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GGCACTCCACCAACAGGTGGGATGCCTCCCCTCTGACTGTACAGCTCAGGTGGGG
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Pred. No. 0;
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(ANDE/) ANDERSSON L.
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Best Local Similarity 97.3%;
Matches 1495; Conservative
2000WO-EP09896.
                                                                                 10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
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Sus scrofa PRKAG3 splice variant DNA
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(ANDE/) ANDERSSON I
(LOOF/) LOOFT C.
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                             TCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGC
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                     GAGCTAGAAGGCCTGCTGGAAGAGAGAGGCCTGCCCTGTGCCTGTCCCCGCAGGCCCCATTT
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The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMFK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting AGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCACCCCCATTTGCTGGTTCAGCTATGA 1600 Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; preprior obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds. New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and ت Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard, Gellin J, Le Roy P, Chardon P; /*tag= a /product= "Sus scrofa Prkaq3 splice variant" TTCAGGTAGGCTCTGCCCTGGGCCATGACACCAGCCT 1637 1494 rrcaggerrerrcageerrecaaaarrgeerrrgeer 1530 NAT RECH AGRONOMIQUE. L.

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                                                                                                                                                                                                                                                                                                                                     CCAACAGGGTGGGACTGCCTCCCCTCTGACTGTACAGCCTCAGCTGCAGCTCCAGCACA 409
from the expression of a functionally altered allele of PRKAG3.
Transpentc animal and host cell transformed with PRKAG3 or a heterotrineric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrKag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                       GGAGAGACCGTTCATGGCCATCCGGGCTGTAACCACCAGCAGAAAGCATGGG
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                                                                                                                                      53 ACCCCTTCCTGGAGCAGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCCTAGAGCAA
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                                                                                                                                                                            Gaps
                                                                                                22; Length 2022;
                                                                                                                   8;
                                                                                C; ...
Score 1172.8; DB 22,
...d. NO. 5.2e-296;
...d. No. 5.2e-217; Indels
                                                                             Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;
                                                                                                          Pred. No. 5.2e-
0; Mismatches
                                                                                                71.2%;
85.7%;
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                                                                                                  1126 TIGGGCATCGGCACATTCCGAGACTTGGCGGGTGCTGGAAACGGGGCCCATCCTGACC
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                                                                                                                                                                                                                                                                         Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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Pred. No. 5.6e-288;
0; Mismatches 210;
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                                                                                                                                                                                                 Plastow
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 89-91; 109pp; English.
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                                                                                                                                                                  (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                 Malek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.3%;
85.8%;
                                                                      10-SEP-2001; 2001WO-US28283
                                                                                                      2000US-231045P.
                                                                                                                     08-JAN-2001; 2001US-260239P. 18-JUN-2001; 2001US-299111P.
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Matches 1316; Conservative
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                                                                                                                                                                                                                                              P-PSDB; AAE22985
                                                                                                                                                                                               MF,
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The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRRAG3: Prkag3 agene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect general for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered alalele of PRRAG3 or a functional and host cell transformed with PRRAG3 or a function and host cell transformed with PRRAG3 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                          PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rogel-Gaillard C;
                                                                                                           complete PRKAG3 cDNA.
                                                                                                                                           subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of discassociated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                          /product= "Sus scrofa complete Prkag3 protein"
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J, Le Roy P, Chardon P;
                                                                                                           subunit muscle-specific isoform,
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ANDE/) ANDERSSON L.
LOOF/) LOOFT C.
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                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..1395
CDNA; 1873 BP
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18-MAY-2000; 2000EP-0401388
                                                                       (first entry)
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AAD03319 standard;
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T; 0 other;

Sequence 1873 BP; 382 A; 580 C; 535 G; 376

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                         Gaps
  Length 1873;
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                        Indels
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Score 1140.4; DB 2;
Pred. No. 1.5e-287;
0; Mismatches 211;
69.2%;
85.7%;
                     Matches 1315; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig wild-type PRRAG3 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
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                                                                                                                                                                                                                                      Malek M, Plastow
                                                                                                                                                                            (IOWA ) UNIV IOWA STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Fig 1; 109pp; English.
                                                      2000US-231045P.
2001US-260239P.
2001US-299111P.
                                                                                                                                                                                                                                   Ciobanu DC,
2001WO-US28283.
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Matches 1315; Conservative
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                                                                                                                                                                                                                                                                                                                        P-PSDB; AAE22984
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10-SEP-2001;
                                                         08-SEP-2000;
08-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                subunit gene
                                                                                                                   18-JUN-2001;
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274 180 331 511 417 571

"Pig PRKAG3 polymorphic variant (PRKAG3-52)"

/product "Pig PF replace (154, A) /*tag= b

/*tag=

Location/Qualifiers 1..1395

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/*tag=

(first entry)

/standard_name= "Single nucleotide polymorphism (SNP)"

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AMP activated protein kinase regulatory gamma subunit; PRKAG3 escreening; meat quality; single nucleotide polymorphism; SNP; gene; variant; ds.
                                      Pig PRKAG3 polymorphic variant DNA (PRKAG3-52)
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                                                                                                                                                                                                                                                           08-SEP-2000; 2000US-231045P.
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18-JUN-2001; 2001US-299111P.
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P-PSDB; AAE22986.
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APCTTCGACACCATGCTGGAGATCAAGAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTG
          GAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTG
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Malek M, Plastow

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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGAAAGAATCCGTGGGAAACGGAGGCCCAAAGCCTTGAGATGGACAAGGCAGAAGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                             Claim 34; Page 93-95; 109pp; English.
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AAD36458 standard; DNA; 1873 BP

AAD36458 ID AAD3 RESULT

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1258 GACCGGATTGTCCGGGAACAGGTGCACCGCCTGGTGCTCGTGGATGAGACCCGGGACCTT 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Pig PRKAG3 polymorphic variant (PRKAG3-199)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "Single nucleotide polymorphism (SNP)"
                                     CIGGGCGIGGTGCCTCTCTGTGATCCTTCAGGCTCTGGTGCTCAGCCCTGCTGGAATT
                                                                                         GATGCCCTCGGGGCCTGAGAACCTTGGAAACCTTTGCTCTCAGGCCACCTGGCACCTCGG
                                                                                                                                            AGCCAGTGAAGGAGC-CGTGGACTCAGCTCTCACTTCCCCTCAGCCCCACTTGCTGGT
                                                                           GATGCCCTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCACCT-GCACACCTGG
                                                                                                                           1531 AAGCCAATGAAGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCCACCCCCATTTGCTGGT
                         TIGGGCGIGGICICCCICICCGACAICCIICAGGCACIGGIGCICAGCCCIGCIGGCAIC
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                                                                                                                                                                                                                                                                                                                                                                AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
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08-JAN-2001; 2001US-260239P.
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                                                   TGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGGCCTGCCCTGTGCCTGTCCCCGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                            1472 GATGCCCTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCACCT-GCACACCTGG
                                   958 TACCGCACCATCCAAGATTTGGGCATCGGCACATCCGAGACTTGGCCGTGGTGCTGGAA
                                                                                                             GTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCCGCTTTGATGTGATTCACCTG
                                                                                                                                                                            1198 ACACTGTGTCTGGAAGGGTCCTTTCCTGCCAGGAGCCTTGGGGGGAAGTCATT
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                                                                                                                                                                                                                                                                                                                                                                             TACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAG
                                                                                                                                                                                                                                                              1352 GACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTC
                                                             ACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
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for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
                                                                                                                                                                          TCAGAAAGAATCCGTGGGAAACGGAGGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCG
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                                                                                                   Gaps
                                                                          Length 1873;
                                                                        69.1%; Score 1138.8; DB 24; Lengt
85.7%; Pred. No. 3.8e-287;
ive 0; Mismatches 212; Indels
                                                Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                  st Local Similarity 85.7 tches 1314; Conservative
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                                                                                                                       GAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCAAGCCTCTG
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   CGGGCAGCCCCTCTATGGGACAGCAGAAGCAGAGCTTTGTGGGGATGCTGACCATCACT
                             CAAGCGGCACCTTTGTGGGACAGCAAAAAGCAGAGCTTCGTGGGGATGCTGACCATCACA
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                                                                                                                                                  Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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The present sequence is a cDNA encoding pig adenosine monophosphate (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.

Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as the constitution and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for encoding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain compounds and is useful in gene therapy.
                          Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma: arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                          1198 TGTCTGGAAGGCGTCCTTTCCTGCCACCCCACGAGACCTTGGGGGAAGTCATTGACCGG
                                                                                                                                                                                                                                                              GTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATGCC
AACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCC
                                                                 CAGCAAACCTACAAACCTGGACATGAGTGTGGGGAGAAGCCCTGAGGCAGAGGACACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1597 ATGATTCAGGTAGGCTCTGCCCTGGGCC 1624
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27-APR-2000; 2000US-0560875.
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB0825-ABBA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, and sequences against the polypeptides, methods of detecting the nucleotides or polypeptides of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby propertides of the invention have homology to known proteins, thereby proteins an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities; seem cell growth factor activity; hammatopolatatory activity; issue growth activity; hammatopolatatory activity; tissue growth activity; hemanatopolates required activities; neceptor or inhabin-related activities; chemotactic or chemokinetic activities; hammatopolates activities; chemotactic or chemotactic activities; neceptor or inhabin-related activities; chemotactic or chemotactic or chemotactic activities; permodely to activities; confidence of involved in oncogenesis, cancer cell proliferation or metastasis.

Companion on their biological activities; polypeptides and nucleicals of involved in oncogenesis, cancer cell proliferation or material schemala, bromediactory activities; cornary heart disease, conditions, e.g., by protein or gene therapy. Such conditions include cancers, hemantopolatic disorders (e.g., mysloid or lympholatic disorders.) chronic inflammatory conditions; cornary heart disease, arterial isonemia, bone disorders (e.g., mysloid or lympholatic activities involved with tissue regeneration and creating infections in additions (e.g., asthma or strain inflammatory activities may be used to promote cell growth. For example, such polypeptides and nuclein or propertion in maintenance 
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                                   Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 3.5e-107
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99.6%;
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P-PSDB; ABB11241.
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1038 GGCCCTCCTTCCTCACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGG 1097

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Similarity
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                                            in intron 6.
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                        1098 CTGTGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTG 1157
                                  301 GGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                         Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of
                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                  intron 4"
                                                           TGTCTGCACTGCCTGTGGTCAACGAATGTGGT 1189
                                                                    TGTCTGCACTGGCTGTGGTCAACGAATGTGGT 452
                                                                                                                                                                                                                                                           /note= "3' portion of intron 22..177
                                                                                                                                                                                                                                                                                                                                                                        /number= "Intron 4"
/note= "5' portion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marklund S;
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       "Intron 3"
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178..541
                                                                                                                                                                                                                                                                                                                                                "Exon 4"
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                                                                                                                     AAH43682 standard; DNA; 989 BP
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                                                                                                                                                                        PRKAG3 intron 2 - intron 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AREX-) AREXIS AB.
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                                                                                                                                                       21-JAN-2002
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a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                 540 AGGTCCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTCCCCAAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA differentially expressed in granulocytic cells #895.
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                                                                                                                                                                                                                                                            Score 407.2; DB 22; Length
Pred. No. 3.2e-96;
                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                       Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                         24.7%;
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                                                                                                                                                                                                                                                                                                                    409; Conservative
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us-09-826-581-5.rng

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated the expression level to an expression level in an unactivated of GCA.

Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a print of expression of the gene is indicative of inflammation.

CC (4) treating (M5) an inflammatory disease, by contacting a subject to a pathogen or sterile inflammatory disease, by contacting a subject to a pathogen or sterile (GCA preferably in an inflammation (especially chronic) in a tissue, an allergic casponse in a subject, exposure of a subject to a pathogen or sterile or response in a subject, exposure of a subject to a pathogen or sterile or response in a subject, exposure of a subject to a pathogen or sterile or response in a subject, exposure of a subject to a pathogen or sterile or response in a subject, seasonse in a subject, an allergic cresponse in a subject, social arthritis, and an analysing or an allergic cresponse in a subject, exposure of a subject to a pathogen or sterile or response in a subject in a subject in a subject in a subject in a subject or a pathogen or sterile or response in a subject in a subject in a subject in a subject in a subject in a subject in a subject or an allergic cresponse in a subject in a subject in a subject i
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                                                                                                       expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents a gene differentially expressed in granulocytes.
                                                                                            Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ie: The sequence data for this patent did not form part
the printed specification, but was obtained in electronic
mat directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for treating one of the above conditions. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 393.4; DB 24; Length
Pred. No. 1.5e-92;
0; Mismatches 311; Indels
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  Vockley J;
     Yamaqa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                        Claim 1; SEQ ID No 895; 114pp; English.
  Weissman SM,
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65.1%;
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                                              WPI; 2002-435328/46.
Beazer-Barclay Y,
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                                                                                                                                                                            drug toxicity
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                                                                                                                                                                                                                                              657 TCATGTCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC 716
                  ACCEGATCCATCECCTECTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA
                                                                                                     537 ACAAGATCCACAGGCTGCCAGTTATTGACCCAGAATCAGGCAATACTTTGTACATCCTCA
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CTCTGGTCTCCATCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1407 ATCTCTTGGGCGTGGTCTCCCTCCGACATCCTTCAGGCACTGGTGCTCA 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pancreatic cancer antigen;
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Ruben SM;

Rosen CA,

us-09-826-581-5.rng

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WPI; 2000-579444/54.

DR P-PSDB, AAB54009.

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New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliotating a medical condition, particular pancreatic PT treating, or ameliotating a medical condition, particular pancreatic PT cancer, or for use in assays for diagnosing a pathological condition - PT cancer, or for use in assays for diagnosing a pathological condition - CC AAB5466. The human pancreatic cancer antigens, given in AAB54008 to AAB5466. The human pancreatic cancer antigens, pave cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, cc in gene therapy. The polynuclecifide and proteins and be used for preventing, treating, or ameliorating a medical condition or in assays (cr diagnosing a pathological condition or a susceptibility to one in a consuject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer.

C Agonists and antagonists to the antigens can be used to design nucleic cancer antigen polyuculectides can be used to design nucleic and diagnostic methods. The proteins can be used to design nucleic can diagnostic methods. The proteins can be used to design nucleic and diagnostic methods. The proteins can be used to design nucleic content near used to purity, detect and target the polypeptides, including proteins can be used to treat or prevent neural, immune system, muscular, correproductive, quastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AA99232 to AA99240 and AAA9447 represent proliferative disorders. AA99232 to AA99240 and AAB5447 represent proliferative disorders. AA9922 to AA99240 and AAB5447 represent proliferative disorders. AA9922 to AA99240.
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Sequence 1691 BP; 458 A; 382 C; 401 G; 449 T; 1 other;

Query Match 23.9%; Score 393.4; DB 21; Length 1691;

Best Local Similarity 65.1%; Pred. No. 1.6e-92;

Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps

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TCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACTTCCGAGACTTGGCTGTGGTGC 1106 987 CACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCCGGCCCTCCT 1046 567 TCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGC 626 TGTATACTTCCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 182 TCACTGACTTCATCCTGGTGCTGCATCGCTACTACAGGTCCCCCCTGGTCCAGATCTATG 806 866 CTCTGGTCTCCATCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGA 926 ACCEGATCCATCCCTCCTTCTTCACCCGGTGTCAGGCAACGTACTCCACATCCTCA 986 543 CCCACAAGCGCATTCTGAAGTTCCTCAAATTGTTTATCACTGAGTTCCCCAAGCCAGAGT 602 TAGTCATCTTCGACCATGCTGGAGATCAAGAGGCCTTCTTTGCTCTGGTGGCCAACG 686 GTGTGCGGGCAGCCCCTCTATGGGACAGCAGAAGCAGAGCTTTGTGGGGGATGCTGACCA 746 AGATTGAACAAAATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGC 1047 627 687 747 807 363 867 927 483 qq à 셤 ŏ ŏ g Ω QQ Qγ QQ ò g à g δ qq

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Search completed: June 13, 2003, 02:59:53 Job time: 601.355 secs

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Title: Perfect score:

Run on:

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Scoring table:

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Database

Searched:

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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR PRimers
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1 (bases 1 to 572)
Fahrentug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
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Fax: 402 762 4390
Email: smith@email.marc.usda.gov
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Score

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                    /note-"Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 190 c 151 g 124 t lothers
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                                                             /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="WARC_2PIG"
/tissue_type="pooled"
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           Plate: 119 row: I column: 11
Seq primer: ATTTAGGTGACACTATAG
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/tissue_type="Adult brain"
//tissue_type="Adult brain"
//note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was prinmed with a NotI-oligo(dT) prinmer. Five prinme end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was constructed by Life Technologies.
Contact: Feng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax: (1) 301 610 8371 Email:
Hilangelifetech.com URL
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1 (bases 1 to 970)
Li,W.B., Gruber,C., Jessee,J., and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope_cns.fr, Web : www.genoscope.cns.fr.
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230 c 217 g 268 t
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                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="cSODN004YN03"
/clone_lb="LTI_FL015_Brn1"
/sex="male"
                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .970
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Tio, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M., Tagawa, A., Takhashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1274 GAAGCCCTGAGGCAGAGGACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCACGAG 1333
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                                                                                                                                                                                                                                                                                                                                                               1034 CCCCGGCCCTCCTTCCTCACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGAC 1093
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTGCTTCAAGCCTCTGGTCTCCATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTAC
                                                                                                                                              241 GACTCCTTTAAGCCGTTGGTCTGCATCTCCCCCAATGCCAGCCTTTTTGATGCCGTCTCC
                                                                                                                                                                                        914 ACCCTCATCAAGAACCGGATCCATCGCCTGCTTCTTGACCCGGTGTCAGGCAACGTA
                                                                                                                                                                                                                                                                             974 CTCCACATCCTCACACACACACCCTGCTCCAGTTCCTGCACATCTTTGGTTCCTTGCTG
                                                                                                                                                                                                                                                                                                 481 ATGGCGTGGTGAGCACCAGCACCATCTATGTGGCTCTGGGCATCTTCGTGCAGCAC
                    BB630381 IREEN full-length enriched, 6 days neonate musculus cDNA clone A030014A04 5', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
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TGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCCGCTTTGATGTGATTC 1226
                                                                                  1227 ACCIGGCIGCCCAGCAAACCIACAACCAGCTGGACAIGAGIGIGGGAGAAGCCCTGAGGC 1286
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Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
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                        810 ATCGATCACATTACTTTGAGGGTGTTCTCAAGTGCTACCTGCATGAGACTCTGGAGACCA 869
                                                                                                                                                                                                                                                                                               870 TCATCAACAGGCTAGTGGAAGCAGAGGTTCACCGACTTGTAGTGGTGGATGAAATGATG 929
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                             614 ACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCT
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Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpl.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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/cell_type="bursa! lymphocyte"
/dev_stage="2-3 weeks old"
238 c 186 g 166 t
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AJ396118 dkf2426 Gallus gallus c
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/clone_lib="dkfz426"
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69.3%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Li.W.B., Gruber.C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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/db_xref="taxon:9606"
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RIKEN integrated sequence analysis (RISA) system--384-format
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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/clone_lib="RIKEN full-length enriched, 6 days neonate
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/dev_stage="6 days neonate"
/lab_host="DH10B"
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was primed with a Notl-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco Ry sites of the pchysport of vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Library was constructed by a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filiang@lifetech.com URL: http://fulllength.invitrogen.com ' I others
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                                                                                                                                                                        /clone="CSODXCOOYYED2"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA
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Full-length cDNA libraries and normalization Unpublished (2001)
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Pred. No. 5.1e-80;
1; Mismatches 289;
                                                       Sequencage
                                              Genoscope - Centre National de Seque
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web
                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                         Location/Qualifiers
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64.9%;
                                     Contact: Genoscope
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="CSOD1082712"
/tissue_type="placenta"
/tissue_type="placenta"
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/note="Wector: pCWNSPORT 6; Site_1: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com  2 others
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AL554278 AL554278.1 GI:12894901 EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1167 TGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTC 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCTGGCTGCCCAGCAAACCTACAACCACCTGGACATGAGTGTGGGGAGAAGCCCTGAGGC 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   692
                                                                                                                                            926
                                                                                                                                                                                                                                                                                986
                                                                                                                                                                                                                                                                                                                            453 ACAAGATCCACACGCCGCTGTTTTTGACCCAGAATCAGGCAATACTTTGTACATCCTCA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         813 ATCGATCACATTACTTTGAGGGTGTTCTCAAGTGCTACCTGCATGAGACTCTGGAGACCA 872
ACATTGAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGC 866
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1085)
                                        753 ATCTGGCAGCAGAAAAGACCTACAACAACCTAGATGTATCTGTGACTAAAGCCTTGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1287 AGAGGACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGGCCCCACGAGAGCTTGGGGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    633 GCACTACCACCCCCGTTATGTGGGCTCTGGGGATTTTTGTACAGCATGGAGTCTCAGCCC
                                                                                                                                            CTCTGGTCTCCATCTCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGA
                                                                                                                                                                                                          393 CGCTTGTCTCCATTTCTCCTAATGCCAGCTTGTTTGATGCTGTCTCTTCATTAATTCGGA
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                                                                                                                                                                                                                                                                                ACCGGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can life ound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM.135 row: k column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1347 TGATCGACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAG 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Context: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM548053.1 GI:18782336
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BM548053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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/note="Organ: lung; Vector: pOTB7; Site_1: Xho1; Site_2:
ECORI: CDNA made by oligo-dT priming. Directionally cloned
into ECORI/Xho1 sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

212 c 235 g 247 t 3 others
                                                                                                                                                                                                                               BQ947745 937 bp mRNA linear EST 21-AUG-2002 AGENCOURT_8863556 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6423989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATG 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGATAGTAAGAAGCAAAGTTTTGTGGGCATGCTGACCATCACTGATTTCATCATATCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTCTCCATCTCTCCTAA 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 AACTTGGAGAGAGGGTGTATCTCCAGGACTCCTTTAAACCGCTTGTCTGCATTTCTCCTAA 240
     895 TCAICAACAGGCTAGNGGGAAGCAGAGTTCACCAACTTGTAATGGNTGGATGAAAAATGA 954
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 937)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapber-centail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information and through the I.M.A.G.E. Consortium/LINL at:
http://inage.lihl.gov
Plate: LLCM2603 row: h column: 06
                                                                               TGGGGGCCAAGGGAATGTATCACTGTCTGACATCTTGCCAGCCCTGGTG 1003
                                                  GCATCTTTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTG 1453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:6423989"
/clone_lib="AH_MCC_18"
/tissue_type="large cell carcinome"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 355; DB 14;
Pred. No. 5.8e-78;
0; Mismatches 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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ilarity 65.6%;
Conservative
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Best Local Si
Matches 531;
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                                                          DEFINITION
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                  RESULT 9
BQ947745
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                                                     δŽ
                                                                                                                  (destroyed): Site_2: NotI: RNA source male hippocampus, age 27. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  987 CACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCCGGCCCTCCT 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .047 TCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGC 1106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1167 TGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTC 1226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     655 GCACTACCACCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535 CCCACAAGCGCATTCTGAAGTTCCTCAAATTGTTTATCACTGAGTTCCCCAAGCCAGGGT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595 TCATGICCAAGICTCTGGAAGAGCTACAGAITGGCACCIAIGCCAAIATTGCTAIGGIIC 654
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                                                                                                          pCMV-SPORT6; Site_1: EcoRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                               4 others
                                                                                                                                                                                                                                                                                                                                                                                     Score 360.6; DB 13; Length
Pred. No. 2.5e-79;
0; Mismatches 323; Indels
                                                                                                       /note-"Organ: brain; Vector:
                                                                                                                                                                                                                                                                                                             286 t
/clone="IMAGE:5732872"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH108"
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Best Local (
                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
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BQ954908 944 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8826665 NIH_MGC_18 Homo sapiens CDNA clone IMAGE:6421343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     582 TGCAGGAGCACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTCATCTTCGACA 641
                                                                                                                                                                                 /tissue_trpe="pooled"
/tissue_trpe="pooled"
/lab_host="DHIDB"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, thymus,
semitendonsus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 AGCT---CGGCCTGGTGGAAGAGGCCGGCCCATTGCCCGTCCCCGCAGGTGCCGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 GCACCCCACACACAGAACGAGACAGCCTCCCCTCTGACTGTACAGCCTCCGGCTTCCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 CCGTGGGAAACGGAGGGCCAAAGCCTTGAG-ATGGACAAGGCAGAAGTCGGTGGAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CCTIGGGGAACAGAGGACCAAGGICTCAAGTATGGAAAAGCCAGGAGGATGTAAAGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           522 CCAAGCTGGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCACTCCACCAACAGGGTGGGACTGCCTCCCCTCTGACTGTACAGCCTCAGCTGCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                       548;
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                                                                                                                                                                                                                                                                                                                                                                                     21.5%; Score 354; DB 13; Length 81.5%; Pred. No. 7.8e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                             95;
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                     adrenal, and endometrium.
173 c 163 g 93
                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                   BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: I column: 16
Seq primer: ATTTAGGTGACACTATAG.
                                                                                  Location/Qualifiers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ954908.1 GI:22370386
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BQ954908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTATGGGA 548
                                                                                                        1, .548
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BQ954908
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1309 AGTCCTTTCCTGCCAGCCCCACGAGAGCTTGGGGGAAGTGATCGACAGGATTGCTCGGGA 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 548)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                      1069 TITGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1128
                                                                                                                                                                                                                                                                                                                                             1129 TGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGG 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                 1189 TCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCCAGCAAACCTA 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1249 CAACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGGGACACTATGTCTGGAGGG 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661 TGTTCTCAAGTGCTACCTGCATGAGA-CTCTGGAGACATCATNCACAGGCTAGTGGAAGC 719
                                                                                                                                                                                                   480
                                                                                                                                                                                                                                                                                                                                                                                       540
                                                                                                                                                                                                                                                                                                                                                                                                                                                     720 AGAGGGTCACCGACTTGTAGTGGTGGATGAAATGATGTGGTCAAGGGAANTGTATCACT 779
                                                                                                                                301 TATTGACCCAGAATCAGGCAATACTTTGTACATCCTCACCCACAAGCGCATTCTGAAGTT 360
                                            241 TGCCAGCTTGTTTGATGCTGTCTCTTCATTAATTCGGAACAAGATCCACAGGCTGCCAGT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
      421 GCTACAGATTGGCACCTATGCCAATATTGCTATGGTTCGCACTACCACCCCCGTCTATGT
                                                                                                                                                                                                                                                                                                                                                                     601 CAACAACCTAGATGTATCTGTGACTAAAGCCTTGCAACATCGATCACATTACTTTGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               b1//5360 548 bp mRNA linear 467815 WARC 2BOV Bos taurus CDNA 5', mRNA sequence. B1775360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1429 CTCCGACATCCTTCAGGCACTGGTGCTCA 1457
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ACCESSION
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AUTHORS
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                                                                                                 107 TGGAGACAGCACCCATCCTGACTGCACTGGACTGTTTGTGGACCGGCGTGTGTCTGCAC 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1346 GTGATCGACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAG 1405
                                                                                                                                                                                                                   TGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCCGCTTTGATGTGATTC 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BJ504184 Tibear EST 08-AUG-2003
BJ504184 MF01FSA CDNA Oryzias latipes CDNA clone MF01FSA006A14 3',
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
                                                                                                                                                          GCACTACCACCCCCCTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC 679
                                                                                                                                                                                                                                                                               TGCCAGTGGTGGATGAGAAGGNGCGTGTGGTGGACATCTACTCCAAGTTTGATGTTATCA 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 728)
Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1227 ACCTGGCTGCCCAGCAAACCTACAACCA-CCTGGACATGAGTGTGGGAGAAGCCCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1286 CAGAGGACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCACGAGAGCTTGGGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="d-rR"
/db_xref="taxon:8090"
/clone="MF01FSA006A14"
/clone_lib="MF01FSA cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="fry stage 40"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 490; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 944)
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                                                                                                 NIH-WGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Rubin Laboratory
cDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information and
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
http://mage.llnl.gov
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: cgapbs-rémail.nin.gov
Tissue Procurement: DCTD/DTP/Gazdar
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lange.llnl.gov
High quality sequence stop: 636.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="mammary adenocarcinoma, cell line"
/lab_host="mammary adenocarcinoma, cell line"
/lab_host="mammary adenocarcinoma;
/note="mammary adenocarcinoma;
/site_2: Sali; Cloned unidirectionally; oligo-dT primed.
/Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
/pull-length sis a NIH_MGC Library."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/db_xref="taxon:9606"
/clone="IMAGE:5392777"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Location/Qualifiers
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/note="Vector: pcMvSpORI 6; Site_l: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL.:
http://fulllength.invitrogen.com"
139 a 222 c 199 g 247 t lothers
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781 AAATGATGTGGTCCAGGGAAATGGTATCACTGTCTGACATCCCTGCAGCCCTGGTGCTCC 840
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
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/db_xref="taxon:9606"
                                               1458 GCCTGCTGGCATGCCTCG 1481
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Query Match
21.1%; Score 346.8; DB 13; Length
Best Local Similarity 65.3%; Pred. No. 6.3e-76;
Matches 555; Conservative 0; Mismatches 292; Indels
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USDA, ARS, US Meat Animal Research Center
DO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
EAX: 402 764 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
Y0.880904.e. Vector identified by cross_match with the -minscore 18
pcr PRimers
FORMARD: AGGAAACAGCTATGACCAT
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1 (bases 1 to 572)

1 (bases 1 to 572)

1 Enking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.

Design and use of two pooled tissue normalized cDNA libraries for Unpublished (2000)
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AJ396118 AJ396118
BB630381 BB630381
AL546987 AL546887
AL555228 AL555228
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1033 GCCCCGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGA 1092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 GCGTGTGTCTGCGCTGCCTGTGGTCAACGGAAACTGGACAGGTAGTGGGCCTCTACTCG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 GCCCCGCCCTCCTTCCTCTACCGCACCATCCAAGATTTGGGCATCGGCACATTCCGAGA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     853 AGGCTGCTTCAAGCCTCTGGTCTCCATCTCTCCTAATGATAGCCTGTTTGAAGCTGTCTA 912
                                                                                                                                                                                                                                                                                                                                  913 CACCCTCATCAAGAACCGGATCCATCGCCTGCTGTTCTTGACCCGGTGTCAGGCAACGT 972
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                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
/note="Yector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
190 c 151 g 124 t l others
                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                       DB 13; Length 572;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                   Pred. No. 1.8e-103;
0; Mismatches 56;
                                                                                                                                                                                                                        Score 456.4;
                                                                 /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
          Plate: 119 row: I column: 11
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGACGAGACCCAGCATC 1409
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                                                                                                                                                                                                                       27.7%;
89.8%;
                                                                                                                                                                                                                                 Local Similarity 89.8 nes 501; Conservative
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KEYWORDS
SOURCE
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AL533446
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/Ussue_type="Adult brain"
//Lissue_type="Adult brain"
//Acts="Vector: pCWYSPORT 6; Site_1: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMYSPORT 6
vector. Library was constructed by Life Technologies.
Contact: Feng Lang Ling Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax: (1) 301 610 8371 Email: ilangalifetech.com URL:
http://fulllength.invitrogen.com"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 TGTATACTTCCTTCATGAAGTCTCATGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 CGCTTGTCTGCATTTCTCCTAATGCCAGCTTGTTTGATGCTGTCTCTTCATTAATTCGGA 449
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                                                                                             Contact: Genoscope
Genoscope - Centra National de Sequencage
BP 191 91006 ENRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 310; Indels
Li, N.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 384; DB 9;
Pred. No. 3.3e-85;
                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="CS0DN004YN03"
/clone_lib="LTI_FL015_Brn1"
                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 685)
Arakawa T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Rouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB650381 RIKEN full-length enriched, 6 days neonate skin Mus musculus cDNA clone A030014A04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                             974 CTCCACATCCTCACACACACACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCTGCTG 1033
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                     481 ATGGCCGTGGTGAGCACCAGCACTCCATCTATGTGGCTCTGGGCATCTTGCTGCAGCAC 540
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                                               241 GACTCCTTTAAGCCGTTGGTCTGCATCTCCCCCAATGCCAGCCTTTTTGATGCCGTCTCC 300
                                                                                                                                                                                                                       914 ACCCTCATCAAGAACCGGATCCATCGCCTGCTTCTTGACCCGGTGTCAGGCAACGTA 973
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URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
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BB630381
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AJ396118
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TGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCCTCTATTCCCCGCTTTGATGTGATTC 1226
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A large database of chicken bursal BSTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 758)
                                                                                               1227 ACCTGGCTGCCCAGCAAACCTACAACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGC
                                                                                                                          1347 TGATCGACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGC
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
1. 758
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                                                                                                                                                                                                                                                                                                                                                                                                     1407 ATCTCTTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGC 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Bursa of Fabricius"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
238 c 186 g 166 t
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Pred. No. 2.9e-84;
0; Mismatches 230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9031"
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/clone_lib="dkfz426"
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/db_xref="taxon_goff=""
/clone_lib="LTI_NFL006_PL2"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pGNVSPORT 6; Site_l: NotI; 1st strand cDNN
was primed with a NotI-ollgo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL548987 LTI_NFL006_PL2 Homo sapiens CDNA clone CS0DI042YD16 5
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                                                                                                   298 ACACCCTTGGCTCAAGCTGTTCCCTTGGCTGAAGCGGAGACCTCCCCCACAGGGTGGGAC 357
                                                                                                                                                                                                                                                       365 TGCCTCCCCTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGGAGCTG 424
                                                                                                                                                                                                                                                                                                                                                        425 GCCACGGAGIICCCAGCCACAGAGGCCIGGGAGIGIGAGCIAGAAGGCCIGCIGGAGAG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 AGGCCTGCCCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGATGACGAA 544
     178 GCTTCCAGATGGACGAGGACAGGAGGCCGTAGAGGAAGCAGAACCACCACGGTTTGGGAGAA 237
                                                                                                                                                    308 ACACCCTTGGCTCAAGCTGATCC---TGCCGGGGTGGGCACTCCACCAACAGGGTGGGAC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     545 CTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGAT
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Pred. No. 6.4e-81;
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length CDMA libraries and normalization

Unpublished (2001)
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http://fulllength.invitrogen.com"
217 c 206 q 255 t
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65.0%;
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
waqi,K., Fullwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawal,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 TGGCCATCACCAGCTGTGACCAGCAGCTCAGAAAGAATCCGTGGGAAACGGAGGGCCCAAA 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 GGGCTGGCCACATGGAGCCCGGGCTGGAGCACGCACTGCGCAGGACCCCTTCCTGGAGC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGAGCTGGCCGCATGGAGCCCGAGCTGGAGCACATTGCCTGGGACCCTGGAGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="A030014A04"
/clone_lib="RIKEN full-length enriched, 6 days neonate
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/dev_stage="6 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
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/clone_lib="LTV NFU006_PL2"
/tissue_type="placenta"
/fissue_type="placenta"
/fissue_type="placenta"
/note="vector: pCMYSPORT 6; Site_l: Not!; ist strand cDNA was primed with a Not!-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMYSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filangelifetech.com URL:
//fulllength.invitrogen.com"
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1085)
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DNA Library Arrayed by: The I.M.-A.E.E. Consortium (LLNL)
DNA Sequencing by Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
flowed through the I.M.-A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM12735 row: k column: 17
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National Institutes of Health, Mammalian Gene Collection (MGC)
Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: ogapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
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http://fulllengulifetch.com URL:
http://fulllengulifetch.com COM URL:
con 202 c 208 g 260 t 2 others
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AL554278 ITI_NFL006_PL2 Homo sapiens CDNA clone CS0D1082XL23 5
    1227 ACCIGGCIGCCCAGCAAACCIACAACCACCIGGACAIGAGIGIGGGGAGAAGCCCIGAGGC 1286
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1 (bases 1 to 940)

Li,W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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Pred. No. 1.8e-79;
); Mismatches 290; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="CSODIOB2YL23"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
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/db_xref="taxon:9606"
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AL554278
AL554278.1 GI:12894901
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/lab_host="DHIDE" phoge resistant)"
//lab_host="DHIDE" phoge resistant)"
//note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using AAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NTH MCC Library."
                                                                                                                                                                                 AGENCOURT 8863556 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:642398955, mRNA sequence.
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895 TCATCAACAGGCTAGNGGGAAGCAGAGTTCACCAACTTGTAATGGNTGGATGAAAAATGA 954
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 937)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2603 row: h column: 06
High quality sequence stop: 611.
Location/Qualifiers
                                         1405 GCATCTCTTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTG 1453
                                                                 955 TGGGGGCCAAGGGAATGTATCACTGTCTGACATCTTGCCAGCCCTGGTG 1003
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Pred. No. 5.8e-78;
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Tissue Procurement: DCTD/DTP/Gazdar
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/db_xref="taxon:9606"
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                                                                                   /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: Not1; RNA source male hippocampus, age 27. Library is oligo-dr primed and directionally cloned (ECORY site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             535 CCCACAAGCGCAITCIGAAGTICCICAAATIGITIAICACIGAGITCCCCAAGCCAGGI 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  655 GCACTACCACCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 TGTATACTTCCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIGTACGAGCTGCCCCTTTATGGGATAGTAAGAAGCAAAGTTTTGTGGGGCATGCTGACCA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 IGGITGIATITGAIACGICCCIGCAGGIGAAGAAAGCIITITTTGCITTGGIGACTAACG
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                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                      DB 13; Length 1085;
                                                                                                                                                                                                                                                                       4 others
                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.5e-79;
0; Mismatches 323; Indels
                                                                                                                                                                                                                                                                       286 t
             /clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                      Score 360.6;
/clone="IMAGE:5732872"
                                                                                                                                                                                                                                                                    251 9
                                                                                                                                                                                                                                                                                                                                   21.9%;
63.4%;
                                                                                                                                                                                                                                                                                                                                                                                564; Conservative
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bp mRNA linear EST 21-AUG-2002
Homo sapiens cDNA clone IMAGE:6421343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522 CCAAGCIGGGCIGGGAIGACGAACTGCGGAAACCCGGCGCCCAGAICTACAIGCGCTTCA 581
                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 CCGTGGGAAACGGAGGCCCAAAGCCTTGAG-ATGGACAAGGCAGAAGTCGGTGGAGGAAG
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                                                                                                                                                                                                                                                                                                                                 Length 548;
                                                                                                                                                                                                                                                                                                                             21.5%; Score 354; DB 13;
81.5%; Pred. No. 7.8e-78;
cive 0; Mismatches 95;
                                                                                                                                                                                                                                                                           93 t
                                                                                                                                                                                                                                                      adrenal, and endometrium.
                                                                                                                                       /clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"

    .548
    /organism="Bos taurus"

                 BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: I column: 16
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                          /db_xref="taxon:9913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           944
NIH_MGC_18
                                                                      Location/Qualifiers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                           163 g
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5', mRNA sequence.
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BQ954908
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KEYWORDS
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Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T.,
Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett,
G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                  TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                     1249 CAACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGGACACTATGTCTGGAGGG 1308
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                                    300
                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                   GCCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCCTGCCAGTGGTGAGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 GCTACAGATTGGCACCTATGCCAATATTGCTATGGTTCGCACTACCACCCCCGTCTATGT
                                                                                                                                                                                                                                                                                         TGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGG
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TGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  548 bp mRNA linear 467815 MARC 2BOV Bos taurus cDNA 5', mRNA sequence. B1775360.1 GI:15776346 EST.
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NO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CICCGACATCCTICAGGCACTGGTGCTCA 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae; Bos.
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AUTHORS

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COMMENT

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BJ504184 728 bp mRNA linear EST 08-AUG-2002 BJ504184 MF01FSA CDNA Oryzias latipes CDNA clone MF01FSA006A14 3',
                                                                                                                                                                1167 TGCCTGTGGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTC 1226
                                                                                                                                                                                                                                                             127 ACCTGGCTGCCCAGCAAACCTACAACCA-CCTGGACATGAGTGTGGGGAGAAGCCCTGAGG 1285
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Oryzias latipes
Bukaryota Metazoa: Chordata, Craniata, Vertebrata; Euteleostomi;
Actinopterygiis Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii: Percomorpha; Atherinomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 728)

Kohara Y., Shin 1,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
                                                                                                                                                                                                                                                                                     620 GCACTACCACCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                         800 CATCGATCACATTACTTTGAGGGTGNTCTCAAGTGCTACCTGCATGAGACTCTGGAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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68.1%; Pred. No. 2e-77;
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/tissue_type="whole embryo"
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/clone_lib="MF01FSA cDNA"
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ECORI: CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                            Dmail: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/ATD/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can
found through the I.M.A.G.B. Consortium/Linl. at:
                   Manmalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.9e-77;
0; Mismatches 312; Indels
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/lab_host="DH10B (phage-resistant)"
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Plate: LLCM2596 row: i column: 24
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/db_xref="taxon:9606"
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MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTCATCTTCGACACC
                                                                     ATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCAGCCCCT
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Email: cgapbs-rémail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

CONA Library Preparation: Life Technologies, Inc.

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LIANL at:
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Plate: LLAM13323 row: n column: 18
High quality sequence stop: 636.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1160 TCTGCACTGCCGTGTGTCAACGAATGTGGGTCAGGTCGTGGGGCCTCTATTCCCGGCTTTGAT 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1220 GTGATTCACCTGGCTGCCCAGCAAACCTACAACCTGGACATGAGTGTGGGGAGAAGCC 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1280 CTGAGGCAGACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCACGAGAGCTTG 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1340 GGGGAAGTGATCGACAGGATTG-CTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGA 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1399 GACCCAGCATCTTTGGG-CGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCA 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                           /clone="INACE:058577"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TICAAGCCICTGGTCTCCATCTCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTC 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 TTGCAACATCGATCACATTACTTTGAGGGTGTTCTCAAGTGCTACCTGCATGAGACTCTG 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 ATTCGGAACAAGATCCACAGGCTGCCAGTTATTGACCCAGAATCAGGCAATACTTTGTAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 CCAGAGTTCATGTCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               680 GCCAACGGTGTGCGGGCAGCCCCTCTATGGGACAGCAGAAGCAGAGGTTTGTGGGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ACTAACGGTGTACGAGCTGCCCCTTTATGGGATAGTAAGAAGCAAAGTTTTGTGGGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGACCATCACTGCATCCTGGTGCTGCATCGCTACTACAGGTCCCCCTGGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ATCTATGAGCTAGAAGAACACAAGATAGAAACTTGGAGAGAGGTGTATCTCCAGGACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   920 ATCAAGAACCGGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAAGGTACTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   980 ATCCTCACACACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .040 CCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   620 TCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TCCAAATIGGTIGIATTTGATACGTCCCTGCAGGTGAAGAAAGCTTTTTTTGCTTTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 GITAICAAICIGGCAGCAGAAAAGACCIACCACAACCIAGAIGIAICIGIGACIAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                              Length 1070;
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                                                                                                                                                                                                                                                                                                                                                                            Score 350.4; DB :
Pred. No. 8.9e-77
                                                                                                                                                                                                                                                                                                      284 t
                                                 /organism="Homo sapiens"
                                                                        /db_xref="taxon:9606
Location/Qualifiers
1. .1070
                                                                                                                                                                                                                                                                                                      263 g
                                                                                                                                                                                                                                                                            Technologies.
247 c
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64.4%;
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987 CACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCCCCCGGCCCTCCT 1046
                                                                                                                                                                                                                                    1047 TCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGC 1106
                                                                                                                                                                                                                                                                                                                               1107 TGGAGACCAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCAC 1166
                                                                                                                                                                                                                                                                                                                                                                                                                            IGCCIGIGGICAACGAAIGIGGICAGGICGIGGCCCICIAIICCCGCITIGAIGIGATIC 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCTGGCTGCCCAGCAAACCTACAACCTGGGCTGGGGTGTGGGGAGAAGCCCTGAGGC 1286
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                                                                                                                                                                                                                                                                 671 GCACTACCACCCCGGTTATGTGGCTTTGGGGGATTTTTGTACAGCATCGAGTCTCAGCCC 730
                                                                                                                                                                                     551 CCCACAAGCGCATTCTGAAGTTCCTCAAATTGTTTATCACTGAGTTCCCCAAGCCAGAGT 610
431 CGCTTGTCTGCATTTCTCCTAATGCCAGCTTGTTTGATGCTGTCTCTTCATTAATTCGGA 490
                                              927 ACCGGATCCATCGCCTGCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATGCTCA 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           731 TGCCAGTGGTGGATGAGAAGGGCGTGTGGTGGACATCTACTCCAAGTTTGATGTTATCA 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: Noti; Site_2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NHE MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 864)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGGACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCACGAGAGCTTGGGG 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI858240 864 bp mRNA linear EST 10-OCT--603384001F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5392777 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/JLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: LLAM12001 row: a column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism~"Homo sapiens"
/db_xref="taxon:9606"
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1. .864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
BI858240
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/clone_1bb="LII_NFL006_PL2"
/clone_1bb="LII_NFL006_PL2"
/clone_lib="LII_NFL006_PL2"
/clone_lib="LII_NFL006_PL2"
/note="Vector: pcWVSpORT 6; Site_1: Not1; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not1 and Eoc Rv sites of the pcWxSpORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Pax: (1) 301 610 8371 Emmil: fliangelifetech.com URL: http://fulllength.invitrogen.com"

39 a 222 c 199 g 247 t lothers
                                                                                                                                                                                                           AL552459 908 bp mRNA linear EST 16-FEB-2001 AL552459 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODIO70YC03 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 TGTATACTICCTICATGAAGTCTCATCGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 TCACTGATTICATCAATATCCTGCACCGCTACTATAAATCAGCCTTGGTACAGATCTATG 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCTGGTCTCCATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGA 926
  781 AAATGATGTGGTCCAGGGAAATGGTATCACTGTCTGACATCCCTGCAGCCCTGGTGCTCC 840
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Pred. No. 1e-76;
1; Mismatches 266; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                              1458 GCCTGCTGGCATGCCTCG 1481
                                                                                             841 CCGGTGGAAGAAAAAAACCCTTG 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                         AL552459.1 GI:12891378
                                                                                                                                                                                                                                                             prime, mRNA sequence.
AL552459
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65.6%;
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                        AL552459
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Search completed: June 13, 2003, 05:58:20 Job time: 4104.65 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-232-463-14
US-09-056-105-18
US-08-299-849B-14
US-08-142-368A-14
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S-08-757-669A-20
S-09-230-371A-20
S-09-165-863-45
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US-08-878-989-14
US-09-272-796-14
US-08-232-463-14
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Maximum Match 100%
Listing first 45 summaries
                                   nucleic search, using sw model
                                                                                                                           IDENTITY_NUC Gapor 10.0 , Gapext 1.0
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                                                                                         US-09-826-581-5
1647
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Match Length
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TITLE OF INVENTION NO. 6124125el AMP Activated Protein Kinase NUMBER OF SEQUENCES: 64
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MEDIUM TYPE: DISKETIE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 390.2; DB 3;
Pred. No. 2.1e-93;
0; Mismatches 313;
       US-08-967-727-13

US-08-037-230D-13

US-09-056-16-9

US-09-103-8408-1

US-09-103-840A-1

US-09-103-840A-1

US-09-103-840A-1

US-09-103-840A-1

US-09-244-585A-2

US-09-359-081-2

US-09-359-081-2

US-09-359-081-2

US-09-359-081-2

US-09-359-081-1

US-09-88-911-15

US-07-88-811-15

US-07-88-811-15

US-07-88-811-15

US-08-910-647-1

US-07-88-910-15

US-08-910-15

US-0
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SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101,146
FILING DATE: US/09/101,146
FILING DATE: US/09/101,146
FILING DATE: US/09/101,146
FILING DATE: US/09/101,146
ATTORNEY/AGENT INFORMATION
NUMBER: JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
NAME: Jane Massey Licata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Jane Massey Licata, Esq. STREET: 66 E. Main Street
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REFERENCE/DOCKET NUMBER: DC-0050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 63, Application US/09101146; Patent No. 6124125; GENERAL INFORMATION:
2531 3 12531 4 11495 4 1125 4 3 4413765 3 4411529 7 1926
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TELEFAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.78;
64.98;
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Best Local Similarity
Matches 578; Conserv
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US-09-101-146-63
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Pred. No. 3.3e-87;
0; Mismatches 334;
                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: RastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
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NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF-0321
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 14:
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62.9%;
                                                                                                                                                                                                    COMPUTER: IBM Compatible
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LENGTH: 1435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear IMMEDIATE SOURCE:
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                                                                             Palo Alto
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; CLONE: 1452972
US-08-878-989-14
                                                                                                                         USA
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                                                                                                 STATE: C. COUNTRY:
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                                                                                                                                                                                                                                              TCACTGATTTCATCATATCCTGCACCGCTACTATAAATCAGCGTTGGTACAGATCTATG 415
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                                                                                                                                                                                                                                                                                                               CICTGGICICCATCICCTAAIGATAGCCIGITIGAAGCIGICIACACCCICAICAAGA 926
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TGTATACTTCCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 235
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                                      TAGTICATICTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08878989 Patent No. 5885803 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
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  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                     14:
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62.9%;
                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 62.9
Matches 567; Conservative
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INFORMATION FOR SEQ ID NO:
                                         TELEFAX: 415-845-4166
                                                                                                                                                                                           TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: PENITUT01 CLONE: 1452972
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US-09-272-796-14
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                                            TCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACTTCCGAGACTTGGCTGTGGTGC 1106
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903 ACCGTTCACAGTATTTTGAAGGTGTTGTGAAGTGCAATAAGCTGGAAATACTGGAGACCA
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                                                                        APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
TITLE OF INVENTION: KINASES
CORRESSONDENCES. 1
CORRESSONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09272796
Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/878,989
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REGISTRATION NUMBER: 36,749
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GENERAL INFORMATION:
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US-09-272-796-14
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1164 CACTGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGA 1223
                                                                                             CCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGG 1103
                                                                                                                                                                                                                        1104 TGCTGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCT 1163
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Fatent No. 6287569
GENERAL INFORMATION:
APPLICANT: KIPPS, THOMAS J.
TILLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR;
TILLE OF INVENTION: PROCESSING
FILLE REPERRACE: 233/221
CURRENT PAPLICATION NUMBER: 60/09/056,105
CURRENT FILING DATE: 1998-04-06
RAALIER APPLICATION NUMBER: 60/043,467
EARLIER APPLICATION NUMBER: 35
NUMBER: OF SEQ ID NOS: 35
SOSTWARE: FASTESQ for Windows Version 3.0
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44.7%; Pred. No. 0.14;
ive 0; Mismatches 198;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-232-463-14/C
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                                                               1407 ATCTCTTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTG 1466
                                                                                                   984 TCACACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCCGGCCCT 1043
963 TCGTGGACAGAATAGTAAGAGCTGAGGTCCATCGGCTGGTGGTGAAATGAAGCAGATA 1022
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2.6%; Pred. No. 0.0027;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DORNER, F.
APPLICANT: SCHEFFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PAPLICATION NUMBER: EP 91 114 300.
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08232463 Patent No. 5670367
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INFORMATION FOR SEQ ID NO: 14:
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LENGTH: 7218 base pairs
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STRANDEDNESS: single
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; CLONE: pTZgpt-Fls
US-08-232-463-14
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Best Local Similarity
Matches 10; Conserv
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ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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TELEX: 89
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Sequence 18, Application US/09056105
Patent No. 6287569
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STREET: 805 Third Avenue
CITY: New York City
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                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 44.4
Matches 159; Conservative
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                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                   GENERAL INFORMATION:
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US-08-299-849B-14
                                                                                                                                                                                                                                                       SEQ ID NO 18
LENGTH: 1022
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 JS-09-056-105-18
                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 AGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCCTAGAGCAAGAAAACAGCAGCTCA 127
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                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.4%; Score 40.2; DB 1; 1
Best Local Similarity 4.5%; Pred. No. 0.55;
Matches 12; Conservative 150; Mismatches 103;
                                                   APPLICANT: DORNER, F.
APPLICANN: SCHEIFLINDER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLEOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 30472/114 IMMU FELECOMMUNICATION INFORMATION:
                                                                                                                                                       ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/232,463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (703)836-9300
(703)683-4109
                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                            Clii.
STATE: VA
COUNTRY: USA
- 22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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RESULT

373 CTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGTGAGGGGCTGGCCACGGA 432 359 CTCGCCTGACGCAGAGTTCCTTGTTCCGAGAAGCACTCCAGTAACAAGGTGGATGAGTTGGC 418 493 CCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAA 552 419 TCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGA 478 433 GTTCCCAGCCACCAGAGGCCTGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGAGGCCTGC 492 613 AACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC 672 539 CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACCTACAC 598 Isolated Nucleic Acid Molecules Useful In Determining Expression of A Tumor Antigen Precursor 48 673 TCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGGACAGCAGAAGCAGAGCTTT 730 553 ACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGC Gaps Sequence 14, Application US/08299849B
Patent No. 5612201
GENERAL INFORMATION:
BEDELICANT: De Plaen, Etienne: Boon-Falleur, Thierry;
APPLICANT: Chomez, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precu ; 0 Length 1022; APPLICANT: KIPPS, THOMAS J.
APPLICANT: KIPPS, THOMAS J.
TILLE OF INVENTION: PROCESSING
FILE REFERENCE: 233,221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER APPLICATION NUMBER: 60/043,467
NUMBER: OF SEC ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0 Pred. No. 0.38; 0; Mismatches 199; Indels DB 4; 2.4%; Score 39.6; 14.4%; Pred. No. 0.3 SOFTWARE: Wordperfect CURRENT APPLICATION DATA:

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978 TCATTITCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGA 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia TITLE OF INVENTION: Tunor Rejection Antigen Precursors, Tumor TITLE OF INVENTION: Rejection Antigens and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.4%; Score 39.6; DB 2; Length 2531;
44.4%; Pred. No. 0.54;
Live 0; Mismatches 199; Indels 0;
                                                                                                                                                                                                                                                                                                              Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hanson, No. 5925729man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUBBER:
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                  SEE: Felfe & Lynch
: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.4
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Wordperfect
                                                                                                                   NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Ly
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                                                                    IBM
                                                                                                                                                                                                                   STATE: New -
                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          673 TCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTT 730
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                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION NUMBER: PCT/US92/04354
PILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/087,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION NUMBER: 07/0807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hanson, No. 5612201man D.
REGISTRATION NUMERS: 30,946
REFERENCE/DOCKET NUMBER: LUD 5355
TELECOMMUNICATION: TELEPHONE: (212) 688-9200
TELEPRAX: (212) 688-9200
INPOMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
  APPLICATION NUMBER: US/08/299,849B
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                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
                      1-SEPTEMBER-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-May-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MAGE-41 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 159; Conservative
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Best Local 8
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Sequence 14, Application US/08037230D
Patent No. 6235525
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
                                                                                                                                                                                                                                                                                                                       978 roatitrorgorocecaagrarceaeccaaeaegeceegececaaaeecaeaarecreea 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                            1098 CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACTACAC 1157
                                   433 GTTCCCAGCCACAGAGGCCTGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGAGGCCTGC 492
                                                                                                                                             918 CTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGC 977
                                                                                                                                                                                           493 CCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAA 552
                                                                                                                                                                                                                                                                                           553 ACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACCTGCTACGATGCCATGGC 612
                                                                                                                                                                                                                                                                                                                                                                                         613 AACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC 672
373 CTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        673 TCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGGACAGCAAAGAAGCAGAGCTTT 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/037,230D
FILING DATE: 26-MARCH-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: 07/807,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Ly
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US-08-037-230D-14
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Patent No. 6025474
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
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                                             613 AACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC 672
                                                                                                                         673 TCTGGTGGCCAACGGTGTGCGGCAGCCCCTCTATGGGACAAGAAGCAGAAGCTTT 730
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44.4%; Pred. No. 0.54;
ive 0; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION UMBER: US/08/967,727
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hanson, No. 6025474man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.4%;
Best Local Similarity 44.4%;
Matches 159; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENCTH: 2531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-DECENPRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
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3402 GAGAGICAICAAAAAITACAAGCGCIGCTIICCIGIGAICIICGGCAAAGCCICCGAGIC 3461
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                                                                                                        553 ACCCGCCCCAGATCTACATGCGCTTCATGCAGGAGCACCCTGCTACGATGCCATGGC 612
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                            493 CCTGTGCCTGTCCCCGCAGGCCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAA 552
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Sequence 17, Application US/09007005B
Sequence 17, Application US/09007005B
GENERAL INFORMATION:
APPLICANT: SCOSIE4, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Roberts, Richard W.
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILLE OF INVENTION: PUSIONS
FILLE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT APPLICATION NUMBER: 06/035,963
EARLIER PLING DATE: 1997-01-27
EARLIER PLING DATE: 1997-01-27
EARLIER PLING DATE: 1997-01-27
EARLIER PLING DATE: 1997-01-27
EARLIER PLING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 17, Application US/09244796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 5.3%
Watches 10; Conservative
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US-09-244-796-17/C
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US-09-007-005-17/c
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                                                                                                                                                                                                                                                                                               373 CTCTGACTGTACAGCCTCCAGCTGCAGGCTCCAGCACAGATGTGGGAGCTGGCCACGGA 432
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Sequence 10, Application US/09056105

Patent No. 6287569

Sequence 10, Application US/09056105

Sequence 10, Application US/09056105

SERVERAL INPORATION:

APPLICANT: KIPPS, THOMAS J.

APPLICANT: WI, YUNOI

TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR

TITLE OF INVENTION: PROCESSING

FILE REPRESENCE: 1337/221

CURRENT APPLICATION NUMBER: US/09/056,105

CURRENT FILING DATE: 1998-04-06

EARLIER PRILING DATE: 1997-04-10

NUMBER OF SEQ ID NOS: 35

SOFTWARE FRANCE PRESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39.6; DB 4; Length 48
Pred. No. 0.69;
0; Mismatches 199; Indels
                                                                                                                                                                                                                      Score 39.6; DB 4; Length 2
Pred. No. 0.54;
0; Mismatches 199; Indels
      14:
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Best Local Similarity 44.4%;
Matches 159; Conservative 0
                                                                                                                                                                                                                    Query Match 2.4%;
Best Local Similarity 44.4%;
Matches 159; Conservative
                                                                                                                      MOLECULE TYPE: genomic DNA
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                    ; NAME/KEY: MAGE-41 gene US-08-037-230D-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                     linear
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954 ACCCGGTGTCAGGCAACGTACTCCACATCCTCACACACAAACGCCTGCTCAAGTTCCTGC 1013
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APPLICANT: Dietrich, Paul S.
APPLICANT: Dietrich, Paul S.
APPLICANT: McGlvern, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: AND USES
FILE REFERENCE: R0043B-REG sequence listing
CURRENT APPLICATION NUMBER: U$/09/404,650
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.4%; Score 38.8; DB 4; Length 289; 5.3%; Pred. No. 0.39; tive 87; Mismatches 93; Indels
                                                                                               APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
                                                                                                                                                              FILE REPERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1998-01-14
SOFTWARR: FASTSEQ for Windows Version 4.0
SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Translation template FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09404650 Patent No. 6309858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
Patent No. 6281344
GENERAL INPORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.4%
Best Local Similarity 5.3%;
Matches 10; Conservative
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; LOCATION: (192)..(6716)
US-09-404-650-1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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US-09-404-650-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
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4229 TTGGGTGAACATCATGTACAATGGACTGGATGCTGTGGACCAGCAGCAGCCTGTGAC 4288
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                                                                              631 CATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCGTGGTCGAACGGTGT 690
                                                                                                                                                                                                                                 751 IGACTICATCCIGGTGCTGCATCGCTACTACAGGTCCCCCCTGGTCCAGATCTATGAGAT 810
                                                                                                                                                                                                                                                                                                              811 TGAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCT 870
                                                                                                                                                         691 GCGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGGATGCTGACCATCAC 750
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Query Match 2.4%; Score 38.8; DB 4; Length 6816; Best Local Similarity 47.5%; Pred. No. 1.3; Matches 115; Conservative 0; Mismatches 127; Indels 0
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Search completed: June 13, 2003, 06:00:59 Job time: 129.419 secs

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Sequence 5, Appli
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Sequence 559, App
Sequence 510, App
Sequence 21109, A
Sequence 2282, Ap
Sequence 2472, Ap
Sequence 1, Appli
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-82-846-559

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US-09-84-761-3373

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US-09-98-476-2282

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US-10-9864-761-693

US-09-918-955-1257

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Sequence 5, Application US/09826581
Patent No. US20020142310a1
GENERAL INFORMATION
APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVERTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 (FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: US 60/195,665
PRIOR FILING DATE: 2000-04-07
                                                                                                                                  Sequence 3, Appli
Sequence 1, Appli
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
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Sequence 2, Appl1
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Sequence 346, App
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Sequence 17480,
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100.0%; Pred. No. 0;
Live 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%;
Matches 1647; Conservative 0
    ; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5
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Db 603 TCATGTCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC 662 Qy	1227 ACCTGGCTGCCCAGCAAACTACAACCTGGACATGGTGTGGGAGAAGCCTGAGGG 1287 ACCTGGCTGCCCAGCAAACTACAACCTGGACATGTGTGGGAGAAGCCTGGGGG 1287 ACTGGCGCAGCAAACCTACAACCTCGGATGTGTGTGGGGGAAG 1287 ACTGGCAAAACATGTCTGAGGAGTTTCCTGCAGCCCAGCGAAGCTTGCAAC 1287 AAGGACACTATGTTGAGGAGTTCTCCAGCTTACCTGCAGCCCAACGCAAGGAAGCTTGGAGAAG 1347 TGATCGACAGTTACTTTGAGGCTTCTCAAGTGCTAGTGAACCTGGAGACCA 1347 TGATCGACAGGATTGTAGAGGCTACACAGGCTGGTGCATGAGACCCAGC 1	Sequence 4, Application (S/09820301) Sequence 4, Application (S/09820301) GENERAL INFORMATION: APPLICANT: Andersson, Leif APPLICANT: Marklund, Stefan TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SI FILE REFERENCE: 11145-007001 CURRENT APPLICATION NUMBER: US/09/826,581 CURRENT APPLICATION NUMBER: US/09/826,581 CURRENT APPLICATION NUMBER: US/09/826,581 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 14 SOFTARRE: FastSEQ for Windows Version 4.0 SEQ ID NO 4 LENGTH: 1014 TYPE: DNA CURGANISM: Homo sapiens US-09-826-581-4	Query Match 16.9%; Score 278.8; DB 10; Length 1014; Best Local Similarity 97.6%; Pred; No. 1.1e-72; Anatches 283; Conservative 0; Mismatches 7; Indels 0; Gaps 0; Qy 1358 Arrecreedencedracencedencernernencencencencencencerrerrencencencencencencencencencencencencence
QY 547 GCGGAAACCCGGCCCAGATCTACATGCGCTTCATGCAGGAGCACCTGCTACGATGC 606 111111111111111111111111111111111111	RESULT 3 US-09-22-297-2 US-09-22-297-2 Sequence 2, Application US/09925297 Patent No. US20020081659A1 GENERAL INFORMATION: TOWNERT RESERVED TOWN TOWNER TOWNER TITLE OF INVERTION: FILE REFERENCE: PA105 CURRENT FILING DATE: 2001-08-10 PRIOR APPLICATION NUMBER: US/09/925,297 CURRENT FILING DATE: 2000-08-10 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 928 SOFTWARE: Patentin Ver: 2.0 SOFTWARE: Patentin Ver: 2.0 LENGTH: 1691 TYPE: DNA SPAURE: FRAURE:	NAME/KEY: misc feature NAME/KEY: misc feature COATION: (1093) COATION: (1093) US-09-925-297-2 Ouery Match 23.9%; Score 393.4; DB 10; Length 1691; Best Local Similarity 65.1%; Pred. No. 1.2e-106; Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0; Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0; Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0; Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0; Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0; Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0; Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0; Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0; Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0; Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0; Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0; Matches 580; Conservative 0; Mismatches 311; Indels 10; Indel	

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10096 ATTTGCATTGAATGATGATACTAACTAAATGGTATCCTCTGCTAGGCGTGCTGCACAACC 10155
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                                556 CGCCCCCAGATCTACATGCGCTTCATGCAGGAGCACCTGCTACGATGCCATGGCAAC 615
                                                                                                            616 TAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCT 675
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APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: DOLUNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REPERENCE: GIN 6400
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CURRENT FILING DATE: 2001-03-29
PRIOR PELICNION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
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Treacy, Maurice
Agostino, Michael J.
Steininger II, Robert J.
Bowman, Michael R.
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LaVallie, Edward R.
Collins-Racie, Lisa A.
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Resnick, Richard J.
Gulukota, Kamalakar
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Wong, Gordon G.
Clark, Hilary
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SEQ ID NO 559
LENGTH: 1446
TYPE: DNA
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APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR ELLING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1129 TGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCGAATGTGG 1188
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Pred. No. 9.3e-40;
0; Mismatches 8; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 70, Application US/10108605
Patent No. US20020160934A1
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                                                 Sequence 3, Application US/09826581 Patent No. US20020142310A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 95.68
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-3
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                       US-09-826-581-3
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Sequence 11096, Application US/09783590

Sequence 11096, Application US/09783590

Patent No. US20020110850A1

GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REPERENCE: PO-16.20
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
FRIOR PILING DATE: 1995-04-12
PRIOR PILING DATE: 1995-04-12
PRIOR PILING DATE: 1994-11-21

PRIOR PRICK APPLICATION NUMBER: 08/346,731

PRIOR PILING DATE: 1994-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   651 AGATCAAGAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCAGCCCCTCTATGGG 710
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EIR INFORMATION: EXPRESSED IN HELAT, SIGNAL = 4.1

HER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9

HER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 3.9

HER INFORMATION: EXPRESSED IN HOUT LIVER, SIGNAL = 3.8

HER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8

HER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 5.3

HER INFORMATION: EXPRESSED IN BOWE MARROW, SIGNAL = 4.8

HER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2

HER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.2%; Score 85; DB 10; Length 378; 94.6%; Pred. No. 3e-15; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                        SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 3373
LENGTH: 378
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   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
                                                               PRIOR FILING DATE: 2001-01-30
PRIOR PEDIACATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PELING DATE: 2001-01-29
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LOCATION: (53)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 49117
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Best Local Similarity 94.6
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 427
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1370 CAGGTACACCAGGCTGGTGCTAGTGGACGAGCACCACCATCTTTGGGCGTGGTCTCCCTC 1429
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                                                                                                                                                                                                                                                            Gaps
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                                                                                                DB 9; Length 1446;
                                                                                             Score 123.6; DB 9; Length
Pred. No. 1.6e-26;
0; Mismatches 134; Indels
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2000-05-3
PRIOR APPLICATION NUMBER: US 60/203,456
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-33
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-06-33
PRIOR FILING DATE: 2000-09-37
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00661
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                                                                                             Query Match 7.5%;
Best Local Similarity 60.4%;
Matches 204; Conservative (
; ORGANISM: Homo sapiens US-09-822-846-559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT: Chen, Wenshang
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL J
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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N: EXPRESSED IN HEART, SIGNAL = 4.1

N: EXPRESSED IN PLACENTA, SIGNAL = 4

N: EXPRESSED IN PLACENTA, SIGNAL = 3.9

N: EXPRESSED IN BULT LIVER, SIGNAL = 5.8

N: EXPRESSED IN BULT LIVER, SIGNAL = 5.3

N: EXPRESSED IN BULT LIVER, SIGNAL = 5.3

N: EXPRESSED IN BULT LIVER, SIGNAL = 4.8

N: EXPRESSED IN LUNG, SIGNAL = 4.2

N: EXPRESSED IN BRAIN, SIGNAL = 4.2

N: EXPRESSED IN BRAIN, SIGNAL = 4.3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DAIE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20146
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/2408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-05-30
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PRIOR APPLICATION NUMBER: PCT/US01/00666
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APPLICATION NUMBER: PCT/US01/00667
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: GB 24263.6
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                             Hanzel, David K.
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COTHER INFORMATIC
US-09-864-761-20146
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Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 CAGCTTGTTTNATGCTGTCTCTTCATTAATTCGGAACAAGATCCACAGGCTGCCAGTNAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 TGAACCCAGNAATCAGGGCAATACTTTGTGACATCCTCACCACAAGCGCCATTCTGAAG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CAGAGGAGGGGTATCTCCAGGACTCCTTTAAACCGCTTGTNTGCATTTNTCCTAATGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        832 CIGGAGGAGATCTACCIGCAAGGCIGCTTCAAGCCICTGGTCTCCATCTCCTAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1008 rccrccacarcrrrgGrrcccrgcrcccc 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: n equals a,t,9, or c NAME/KEY: misc feature LOCATION: (350)
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                                                                                          OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (409)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (411)
LOCATION: (73)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                                                                                             OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (259)
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                                                                                                                                                                                                    OTHER INFORMATION: n equals a, t, g, or
                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n equals a, t, g, or
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Best Local Similarity 59.0
Matches 124; Conservative
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                                                                                                                                                                                                                           NAME/KEY: misc feature LOCATION: (245)
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US-09-864-761-20146/c
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651 AGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCTC 704

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us-09-826-581-5.rnpb

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SEQ ID NO 2472
LENGTH: 897
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LENGIH: 821
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APPLICANT: Lillie, James
APPLICANT: Mang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
3.2%; Score 53.4; DB 9; Length 457; 53.6%; Pred. No. 7.8e-06; tive 0; Mismatches 96; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FLING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
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                                                                                                                                   Sequence 2282, Application US/10198846 Publication No. US20030099974A1 GENERAL INFORMATION:
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LOCATION: 2, 3, 4, 5
OTHER INFORMATION: n = A,T,C or G
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Matches 111; Conservative
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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US-10-198-846-2472/C
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APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 :
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
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                                                        NAME/KEY:
NAME/KEY:
NAME/KEY:
LOCATION: 2, 16, 22, 23, 27, 28, 30, 36, 39, 73, 462, 481, 540, 559, 10CATION: 590, 604, 634, 636, 676, 680, 772, 774, 809, 849, 870, 873, 10CATION: 876, 886, 893, 895, 895, 897
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                    3.2%; Score 52.2; DB 9; Length 897; 56.8%; Pred. No. 2.2e-05; Live 0; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 821;
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OF INTILE OF INVENTION: 1-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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100.0%; Pred. No. 2.4e-05;
Live 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030073623A1
GENERAL INFORMATION:
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; Patent No. US20020142310A1
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Best Local Similarity 100.0%
Matches 52; Conservative
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Matches 96; Conservative
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US-09-826-581-1
ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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US-09-918-995-16257
                                                                                                                                                                                         ; OTHER INFORMATI
US-10-198-846-2472
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1369 GCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTCTTGGGCGTGGTCTCCCT 1428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.6%; Score 43.4; DB 10; Length 458; Best Local Similarity 64.4%; Pred. No. 0.0073; Matches 65; Conservative 0; Mismatches 36; Indels 0
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.8

OTHER INFORMATION: EXPRESSED IN PACEMENA, SIGNAL = 7

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.2

OTHER INFORMATION: EXPRESSED IN BH2100, SIGNAL = 6.5

OTHER INFORMATION: EXPRESSED IN HB1100, SIGNAL = 6.5

OTHER INFORMATION: EXPRESSED IN HB1100, SIGNAL = 6.5

OTHER INFORMATION: EXPRESSED IN HB14, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN BAULT LIVER, SIGNAL = 4.7

OTHER INFORMATION: EXPRESSED IN BAULT SIGNAL = 5.4

OTHER INFORMATION: EXPRESSED IN BALIN, SIGNAL = 5.4

US-09-864-761-693
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PRIOR APPLICATION NUMBER: PCT/USO1/00661
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PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SECTIOR 0633
LENGTH: 458
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ORGANISM: Homo sapiens
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Patent No. US20020048763A1
GENERAL INPORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/20,456
PRIOR PTLING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-10-04
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PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-16257
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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GEALRQRTLCLEGGULSCOPHESLGEVIDRIAREQVHRLVUNDETQHLLGGVVSLSDILQ
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                                                                                                          100 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCGGTCC 159
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Ernst (DE)
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Variants of the gamma chain of ampk, dna sequences encoding the
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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Length 2109;
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Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
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Query Match
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Matches 61; Conservative
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TQHLLGVVSLSDILOALVLSFAGTDALGA"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE A RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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100.0%; Pred. No. 5.6e-08;
.ive 0; Mismatches 0; Indels
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AX099776
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                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                   Location/Qualifiers
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LQGCFKPLVSISPNDSLFEAVYTLIRNRIHELPVLDPVSGNVLHILTHHRELLKFLHIP
GSLLPRPSFLYRTIQDLGITGFRBLAVVLETAPILTALDIFVDRNSGLPVVNBCGQV
VGIZSRFDVIHLAAQQYYNHLDMSVGBALRKRTLCLEGVLSCQPHESLGEVIDRIARE
QVHRLVLVDFFQHLLGVVSLSDILQALVLSPAGIDPSGPEXI
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SSERIRGKRRAKALKWTRQKSVEEGEPPGQEEPSRPEABENGLEEATFPKTTPLAQA
DPAGVGTPPTGWDCLPSDCTASAAGSTDDVELATEFPATEAMECELEGLLEERPALG
LSPQAPFPKLGWNDELRFGAQIYMRFIEBHYCYDAMATSSKLVIFDTMLEIKKARPA
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Arexis AB (SE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2290)
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/protein_id="CAB65117.1"
/db_xref="GI:6688201"
                                                                                                                                              Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
Blochem. J. 346 Pt 3, 659-669 (2000)
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Carling,D.
Submitted (L2-CCT-1999) Carling D., Cellular Stress Group, M Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 OWN, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="AMPK gamma 3"
/function="AMP-activated protein kinase regulatory
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/db_xref="taxon:9606"
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RFWQEHTCYDAMATSSKIV1FDTMLEIKKAFPALVANGVRAAPLMDSKKQSFVGMLTI
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KNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSV
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AJ249977 AJ249977.1 GI:6688200 AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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; Pred. No. 5.4e-08;
0; Mismatches 0; Indels
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/db_xref="G1:8215682"
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/chromosome="2"
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1. .2115
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                                                                                               Homo sapiens
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Budguslavkiy, Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boughslavkiy, L., Boukhagiler, B. Brown, A., Burkett, G., Boughslavkiy, L., Boukhagiler, B. Brown, A., Burkett, G., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, W., Doyle, M., Ferreita, P., Fitzhaph, W., Gage, D., Gand-Pierre, N., Gant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illew, I., Johnson, R., Mocker, M., Kann, L., Kartats, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Mcherters, R., Mcdrin, J., Lakocque, K., Liau, G., Locke, K., Macdonald, P., Marquis, N., Mchan, P., McGrthy, W., McBan, P., McGurk, A., McKernan, K., Mcheters, R., McIrin, J., Maneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Mirphy, T., Naylor, J., Mihova, T., Miranda, C., Menga, V., Morrow, J., Wirphy, T., Schoen, P., Schoen, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Schjanovic, N., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Taylis Sol, A., Sercet, Cambridge, MR 02141, USA
All repeats were identified using Repeatmaker:
Smit, A., R., & Green, P., (1961–1997)
Smit, A., & Green, P., (1961–1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACUZ/416 152129 bp DNA linear HTG 07-JUN-2000 HOMO sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32 unordered pleces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152129)
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                            Length 989;
                                                                                                                                                                Score 51; DB 6; Length your,
Pred. No. 5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-504G11
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                                                                                                                                                                                         ch 83.6%; Score 51; DB 1 Similarity 100.0%; Pred. No. 5e-51; Conservative 0; Mismatches
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                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
306 c 286 q 166
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Location/Qualifiers
1. .989
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
Consensus quality: 135376 bases at least Q40 Consensus quality: 14364b bases at least Q30 Consensus quality: 146503 bases at least Q20 Insert size: 161000; agarose-fp Insert size: 164009; sum-of-configs Quality coverage: 3.1 in Q20 bases; sum-of-configs Quality coverage: 3.3 in Q20 bases; sum-of-configs
                                                                                                                                                                                                                                                                                                                                                            1006 1105; gap of 100 bp 1106 2402: contig of 1297 bp in length 2403 2502; gap of 100 bp 2503 3823: contig of 1321 bp in length 3824 3923; gap of 100 bp 3924 5020: contig of 1097 bp in length
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12556: contig of 2473 bp in length
12656: gap of 100 bp
15043: contig of 2387 bp in length
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27059: contig of 2640 bp in length
27159: gap of 100 bp
30170: contig of 3011 bp in length
30270: gap of 100 bp
33968: contig of 3698 bp in length
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38179: contig of 4111 bp in length
38279: gap of 100 bp
42366: contig of 4087 bp in length
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101193: contig of 7779 bp in length
101293: gap of 100 bp
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12928: contig of 2362 bp in length
128: gap of 100 bp
24319: contig of 2291 bp in length
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60595: contig of 4624 bp in length
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contig of 5900 bp in length
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73218: contig of 6523 bp in length
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7115: contig of 3797 bp in length
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93315 93414: gap of
93415 101193: contig
101194 101293: gap of
101294 113090: contig
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19567 21928: conti
21929 22028: gap of
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113091 113190: gap of 100 bp
113191 123496: contig of 10306 bp in length
123497 123596: gap of 100 bp
123597 137937: contig of 14241 bp in length
137838 137937: gap of 100 bp
137938 152129: contig of 14192 bp in length.
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7648. .9983
// Octe...'s seembly_fragment"
10084. .12556
// Note...'s seembly_fragment"
// Note...'as sembly_fragment"
1544. .17123
// Octe...'as seembly_fragment"
15144. .17123
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22029 .24319
/note-assembly_fragment"
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/note-assembly_fragment"
30271 .33968
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38280 .42366 .42366 .42366 .42366
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46466. .51285
/note="assembly_fragment"
51386. .55871
/note="assembly_fragment"
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'note="assembly_fragment"
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/note="assembly_fragment"
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101294. .113090
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/note="assembly_fragment"
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/note="assembly_fragment"
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19567. .21928
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Materian Machinesion Submitted (09-JAN-2002) Department of Genetics, Washington Submitted (09-JAN-2002) Department of Genetics, Washington Dilversity, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 8, 2001 this sequence version replaced gi:13431203.
                                                                                                                                                                                                                                                          AC009974 206854 bp DNA linear PRI 09-JAN-2002
Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
AC009974
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Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 206854)
Waterston, R.H.
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Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 206854)
Waterston, R.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 206854)
Sulston,J.E. and Waterston,R.
                                                      Gaps
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
6 (bases 1 to 206854)
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                                                                                                                           2925 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAAGCCACCACCAGGTCAGGGGGAAGGT 2875
                                                                                                 1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGT 51
                                                      ;
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     Length 152129;
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459119
Unpublished (2001)
3 (bases 1 to 206854)
Waterston,R.H.
83.6%; Score 51; DB 2; Length 152
100.0%; Pred. No. 2e-05;
ive 0; Mismatches 0; Indels
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Contact: sapiens@watson.wustl.edu
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Genome Res. 8 (11), 1097-1108 (1998)
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Query Match
Best Local Similarity 100.4
Matches 51; Conservative
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MEDLINE
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/note="similar to Mus musculus EST AI196847 (NID:g3749453)
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594. .763
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594. .763
                                                   /note="match to EST BE908408 (NID:g10402954)"
281. .344
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281. .344
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/note="match to EST BF183086 (NID:g11061273)"
594. .763
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281. .344
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594. .763
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599. .763
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(NID:914565249)"
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(NID:q14565249)"
967. .1085
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100.0%; Pred. No. 1.9e-05;
ive 0; Mismatches 0;
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                                                                                      Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wastl.edu/ssc
                                                                                                                                                                                                                                The RCI-II human BAC library was made from the blood of one male donor, as described by Geogawak. Woon, Pr., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1988) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281. .344
/note="match to EST BE047599 (NID:98364652) tz39c01.y1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note-"match to EST BE047599 (NID:98364652) tz39c01.y1"
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  more than one subclone; and the assembly was confirmed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match to EST BG477625 (NID:g13409904)"
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/note="match to EST BE314060 (NID:99134719)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"similar to Homo sapiens EST BIll4348
(NID:g14565249)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                     (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
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                                                                       MAPPING INFORMATION:
                                                                                                                                                                                                               SOURCE INFORMATION:
                        restriction digest
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GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
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KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mSFLEQGESRSWPSRAVTTSSERSHCDQGNKASRWTRQEDVEBG
GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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                                         Milan, D., Jeon, J.T., Looft, C., Amarger, V., Roblo, A., Mardon, J.T., Looft, C., Amarger, V., Roblo, A., Reinsch, N., Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N., Kalm, E., Le Roy, P., Chardon, P. and Andersson, L. Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
1. 1873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"AMP-activated protein kinase gamma subunit"
/protein_id="AAF73988.1"
/db_xref="GI:8215684"
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Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 1873;
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Pred, No. 0.021;
                                                                                                                                                                                                                                                                                                                                                      /tissue_type="skeletal muscle"
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                                                                                                                                                                                                                   Location/Qualifiers
1. .1873
/organism="Sus scrofa"
/db_xref="taxon:9823"
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                                                                                                                                                                                                                                                                                                             /chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                    /gene="PRKAG3"
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Sus scrofa
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ACCESSION
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AX099800
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AUTHORS
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JOURNAL
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LWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVS
ISPNDSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFL
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HLAAQQTYNHLDMNVGEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLYLVDE
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Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P. and Andersson, L.
                                                                                           PAT 02-APR-2001
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                           Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof Patent: WO 0120003-A i 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR); Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE) Location/Qualifiers
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Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
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                                                                                                                                                                                                                                                                 Mammalia; Butheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 1867)
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583 c 529 g 375 t
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                                                                                Sequence 1 from Patent W00120003.
AX099774
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/db_xref="GI:13538809"
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/organism="Sus scrofa"
/db_xref="taxon:9823"
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/translation-"MSFLEQGESRSWPSRAVTTSSERSHGDQGTKASRWTRQEDVEEG
GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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KNRTHELPULDPVSGAVLHILTHFRELKELHIFGTLLERSPELKRTIODLGIGFREDL
AVVLETAPTLITADIFVDRAVSALPVNNETGQVVGIXSREDVIHLAAQQTYNHLDMNV
GEALRQRTLCLEGGULSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSESDILQ
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meet quality traits
Patent: WO 10250-A 3 14-MAR-2002;
Iowa State University Research Poundation, Inc. (US)
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Pred. No. 0.021;
0; Mismatches 12;
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1. .1395
/note="unnamed protein product"
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/db_xref="G1:21261109"
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les 49; Conservative (
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Sus scrofa
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DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
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TDFILVHTRYRGSPLVQLYEIEBHKIETWREITLQGCFKFPLVSISBNDSLFEAYYALI
KNRIHRLPVLDPVGGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
AVVEETAPLILTAAQOTYNHLDMY
GEALRORTLCLEGGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLCAVSESDILQ
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DSNITDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 022085-A 1 14 *MAR.2002.
Iowa State University Research Foundation, Inc. (US)
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'organism="Sus scrofa"
               /db_xref="taxon:9823"
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Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
Patent: WO 022085-A 9 14 *MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 7 14 MAR-2002,
Iowa State University Research Foundation, Inc. (US)
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PRKAG3

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Human calcium acti T. thermophilus ga Thermus thermophil

AAX24825 AAT06978 AAX21373 AAZ23900 ABK95404

Human IKca channel

Calcium activated

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/note= "Causes R340W"
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/label= "C230G"
/note= "Causes P71A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "PRKAG3"
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                                                                                                                                                                                                                                                                                                                                                                                      AAH43685 standard; cDNA; 1647 BP.
21-JAN-2002 (first entry)
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(KALM/) KALM E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC 60
                                                                                                                                                                                                                                                      New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopthy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                  AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 103, variation may be a substitution of a T for a C at nucleotide 103, resulting in the amino acid substitution R340W. There may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on
                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the full length cDNA encoding the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 61; DB 22; Length 1647; 100.0%; Pred. No. 6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             position 1 of the open reading frame.
                                                                                                                                                                        Andersson L, Luthman H, Marklund S;
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                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 5; 25pp; English.
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                                                                    06-APR-2001; 2001WO-SE00765.
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Matches 61; Conservative
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                                                                                                                                         (AREX-) AREXIS AB.
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WO200177305-A2
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                                    18-OCT-2001.
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The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, berkad3 whataion in Prkad3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence cativity, and for restoring a normal AMPK function. PRKAG3 sequence evaluation, genetic testing and prognosis of a metabolic disorder. The genetic polymorphic marker linked to a sequence encoding PRKAG3, are a genetic polymorphic marker linked to a sequence encoding PRKAG3. The section of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a respective compounds able to modulate AMPK activity. Nucleic activity in a sequence encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or a masser.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robic A, Rogel-Gaillard C;
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/product= "Human Prkag3 protein"
1390..2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andersson L, Looft C, Kalm E, Milan D, Robic Iannuccelli N, Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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                                                                                                                                                                                                                                                                                                   11-SEP-2000; 2000WO-EP09896.
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18-MAY-2000; 2000EP-0401388.
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AAH43682 standard; DNA; 989 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a recenting compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRRAG3 and is useful in gene therapy.
                                                                                                                                                                                                         PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                 Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
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                                                                                                                                                                      gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Human complete Prkag3 protein"
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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18-MAY-2000; 2000EP-0401388.
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13-JUN-2001
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New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRRAG3). Detecting the presence of the PRRAG3 DNA, or a variant, (PRRAG3). Detecting the presence of the PRRAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A, in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                  Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAH43681-84 represents genomic fragments
                                                                                                metabolic disease; diabetes; obesity; substitution; ds
                                                                                                                                                                                                               intron 2"
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r= "Intron 3"
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542..945
/*tag= d
----- "Exon 4"
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                                                        PRKAG3 intron 2 - intron 4.
                         21-JAN-2002 (first entry)
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Gaps ö

Indels

DB 22; Length 2115;

Pred. No. 6.1e-10; 0; Mismatches

100.0%; Score 61; 100.0%; Pred. No. 6

61; Conservative

Matches

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Best Local Similarity

Query Match

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1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC

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WPI; 2001-244810/25.
P-PSDB; AAE00222.
                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome 15; ss.
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(ANDE/) ANDERSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOOFT C.
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                                                                                                                                                                                                                               PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                                                        gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                               1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGT 51
                                                  ö
                                                                                                                                                                                                    Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                            Length 989;
                                                0; Indels
                                                                                                                                                                                                                                                                                                                                            /*tag= b
Product= "Sus scrofa PRKAG3 protein"
1390..1867
        Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
                          Score 51; DB 22;
Pred. No. 7.5e-07;
; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
                             Score 51;
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                   83.6%; Sc.
100.0%; Pred
0; V
                                                                                                                                        AAD03295 standard; cDNA; 1867 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Fig 2; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-1999; 99EP-0402236.
18-MAX-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                 472..1389
/*tag= b
                                                                                                                                                                                (first entry)
                                                51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-244810/25.
                                       Similarity
                                                                                                                                                                                                                                                               chromosome 15; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                              WO200120003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersson L,
                                                                                                                                                                               13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-2001
                                                                                                                                                                                                                                                                                   Sus scrofa.
                           Query Match
Best Local S:
Matches 51;
                                                                                                                                                            AAD03295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOOF/)
                                                                                                                                                                                                                                                                                                     Key
5'UTR
                                                                                                                                                                                                                                                                                                                                                                 3'UTR
                                                                                                                      RESULT 5
                                                                                                                              AAD03295
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such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and lits functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transpenic animal and host cell transformed with PRKAG3 or a cheterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrKaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robic A, Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "Sus scrofa complete Prkag3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41.8; DB 22; Length 1867; Pred. No. 0.00058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.00/
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAT RECH AGRONOMIQUE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD03319 standard; cDNA; 1873 BP.
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80.3%;
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18-MAY-2000; 2000EP-0401388.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 68.55
Best Local Similarity 80.3°
Matches 49; Conservative
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1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCGGTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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/product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
                                  /*tag* e
/standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., plays to determine those most likely to exhibit improved meat quality traits and to produce larger litters.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is pig wild-type PRKAG3 gene.
                                                                                                                                                                                                                                                                                                                                                                                 Malek M, Plastow G;
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    replace (599, A) /*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD36457 standard; DNA; 1873 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Fig 1; 109pp; English.
                                                                                                                                                                                                                                    08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                        10-SEP-2001; 2001WO-US28283.
                                                                                                                                                                                                                                                                                                                                                                               Rothschild MF, Clobanu DC,
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    variation
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Matches
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                                                                                                                                                      The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3: PrkAG3 gene is located in the RN locus of chromosome 15. Mutation in PrkAG3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders sasociated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Primers that can detect or peferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3 are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3 or a franspenic animal and host cell transformed with PRKAG3 or a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence encoding the first cystathione beta synthase (CBS) domain
New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
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/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41.8; DB 22; Length 1873;
Pred. No. 0.00058;
0; Mismatches 12; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRKAG3 and is useful in gene therapy,
                                                                                                                  Claim 12; Page 62-64; 71pp; English.
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80.3%;
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Best Local Similarity 80.3
Matches 49; Conservative
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The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
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/product= "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
                      /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                             Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.5%; Score 41.8; DB 24; Length 1873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                                                                                                     Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.00058;
0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 98-100; 109pp; English.
                                                                                                                                                                                                                       (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..1395
       replace (595, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD36460 standard; DNA; 1873 BP.
                                                                                                                                                            2000US-231045P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.38;
                                                                                                                              10-SEP-2001; 2001WO-US28283.
                                                                                                                                                                          08-JAN-2001; 2001US-260239P. 18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                                                    Rothschild MF, Ciobanu DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 80.3
Matches 49; Conservative
                                                                                                                                                                                                                                                                                WPI; 2002-393850/42.
P-PSDB; AAE22987.
                                                                   WO200220850-A2
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                                                                                                                                                                                                                                                                                                                                                                             subunit gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 A 61
                                                                                                                                                            08-SEP-2000;
                                                                                                 14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa.
       variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD36460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Pig PRKAG3 polymorphic variant (PRKAG3-199)"
                                                                                                                                                                                                                                                                                                                          Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PRKAG3-30)
                                 /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein thase requiatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant DNA (PRRAG3-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41.8; DB 24; Length 1873;
Pred. No. 0.00058;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                  Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 89-91; 109pp; English.
                                                                                                                                                                                                                    (IOWA ) UNIV IOWA STATE RES FOUND INC.
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1..1395
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replace (89, C)
/*tag= b
                                                                                                                                                                                                                                                  Rothschild MF, Ciobanu DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ilarity 80.3%;
Conservative
                                                                                                                                                       08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                          10-SEP-2001; 2001WO-US28283
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Matches 49; Conserv
                                                                                                                                                                                                                                                                                               P-PSDB; AAE22985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A 166
                                                              WO200220850-A2
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                                                                                                                                                                                                                                                                                                                                                                          subunit gene
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                                                                                              14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD36459;
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/product= "Sus scrofa Prkag3 splice variant"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.5%;
80.3%;
                                                                     11-SEP-2000; 2000WO-EP09896.
                                                                                            99EP-0402236.
                                                                                                     18-MAY-2000; 2000EP-0401388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Conservative
                                                                                                                                                                                                                       WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                   P-PSDB; AAE00224
                                                                                                                                                                                                   Cannuccelli N,
                        WO200120003-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 A 61
                                                                                                                                                                                       Andersson L,
                                                                                          10-SEP-1999;
                                              22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD36458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                           myopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., plgs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRŘAG3; diabetes; obesity; myopathý; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                                                                                                                                                                                                           Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma subunit gene
                     /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.5%; Score 41.8; DB 24; Length 1873; 80.3%; Pred. No. 0.00058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                    Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                      Disclosure; Page 102-104; 109pp; English.
                                                                                                                                                              (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa PRKAG3 splice variant DNA.
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replace (599, A)
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                                                                                                               08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                    Rothschild MF, Ciobanu DC,
                                                                                          10-SEP-2001; 2001WO-US28283.
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/*tag= a
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          /*tag=
                                                                                                                                                                                                           WPI; 2002-393850/42.
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                                                                                                                                                                                                                      P-PSDB; AAE22988
                                            WO200220850-A2
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                                                                   14-MAR-2002
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variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD03321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism cuch as myopathy and cardiovascular diseases, to modulate AMPK cucivity, and for restoring a normal AMPK function. PRKAG3 sequence activity, and for restoring a normal AMPK function. PRKAG3 sequence conditis functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Primers that can detect or sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3 or a renasenic animal and host cell transformed with PRKAG3 or a resuguence ancoding PRKAG3 is useful for detecting mutations in a PrKAG3 gene, or a maceding PRKAG3 is useful for detecting mutations in a PrKAG3 domain a function or the presence of the first cystathione beta synthase (CBS) domain and a maceding presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the 
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                                                                                                                                                                                                                                                                                                                         Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Pred. No. 0.00059;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRKAG3 and is useful in gene therapy.
(INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDER, ANDERSSON L.
(LLOGF/) LOOFT C.
(KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 69; 71pp; English.
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Sus scrofa

variation

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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                                     AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; polymorphism; short interspersed element; pig; SINE; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_type= "DIRECT"
/note= "Direct repeat present between short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1095 BP; 233 A; 315 C; 267 G; 278 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plastow G;
                         PRKAG3 gene 5' flanking region with SINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interspersed element (SINE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                                     Location/Qualifiers
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Best Local Similarity 74.5%;
Matches 38; Conservative 2
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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/number= 1
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826..979
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/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                             "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
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                                                                  AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
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Pred. No. 0.0018;
0; Mismatches 13; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malek M, Plastow G;
                            Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
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                                                                                                                                                                                                                                                                  Location/Qualifiers
1..1395
/*tag= a
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78.78;
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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RESULT 13

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Query Match

Matches

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                            DNA encoding novel human diagnostic protein #20327.
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               AAS84523 standard; cDNA; 2541
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                                                                            13-FEB-2002 (first entry)
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AAS84523
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                                                                                                                                             Pig PRKAG3 gene 5' flanking region including exon and intron.
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Pred. No. 0.94;
1; Mismatches
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                                               AAD36462 standard; DNA; 808 BP.
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Local Similarity 74.5%;
Les 38; Conservative
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18-JUN-2001; 2001US-299111P.
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539..692
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Matches
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               RESULT 14
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                                AAD36462
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Tang YT;

2000US-0649167.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chalm reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating clisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clasponshie, for emposite, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and to produce other types of data and products dependent on DNA and amino acid sequences. AAS$4197-AAS$4564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPPO
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Pred. No. 43;
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Best Local Similarity 67.3%;
Matches 37; Conservative (
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                            OM nucleic - nucleic search, using sw model
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Perfect score:
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SUMMARIES			Description		BB628877 BB628877	BB629521 BB629521	BB630381 BB630381	AW356079 38073 MAR		BF890374 291826 MA
			日		BB628877	BB629521	BB630381	AW356079	AW427435	BF890374
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	æ		Length	- 1	621	655	685	399	422	444
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			Score		38.6	38.6	38.6	37	37	34.2
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RIKEN integrated sequence analysis (RISA) system--384-format RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1711 (2000)

Konno, M., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishi, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                         Arakawa,T., Carnincia, P. Pukuda,S., Furuno,M., Hanagaki,T., Hara,A. Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hitamoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Muramatsu,M. and Hayashizaki,Y. Takeda,Y., Tanaka,T., Toya,T., RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
"S., Kwadi,U., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9226
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
             BB629521 RIKEN full-length enriched, adult male bone Mus musculus cDNA clone 9830138C07 5', mRNA sequence.
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/clone_lib="RIKEN full-length enriched, adult male bone"
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Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
                                                                                                                                                                                                                                                                                                                                                                                                     sequencing pipeline with 384 multicapillary sequencer. Genome Res. . . 10 (11), 1757-1771 (2000)
Konno, B., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
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Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayateu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Ress. 10 (10), 1617-1630 (2000)
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Pred. No. 0.17;
0; Mismatches 14; Indels 0;
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DB630381 RIKEN full-length enriched, 6 days neonate skin Mus musculus cDNA clone A030014A04 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encyclopedia: real-time sequence clustering for construction of a nonredundant CDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                            3^\prime\,] . CDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu.W., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper_selected cDNAs to
prepare full-length cDNA libraries for rappid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1.7-22 Suehiro-cho, "Surummi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                    63.3%; Score 38.6; DB 10; Length 655; 77.0%; Pred. No. 0.17;
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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Manmalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Pred. No. 0.17;
0; Mismatches 14; Indels 0;
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/dev_stage="6 days neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A030014A04"
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1 Similarity 77.0%;
47; Conservative (
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Smith,T.P.L., Grosse,W.W., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E. Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
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                                                                                                                                                                                                             /note="Vector: pcMv SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                          Query Match 60.7%; Score 37; DB 10; Length 422; Best Local Similarity 75.4%; Pred. No. 0.46; Matches 46; Conservative 0; Mismatches 15; Indels
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BF890374
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PO Box 166, Clay Center, NE 68933-0166, USA
121: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
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                                                                                                /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                     /clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH108"
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/clone_lib="MARC 3BOV"
/tissue_type="pooled"
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  Plate: 32 row: F column: 22
Seq primer: ATTTAGGTGACACTATAG.
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Plate: 57 row: H column: 11
Seq primer: ATTTAGGTGACACTATAG.
                                                     Location/Qualifiers
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                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
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1 (bases 1 to 422)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Cass, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from testis, thymus, samitendonosus muscle, longissimus muscle, panorreas,
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PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
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PO Box 166, Clay Center, NE 68933-0166, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adrenal, and endometrium.
                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .399
/organism="Bos taurus"
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Plate: 17 row: P column: 9
Seq primer: ATTTAGGTGACACTATAG.
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FORWARD: AGGAAACAGCTATGACCAT
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PCR PRimers
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AW427435.1 GI:6955382
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Contact: Smith TPL
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Fax: 402 762 4390
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Best Local Similarity
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AW427435
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EST 25-APR-2001

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Gaps ; 0 S

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AI664508 516 bp mRNA linear EST 10-MAY-1999 uk25b05.yl Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:1970001 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                              Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(pases 1 to 516)

Marra,M. Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:986741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Other_ESTS: uk25b05.x1
Contact: Marra MyMashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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139 c 171 a
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    .516
    /organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL"
                                                                                                                                                                                                                    AI664508.1 GI:4768091
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                                                                                                                                                                                                                                                           house mouse.
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    61 A
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A1664508
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 548)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
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Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle. I 147 c 139 g 67 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                       Length 444;
                                                                                                                                                                                                                                                                                                                                   50 548 bp mRNA linear MARC 2BOV Bos taurus CDNA 5', mRNA sequence.
                                                                                                                                                            Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                          13;
                                                                                                                       DB 12;
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173 c 163 q 93 t
                                                                                                                   ch 56.1%; Score 34.2; Di Similarity 76.4%; Pred. No. 3; 42; Conservative 0; Mismatches
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Seg primer: ATTTAGGTGACACTATAG.
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/clone_lib="MARC 2BOV"
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1..548
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72.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.4
Best Local Similarity 72.1
Matches 44; Conservative
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Fax: 402 762 4390
                                                                                                                     Query Match
Best Local Similarity
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BI775360
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/iissue_type="whole embryo"
/dev_stage="stage 25"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleusiomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                            Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BJ080431 669 bp mRNA linear EST 12-DEC-2 BJ080431 NIBB Mochil normalized Xenopus tailbud library Xenopus laevis cDNA clone XL075jl6 3', mRNA sequence.
BJ080431 GI:17574127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIBB Mochii normalized Xenopus tailbud
                                            Medicago truncatula stem library
Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7568111.
Contact: Dixon RA
Plant Biology Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clome_in____/dissue_type="stem"
/dissue_type="stem"
/dev_stiage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
107 c 137 g 200 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 45.9%; Score 28; DB 10; Length 618; Similarity 77.3%; Pred. No. 2e+02; 34; Conservative 0; Mismatches 10; Indels
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                   The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, Tel: 580 221 7302
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .Gla
. /organism="Medicago truncatula"
/db_xref="taxon:3880"
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National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="NF063H10ST"
/clone_lib="Developing stem"
                                                                                                                                                                                                                                                  Email: radixon@noble.org
Insert Length: 660 Std Brror: 0.00
Plate: 063 row: H column: 10
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Xenopus laevis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tshini@genes.nig.ac.jp.
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Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus.
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/clone="madd7al"
/clone="madd7al"
/clone=lib="aspergillus nidulans 24hr asexual
developmental and vegetative coNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="vector: pBlueScript SK-; Site_l: EcoKI: Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript
a 118 c 96 9
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    EST 31-JUL-1998
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AA787203 365 bp mRNA linear EST 31-JUL-199 m8d07a1.rl Aspergillus nidulans 24hr asexual developmental and vegetative CDNA lambda zap library Emericella nidulans CDNA clone
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGGTCC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW693375 618 bp mRNA linear EST 20-DEC-2
NF063H10ST1F1000 Developing stem Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                   Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
Prade,R. and Roe,B.
                                                                                                                                                                                                                                                                                                                                                                              Contact: Bruce A. Roe, University of Oklahoma, broecou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
1 (bases 1 to 365)
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                                                                                                                                                                                                                                                                                                               An Aspergillus nidulans EST Database Unpublished (1998)
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Pred. No.
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Location/Qualifiers
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                                                                 m8d07a1 5', mRNA sequence
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                                                                                                           AA787203.1 GI:2847434
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ilarity 67.2%;
Conservative
                                                                                                                                                     Emericella nidulans.
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Medicago truncatula
                                                                                                                                                                            Emericella nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: broe@ou.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 405 325 4912
Fax: 405 325 7762
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AW693375
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BM466469
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                                                                                                                               Gallus gallus
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Matches 37; Conserv
                                                                                                              chicken.
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1 243 c 241 g 161 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 808)
                                                                                                                                                                                                      BM489457
pgm2n.pk010.p18 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA
                                                                                                                                                                                     9
according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute). " 1 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:3493458"
/clone=lib="mcLcGAA_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Cloud through the I.M.A.G.E. Consorthum/LLNL at:
http://image.llnl.gov
Plate: LLAMBS40 row: n column: 19
High quality sequence stop: 652.
Location/Qualifiers
                                                                                                                                                                                 1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: gapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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                                                                                                              Length 669;
                                                                                                                                                20; Indels
                                                                                                          Score 28; DB 13;
Pred. No. 2e+02;
0; Mismatches 20;
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/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                     BE306360.1 GI:9159452
                                                                                                            45.9%;
66.7%;
                                                                                                                                                40; Conservative
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/dev_stage="Breast,leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,11 weeks);growth plate(ld,7d,14d post-hatch)" /lab_host="E. coli EMDH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
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AGENCOURT_6456404 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5579448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="pgm2n.pk010.p18"
/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves: Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 590)

1 (bases 1 to 590)

2 ogburn, A. and Monsonego-Ornan, B. BSTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate CDNA library, USDA/IFAFS Animal Genome
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
clone pgm2n.pk010.p18 5' similar to ref|NP_060575.1 (NM_018105)
hypothetical protein FLJ10477 [Homo sapiens] dbj|BAA91635.1|
(AK001339) unnamed protein product [Homo sapiens], mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Epiphyseal Growth Plate cDNA library (pgm2n) /sex="Male and Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 590;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cogburn@udel.edu, www.chickest.udel.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27.4; DB 13;
Pred. No. 3e+02;
0; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822

    .590
    /organism="Gallus gallus"

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/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Larry A. Cogburn
University of Delaware
                                                                                                                       BM489457.1 GI:18610388
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/organism-"Homo sapiens"
/db_xref"*taxon:9606"
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/clone=lib="NHH_MGC_67"
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/lab_host="DH10B (phage-resistant)"
/inche="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAMI2336 row: c column: 01

High quality sequence stop: 681.

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:
http://image.lnl.gov
Plate: LLAM10330 row: h column: 16
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Kanith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 others
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/clone_lib="WCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH108"
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/db_xref="taxon:10090"
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Location/Qualifiers
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Sequence 7, Appli
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Patent No. 5449756
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Patent No. 5449756
                                                                                                                                 (without alignments)
4027.262 Million cell updates/sec
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Sequence 3,
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Sequence
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-750-222h-1

US-08-15-652B-1

US-08-254-353h-1

PCT-US92-053+4h-1

PCT-US95-07044-1

US-09-750-580-4

US-08-41-777h-7

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US-09-103-840A-1
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US-09-750-580-1
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US-09-021-715-3
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5198359-5
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US-07-918-314-5
                                                                                                                                                                                                                                                                                                                           441362 seqs, 153338381 residues
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                                                                         nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5198359-1
                                                                                                                                                                                                                                                                     IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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length: 2000000000
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                                                                                                            Sequence 214, App
Sequence 39, Appl
Sequence 13, Appl
Sequence 14, Appl
                                                                                                                                                                                                                                              Sequence 1, Appil
Sequence 10, Appi
Sequence 10, Appi
Sequence 10, Appi
Sequence 4, Appil
Sequence 1, Appil
Sequence 20, Appil
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Sequence 2, Sequence 1,
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MINAMOTO, SEJIRO; KONO, TAKESHI; DOI, TAKESHI; MIYASAKA, MASAYUKI;
TSUDO, MITSURU; KARASUYMA, HAJIME
TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/487,059
FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.0%; Score 25; DB 6; Length 4035; 64.9%; Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Indels
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us-09-182-145-14

us-09-182-145-14

us-09-182-145-14

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Pred. No. 16;
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FILING DATE: 9-UOL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 865,155
FILING DATE: 08-APR-1992
APPLICATION NUMBER: 487,059
FILING DATE: 05-MAR-1990
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Best Local Similarity 64.99
Matches 37; Conservative
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Best Local Similarity 64.9°
Matches 37; Conservative
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;Patent No. 5198359
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tive 0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PSTERIN PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,222A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,353
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                  ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                      BMP-9 COMPOSITIONS
                                    Sequence 1, Application US/08750222A
Patent No. 6034061
                                                                           GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Gozen, John M.
APPLICANT: Celeste, Anthony J.
APPLICANT: Thies, Scott
APPLICANT: Thies, Scott
ITILE OF INVENTION: BMP-9 COMPOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kapinos, Ellan J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA
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STRAIN: C57B46xCBA
TISSUE TYPE: liver
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Best Local Similarity 65.5%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: mat_peptide
LOCATION: 1564..1893
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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610..1896
                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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POSITION IN GENOME:
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ANTI-SENSE: N
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NAME/KEY:

LOCATION:

US-08-750-222A-1
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RESULT 4
US-08-750-222A-1
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                                                                                                                                                                                                                                                                ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PARENTING FREEDRE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,132A
                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Repinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFRENCE/DOCKET NUMBER: GI 5186A
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-181
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDENMES: double
                                                                                            Sequence 1, Application US/08050132A Patent No. 5661007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mus musculus
STRAIN: C57246xCBA
TISSUE TYPE: liver
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat_peptide
LOCATION: 1564..1893
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610..1896
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POSITION IN GENOME:
UNITS: bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION:
US-08-050-132A-1
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FEATURE:
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US-08-050-132A-1
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                                                                       APPLICANT: ROCHE, VICKI A.
APPLICANT: ROCHE, VICKI A.
APPLICANT: Geleste, Anthony J.
APPLICANT: Celeste, Anthony J.
APPLICANT: Thies, Sectifiery
APPLICANT: Thies, Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/254,353A
FILING DATE:
CLASSIPICATION: 4355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Rapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 876-1170
TELEFAX: (617) 876-1170
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nuclet acid
STRANDEDNESS; double
US-08-254-353A-1; Sequence 1, Application US/08254353A; Patent No. 6287816; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: Mouse liver CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
STRAIN: C57B46xCBA
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1..2447
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POSITION IN GENOME:
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ORIGINAL SOURCE:
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COUNTRY: US
ZIP: 02140
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FEATURE:
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US-08-254-353A-1
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                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs – 87 CambridgePark Drive
CITY: Cambridge
                                                                                              APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
APPLICANT: Song, Jeffrey
APPLICANT: Thies, R. Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/815,652B
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                       Sequence 1, Application US/08815652B Patent No. 6034062 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
STRAIN: C57B46xCBA
TISSUE TYPE: liver
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Best Local Similarity 65.55
Matches 36; Conservative
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LOCATION: 1564..1893
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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610..1896
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POSITION IN GENOME:
UNITS: bp
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ORIGINAL SOURCE:
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LOCATION:
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US-08-815-652B-1
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                  US-08-815-652B-1
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                                                                                                                                                                                                                                                                                                     STATE:
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APPLICANT: Rosen, Vicki A.
APPLICANT: Rosen, Vicki A.
APPLICANT: Rosen, John M.
APPLICANT: Celeste, Anthony J.
TILE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/ACBRY INCRMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERRENCE/DOCKET NUMBER: GI 5186C-PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 876-1210
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
Sequence 1, Application PC/TUS9507084 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
STRAIN: C57B46xCBA
TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 65.58
Matches 36; Conservative
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POSITION IN GENOME:
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FEATURE:
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PCT-US95-07084-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-750-580-4
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40.3%; Score 24.6; DB 5; Length 2447;
Best Local Similarity 65.5%; Pred. No. 20;
Matches 36; Conservative 0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05374A
FILING DATE: 19920625
CLASSIFICATION:
                                                                                                                                                                                  ADDRESSE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
STRIT: Cambridge
                                                                                                         APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCREEY KAPINOS, Ellen J.
REGISTRATION NUMBER: 32,245
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                       Sequence 1, Application PC/TUS9205374A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diaming TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse liver CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
STRAIN: C57B46xCBA
TISSUE TYPE: liver
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide LOCATION: 1564 .1893
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NAME/KEY: CDS
.^^*TON: 610..1896
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POSITION IN GENOME:
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PCT-US92-05374A-1
                                   RESULT 7
PCT-US92-05374A-1
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PCT-US95-07084-1
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40.3%; Score 24.6; DB 5; Length 2447; 65.5%; Pred. No. 20;
tive 0; Mismatches 19; Indels 0;
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ZIP: 19406-0939

COMPUTAT: USA

MEDIUM TYPE: Floppy disk

COMPUTER: IBW PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NORMER: US/08/451,777A

FILING DATE: 26-MAX 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
ADDRESSEE: Intellectual Property
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-451-777A-7/c

Sequence 7, Application US/08451777A

Patent No. 578923

GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stanbollan, Dwight
APPLICANT: Stanbollan, Dwight
ITILE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 40.3%; Score 24.6; DF Best Local Similarity 70.2%; Pred. No. 22; Matches 33; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: primer_bind
LOCATION: 320..338
OTHER INFORMATION: 17-42-319.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
LOCATION: 3214..3232
OTHER INFORMATION: 17-41-250.mis complement
                                                                                                                     NAME/KET: primer_bind
LOCATION: 1632.12651
LOCATION: 1632.12651
COTHER INFORMATION: 17-40.rp complement
NAME/KET: primer_bind
LOCATION: 2964.13984
OTHER INFORMATION: 17-41.pu
NAME/KET: primer_bind
LOCATION: 3432..14454
OTHER INFORMATION: 17-41.rp complement
NAME/KET: primer_bind
LOCATION: 3432..14454
OTHER INFORMATION: 17-41.rp complement
NAME/KET: primer_bind
LOCATION: 300..318
OTHER INFORMATION: 17-42-319.mis
                              NAME/KEY: primer_bind
LOCATION: 1441..12461
OTHER INFORMATION: 17-39.rp complement
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APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-28P-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_binding
LOCATION: 307..331
OTHER INFORMATION: 17-42-319.probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: primer_bind
LOCATION: 3194.,3212
OTHER INFORMATION: 17-41-250.mis
OTHER INFORMATION: 17-40.pu
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LOCATION: 3201..3225
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APPLICANT: Bouguelert, Aymeric
APPLICANT: Bouguelert, Aymeric
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REPERENCE: 89.05.C1P
CURRENT APPLICATION NUMBER: US 09/599,362
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR PLING DATE: 2000-06-21
PRIOR PLING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: US 60/113,686
PRIOR PLING DATE: US 60/114,032
PRIOR PLING DATE: US 60/141,032
PRIOR PLING DATE: DESECT AND SECONDAL AN
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OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
OTHER INFORMATION: 1.1022
OTHER INFORMATION: 1.-42.pu
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OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
NAME/KEY: conflict
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OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: conflict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 17-42-319 : polymorphic base C or T NAME/KEY: allele
                                                                                                                           Dumas Milne Edwards, Jean-Baptiste
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LCCATION: 553.11575
ULCCATION: 553.11575
ULCATION: 553.11576
NAME/KEY: primer_bind
LOCATION: 899.11920
OTHER INFORMATION: 17-39.pu
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LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: exon 4
NAME/ERF: misc_feature
LCCATION: 3941..5381
OTHER INFORMATION: 3'regulatory region
                          Denison, Blake
Bour, Barbara
Bihain, Bernard
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OTHER INFORMATION: exon 2
NAME/KEY: exon
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OTHER INFORMATION: exon 1
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1613..1724
OTHER INFORMATION: exon 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 2243..3940
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LOCATION: 319
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                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-451-777A-7

Matches

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5363 AAGGAACAACTCAGTGTGGGCAGCGGCCAGCCAGTCAAGAGCATGGGCCCTGG 5309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                  APPLICANT: Strambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKille Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road/UW220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: 709 Sweeland Road/UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 24.6; DB
; Pred. No. 23;
0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/451,777
FILING DATE: 26-MAY-1995
APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: EAGLE, Alissa M.
REGISTRATION NUMBER: 37,126
REFERENCE/DOCKET NUMBER: P50268-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 7, Application PC/TUS9506743; GENERAL INFORMATION:
                                                                                                                                        Sequence 7, Application US/08998208
Patent No. 5880105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-998-208-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.3%;
Best Local Similarity 65.5%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 7676 base pairs
                                                                                                                                                                                                                                                                                                                                                                                      CITY: King of Prussia STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-06743-7/C
                                                                                                                   JS-08-998-208-7/c
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                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 19; Indels
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CURRENT APPLICATION DATA:
APPLICATION VUNBER: US/08/451,778A
FILNG DATE: 26-MAY-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREE: 709 Swedeland Road/UW220 CITY: King of Prussla STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
ATTLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
REGISTRATION NUMBER: 37,126
REPERBNCK-POCKET NUMBER: P50268-1B
TELECOMUNICATION INFORMATION:
TELEPHONE: 610-270-5904
TELEPHONE: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P50268-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 7, Application US/08451778A; Patent No. 5830649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAME: Eagle, Alissa M.
REGISTRATION NUMBER: 37,126
REFERENCE/COCKET NUMBER: P5(
TELECOMMUNICATION INFORMATION:
TELECHONE: 610-270-5364
                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                            36; Conservative
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TYPE: nucleic acid
                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19406-0939
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Best Local Similarity
                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-08-451-778A-7/C
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COUNTRY:

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US-08-451-778A-7

Matches

```
LOCATION: 1239

DTHER INFORMATION: 20-828-311 : polymorphic base C or T

NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: 20-841-149 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer_bind
LOCATION: 12029.12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
LOCATION: 12581..12603
LOCATION: 14992..15012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: 20-842.rp complement
NAME/REY: primer_bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement
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NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 15969.17969
OTHER INFORMATION: 3'regulatory region
                                                                                                                                OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 20-853-415
NAME/KEY: primer_bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: 45442
OTHER INFORMATION: 20-842-115
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LOCATION: 42572.42591
OTHER INFORMATION: 20-841.rp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 17-42-319
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LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
                                                                                                                                                                                                     OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                     OTHER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: exon 3
                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 14271...15968
OTHER INFORMATION: exon
NAME/KEY: misc_feature
LOCATION: 15969..17969
                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: 13470..13526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: primer_bind
LOCATION: 45863..45883
                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                              LOCATION: 12947..12958
                                                                                                                                                                                                                                                                                                             13641..13752
                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind LOCATION: 1357..1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
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LOCATION: 42218
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                                                                                                                                                     NAME/KEY: exon
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  LENGTH: 81001
                                                                                                              COCATION:
                                                                                                                                                                                                                                                                                                                 COCATION:
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APPLICANT: Dumas Milne Lu.....
APPLICANT: Duclert, Aymeric
APPLICANT: BouqueLeret, Lydie
APPLICANT: BouqueLeret, Lydie
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Ebbets-Reed, Dana
TILE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
CURRENT APPLICANTON NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR APPLICATION NUMBER: PCT/IB09/02058
PRIOR PILING DATE: 2000-06-21
PRIOR PILING DATE: 1999-112-20
PRIOR PILING DATE: 108 94/469/099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.3%; Score 24.6; DB 5; Length 7676; Best Local Similarity 65.5%; Pred. No. 23; Matches 36; Conservative 0; Mismatches 19; Indels 0.
                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yen, Frances
Denison, Blake
Bour, Barbara
Bihain, Bernard
Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION
PRIOR FILING DATE: 1999-12-20
PRIOR PPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/141,032
                                                                                                                                                                                                                                     CLASSICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23-SED-1944
ATTORNEY/AGENT INFORMATION:
NAMM: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REGISTRATION NUMBER: 960268-1
TELECOMMUNICATION INFORMATION:
TELEFRAX: 610-270-5024
TELEFAX: 610-270-5034
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/06743 FILING DATE:
                                    ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09750580 Patent No. 6455280 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06743-7
Pennsylvania
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US-09-750-580-1
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APPLICANT:
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APPLICANT:
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APPLICANT:
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SEQ ID NO 1
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APPLICANT: FLEISCHMAN, Robert D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 40.3%; Score 24.6; DB 4; Length 81 Best Local Similarity 70.2%; Pred. No. 29; Matches 33; Conservative 0; Mismatches 14; Indels
                                                                                                               OTHER INCORATION: 1220.

NAME/KEY: primer_bind
LOCATION: 1240. 1258

OTHER INCORATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 12328.1246

OTHER INCORATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12384.1256

OTHER INCORATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 12322.1256

OTHER INCORATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 1522..1250

OTHER INCORATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 1522..1250

OTHER INCORATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 42219..4237

OTHER INCORATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 4542:.4541

OTHER INCORATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..4561

OTHER INCORATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..4561

OTHER INCORATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 4542:.4561

OTHER INCORATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 77039..77057

OTHER INCORATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
LOCATION: 1227. 1251
LOCATION: 1277. 1251
LOCATION: 1277. 1255
LOCATION: 12335. 12359
OTHER INFORMATION: 17-42-319.probe
                                           OTHER INFORMATION: 20-853.rp complement NAME/KEY: primer bind LOCATION: 1220..1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INCORMATION: 17-41-250.probe
NAME/KEX: misc_binding
COTHER INCORMATION: 17-41-250.probe
COTHER INCORMATION: 20-841-149.probe
NAME/KEY: misc_binding
COTHER INCORMATION: 20-841-149.probe
COTHER INCORMATION: 20-842-115.probe
NAME/KEY: misc_binding
LOCATION: 7046..77070
COTHER INCORMATION: 20-853-415.probe
US-09-750-580-1
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US-09-103-840A-2/C
; Sequence 2, Application US/09103840A
; Patent No. 6284328
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_binding
LOCATION: 15229..15253
primer_bind
77166..77185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
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OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence;
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ACAAGGCAGAAGTCGGTGGAAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC
APPLICANT: WHITE, Owen R.
APPLICANT: PRASER, Claire M.
APPLICANT: VENIER, Claire M.
APPLICANT: VENIER, Claire M.
APPLICANT: VENIER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILLE REPERENCE: 24566-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
SOFTWARE: PATENTING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 39.7%; Score 24.2; DB 4; Length 4 Best Local Similarity 62.3%; Pred. No. 40; Matches 38; Conservative 0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June 13, 2003, 06:01:06
Job time: 11.6452 secs
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3821367 A 3821367
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                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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9

Gaps

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Sequence 5, Appli
Sequence 1640, Ap
Sequence 1640, Ap
Sequence 67, Appl
Sequence 32, Appl
Sequence 30, Appl
Sequence 69, Appl
Sequence 2184, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 817, App
Sequence 9241, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 2228, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 5478, Ap
                                                                                                               (without alignments)
4579.068 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                              June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds
                                                                                                                                                                                            1 acaaggcagaagtcggtgga.....gggggaaggtcccggtcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2. /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
3. /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/NSO8_PUBCOMB.seq:*
3. /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
4. /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
5. /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-826-581-2

US-09-960-352-1640

US-10-175-523-67

US-09-995-793A-32

US-09-995-793A-31

US-09-997-768A-31

US-09-977-768A-31

US-09-877-868-69

US-09-873-658-69

US-09-880-107-2184

US-09-764-891-9241

US-09-764-891-9241

US-09-764-891-9241

US-09-764-891-9241

US-09-764-891-9241

US-09-764-891-9241

US-09-764-891-9241
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0 US-09-751-877-1

US-09-764-891-5478

US-09-764-891-10205
                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        1029858 segs, 724030393 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                US-09-826-581-5_COPY_200_260
61
                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_NA:*
                                                                nucleic search, using sw model
                                                                                                                                                                                                                         IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
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Match Length DB
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4034
8670
33795
2996
5312
5312
5312
5381
8095
8095
8095
14040
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Maximum DB
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Sequence 5, Application US/09826581
Fatent No. US20020142310A1
GENERAL INFORMATION:
APPLICANT: AACHERSON. Leif
APPLICANT: AATHUNG Stefan
FILE REFERENCE: 11145-007001
CURRENT APPLICANTION NUMBER: US/09/826,581
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOUTHARE: PASLESC for Windows Version 4.0
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                                             Sequence 950, App Sequence 950, App Sequence 875, Appli Sequence 1952, A Sequence 11952, A Sequence 12192, A Sequence 131, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 71, Appli Sequence 71, Appli Sequence 6537, Ap Sequence 2637, Ap Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence 298, Appli Sequence
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                                                                                      US-09-764-891-8575
US-10-199-550-1
US-10-199-864-761-19652
US-10-198-846-9038
US-10-198-846-12192
US-10-198-846-4363
US-10-198-846-4363
US-09-895-298-16
US-09-895-298-16
US-09-139-254-16
US-09-139-254-16
US-09-900-274-1
US-09-962-832-154
US-09-864-761-19511
US-09-294-093B-950
US-09-864-761-5
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-960-352-9061

US-09-822-849A-49

US-09-922-598-298

US-09-989-298A-298

US-09-989-735-298

US-09-989-444-298

US-09-989-730-298
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Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                  US-09-764-090-71
US-09-764-891-5637
US-09-764-891-5639
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US-09-826-581-2
; Sequence 2, Application US/09826581
; Patent No. US20020142310A1
; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5
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TYPE: DNA
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Sequence 32, Application US/09995793A
Publication No. US2003005446A1
GENERAL INFORMATION:
APPLICANT: Weber, Bernard H.F.
APPLICANT: Stochr, Heidi
TITLE OF INVENTION: NO. US20030054446Alel retina-specific human proteins C7orf9, CURRENT APPLICATION NUMBER: US/09/995,793A
FILE REFERENCE: 033488-01
CURRENT APPLICATION NUMBER: US/09/995,793A
FILEN DATE: 2001-11-29
FRICK APPLICATION NUMBER: 60/253,751
FRICK PRICK APPLICATION NUMBER: 60/253,751
FRICK PRICK APPLICATION NUMBER: 60/253,751
FRICK PRICK APPLICATION NUMBER: 500-11-29
SOFTWARE: PatentIN version 3.1
SEQ ID NO 32
LENGTH: 560
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                      TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS) FILE REFERENCE: 3235/14795-US3
CURRENT APPLICATION NUMBER: US/10/175,523
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGT 58
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tive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature; OTHER INFORMATION: genomic DNA, Exon from 101 to 460 US-09-995-793A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.3%; Score 27; DB 9;
85.7%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                           PRIOR FILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-05
PRIOR PRINC APPLICATION NUMBER: US 60/325,150
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-05
PRIOR FILING DATE: 2001-11-14
PRIOR PLING DATE: 2001-11-14
PRIOR PLING DATE: 2001-11-14
PRIOR PLING DATE: 2002-01-18
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PATENTIN VERSION 3.1
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Sequence 30, Application US/0995793A
Publication No. US20030054446A1
GENERAL INFORMATION:
APPLICANT: Weber, Bernard H.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.9%
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Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-175-523-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 74868
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US-09-995-793A-32
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                APPLICANT: Andersson, Leif
APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Hoiger
APPLICANT: Markund, Staffan
TITLE OF INVENTION: VARANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagn, Negappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERBNCE: 16511.006/37-21(10298)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1640
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Bos taurus
OTHER INFO:WATION: Clone ID: 08-1,18188-005-01-87
                                                                                                                                                                                                                                                                                                                                                                                                83.6%; Score 51; DB 10; I
100.0%; Pred. No. 5.8e-08;
Live 0; Mismatches 0;
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Publication No. US20030096264A1
GENERAL INFORMATION
APPLICANT: Brockman, Jeffrey
APPLICANT: Evans, David
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Hook, Derek
Klimczak, Leszek
Laeng, Pascal
Palfreyman, Michael
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Best Local Similarity 100.0
Watches 51; Conservative
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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US-10-175-523-67/c
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APPLICANT:
APPLICANT:
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5 GGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCCA 61
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  TITLE OF INVENTION: Methl and Meth2 Polynucleotides and Polypeptides CURRENT APPLICATION NUMBER: US/09/373,658
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 125
SEG ID NO 69
LENGTH: 8670
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Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REPRENEUR: 44921-2028 WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L25880 US-09-880-107-2184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 CAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGT
                                                                                                                                                                                                                                                                                               Score 25; DB 9; Length 8670;
Pred. No. 12;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Unknown Organism:Unknown US-09-373-658-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24.8; DB 10;
Pred. No. 12;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 179, Application US/09822830A
Patent No. US20020142952A1
GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agostino, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Howes, Steven H.
Resnick, Richard J.
Gulukota, Kamalakar
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64.98;
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Best Local Similarity 67.3%;
Matches 35; Conservative C
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                                                                                                                                                                                                                                                                                                                   Local Similarity 64.9 nes 37; Conservative
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Clark, Hilary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                         TYPE: DNA ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-822-830A-179
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APPLICANT:
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APPLICANT: Stoehr, Heidi
TITLE OF INVENTION: No. US20030054446Alel retina-specific human proteins C7orf9, C12d
FILE REFERENCE: 033488-001
CURRENT APPLICATION NUMBER: US/09/995,793A
CURRENT FILING DATE: 2001-11-29
PRIOR PRICATION NUMBER: 60/253,751
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 301, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; OTHER INFORMATION: artificial sequence, Translation start at 347, stop at 604
US-09-995-793A-30
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Pred. No. 13;
0; Mismatches 20; Indels (
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CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR PLILNG DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR PLILNG DATE: 2000-09-28
PRIOR PLILNG DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
SOFTWARE: PatentIn version 3.0
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Ruben, Steven M.
Jonak, Zdenka L.
Trulli, Stephen H.
Fronwald, James A.
Terrett, Jonathan A.
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64.98;
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64.9%;
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Best Local Similarity 64.91
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Best Local Similarity 64.95
Matches 37; Conservative
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US-09-373-658-69/c
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                   TYPE: DNA
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R FILING DATE: 2000-08-14

R APPLICATION NUMBER: 60/236,369

R FILING DATE: 2000-09-29

R APPLICATION NUMBER: 60/224,519

R APPLICATION NUMBER: 60/220,964

R APPLICATION NUMBER: 60/220,964

R APPLICATION NUMBER: 60/220,964

R APPLICATION NUMBER: 60/220,964

R APPLICATION NUMBER: 60/241,809
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R FILING DATE: 2000-09-29
R FILING DATE: 2000-10-29
R FILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/237,038
R FILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/251,868
FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/229,344
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APPLICATION NUMBER: 60/229,343
FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,287
FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,513
FILING DATE: 2000-09-05
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/249,299
FILING DATE: 2000-111-17
APPLICATION NUMBER: 60/236,327
FILING DATE: 2000-09-29
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FILING DATE: 2000-11-01
APPLICATION NUMBER: 60/225,268
FILING DATE: 2000-08-14
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FILING DATE: 2000-09-05
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FILING DATE: 2000-12-08
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FILING DATE: 2000-09-08
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FILING DATE: 2000-10-02
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           APPLICATION NUMBER: 60/228,924
                                                       APPLICATION NUMBER: 60/224,518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/236,368
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FILING DATE: 2000-10-02
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APPLICATION NUMBER: 60/249,210
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS TELLE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILLING DATE: 2001-03-29
PRIOR PRILING DATE: 2001-03-29
PRIOR PRILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                              Score 24.6; DB 10; Length 2996; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA118C1
CURRENT APPLICATION NUMBER: US/10/091,572
CURRENT FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 19; Indels
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PRIOR APPLICATION NUMBER: 09/764,850
PRIOR PLICATION NUMBER: 09/764,850
PRIOR PLICATION NUMBER: 00/719,065
PRIOR PLICATION NUMBER: 60/19,065
PRIOR PLICATION NUMBER: 60/19,065
PRIOR PLICATION NUMBER: 60/214,886
PRIOR PLICATION NUMBER: 60/217,487
PRIOR PLICATION NUMBER: 60/225,758
PRIOR PLICATION NUMBER: 60/220,963
PRIOR PLICATION NUMBER: 60/220,963
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PRIOR PLICATION NUMBER: 60/220,270
PRIOR PLICATION NUMBER: 60/230,334
PRIOR PLICATION NUMBER: 60/231,274
PRIOR PLICATION NUMBER: 60/231,223
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Publication No. US20030054373A1
GENERAL INFORMATION:
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Best Local Similarity 65.5%;
Matches 36; Conservative C
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LENGTH: 2996
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PRIOR PELING DATE: 2000-01-17
PRIOR PELING DATE: 2000-06-22
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APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: APOLIPOPROTEIN A-IV-RELATED PROTEIN: POLYPEPTIDE, POLYNUCLECTI
TITLE OF INVENTION: SEQUENCES AND BIALLELIC MARKERS THEREOF.
FILE REFERENCE: GENSET.50CP2C
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: 9C006
CURRENT ENLING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: 9tentin Ver. 2.0
SEQ ID NO 9241
LENGTH: 5312
                                                                                                                                                                                                                               19; Indels
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                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                             Query Match 40.3%; Score 24.6; Best Local Similarity 65.5%; Pred. No. 18; Matches 36; Conservative 0; Mismatches
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CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR PILING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-21
PRIOR PELING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 69/469/099
PRIOR PILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR PILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR PILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9241, Application US/09764891; Publication No. US20030077808A1; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09842364 Publication No. US20030032783A1 GENERAL INFORMATION:
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Best Local Similarity 65.5%;
Matches 36; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yen-Potin, Frances
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Bour, Barbara
Bihain, Bernard
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SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT:
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us-09-826-581-5_copy_200_260.rnpb

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OTHER INFORMATION: 17-39-343: T in ref genbank AC007707
NAME/KEY: conflict
LOCATION: 1447
OTHER INFORMATION: 17-40-202: G in ref genbank AC007707
NAME/KEY: primer_bind
LOCATION: 1.11022
OTHER INFORMATION: 17-42.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 17-42-319 : polymorphic base C or T NAME/KEY: allele LOCATION: 3213 OTHER INFORMATION: 17-41-250 : polymorphic base C or T
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LOCATION: 3194.3212
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NAME/KEY: primer_bind
LOCATION: 3214.3232
UCHER INFORMATION: 17-41-250.mis complement
NAME/KEY: misc_binding
LOCATION: 307.331
                                                                                                     NAME/KEY: misc_feature
LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
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NAME/KEY: misc_feature
LOCATION: 3941..5381
OTHER INFORMATION: 3'regulatory region
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LOCATION: 553..11575
OTHEK INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 899..11920
OTHER INFORMATION: 17-39.pu
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IAME/KEY: primer_bind
OCATION: 1441..12461
PHER INFORMATION: 17-39.rp complement.
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LOCATION: 1632..12651
OTHER INFORMATION: 17-40.rp complement
NAME/KEY: primer_bind
LOCATION: 2964..13984
OTHER INFORMATION: 17-41.pu
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LOCATION: 3432..14454
OTHER INFORMATION: 17-41.rp complement
NAME/CT: primer_bind
LOCATION: 300..318
OTHER INFORMATION: 17-42-319.mis
                                                                                                                                                                   NAME/KEY: exon
LOCATION: 919..930
OTHER INFORMATION: exon 1
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THER INFORMATION: exon 2
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OTHER INFORMATION: exon 3
                                                              ORGANISM: Homo sapiens
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LOCATION: 320..338
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SEQ ID NO 4
LENGTH: 5381
                                              TYPE: DNA
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APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Denison, Blake
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara

APPLICANT: Blhain, Bernard

APPLICANT: Budgets Reed, Jean-Baptiste
APPLICANT: Bouquelret, Lydie
APPLICANT: Relets Reed, Dana
APPLICANT: Salter-Cid, Luisa

ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH

FILE REFERENCE: 89.US3.REG

CURRENT FILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patent.pm

SEQ ID NO 4

LENGTH: 5381
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                                                                                                                                Query Match
40.3%; Score 24.6; DB 9; Length 5;
Best Local Similarity 70.2%; Pred. No. 18;
Matches 33; Conservative 0; Mismatches 14; Indels
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OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
NAME/KEY: conflict
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LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
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NAME/KEY: misc_feature
LOCATION: 3941.5381
OTHER INFORMATION: 3'regulatory region
; OTHER INFORMATION: 17-42-319.probe
; NAME/KEY: misc_binding
; LCCATION: 3201..325
; OTHER INFORMATION: 17-41-250.probe
US-09-842-364-4
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Patent No. US20020142949A1
GENERAL INFORMATION:
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OTHER INFORMATION: 17-42.pu
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LOCATION: 1442..1498
OTHER INFORMATION: exon 2
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OTHER INFORMATION: exon 1
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ORGANISM: Homo sapiens
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LOCATION: 319
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US-09-880-107-2228/C

Sequence 2228, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Wockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer; TITLE COF INVENTION: Gene Expression Profiles in Liver Cancer; FILE EFFERENCE: 44921-5028-WO.

CURRENT FILING DATE: 2001-06-14

PRIOR PILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-10-02

NUMBER OF SEQI ID NOS: 3950

SOFTWARE: PatentIn Ver. 2.1

SEQI ID NO 2228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 40.3%; Score 24.6; DB 10; Length Best Local Similarity 70.2%; Pred. No. 18; Matches 33; Conservative 0; Mismatches 14; Indels
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LOCATION: 1441..1240. Pu
LOCATION: 1441..1240. Pu
CUTHER INCORMATION: 17-39.rp complement
NAME/KEY: primer_bind
LOCATION: 1622..12651
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NAME/KEY: primer_bind
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CUTHER INCORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 3004..13984
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NAME/KEY: primer_bind
LOCATION: 300..318
CUTHER INCORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 300..318
CUTHER INCORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 320..338
CUCATION: 320..338
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NAME/KEY: primer_bind
LOCATION: 553.11575
UCHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 899..11920
OTHER INFORMATION: 17-39.pu
NAME/KEY: primer_bind
LOCATION: 1246..12267
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LOCATION: 307..331
OTHER INFORMATION: 17-42-319.probe
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; OTHER INFORMATION: 17-41-250.probe
US-09-751-877-4
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ORGANISM: Homo sapiens
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LOCATION: 3214..3232
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June 13, 2003, 01:49:14 ; Search time 192.613 Seconds (without alignments) 9216.782 Million cell updates/sec 61 US-09-826-581-5_COPY_529_589 61 1 gggctgggatgacgaactgc.....acatgcgcttcatgcaggag 4109280 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 2054640 segs, 14551402878 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 em_htgo_hum:* em_htgo_mus:* em_htgo_other:* em_sts:*
em_un:*
em_vi:*
em_htg_hum:*
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em_ov:*
em_pat:*
em_ph:*
em_pl:* GenEmbl:* Title: Perfect score: Sequence: Scoring table: Database : Searched: Run on:

Pred. No. is the number of results predicted by chance to have a

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0 0		61	90	152129		AC027416	ACO	27416 Homo	sapi
			94.	2290		HSA249977	AJZ	49977 Homo	sapi
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11				1873		AX099800	AXO	99800 Sequ	ance
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26			m 6	10346		AE009112	AEO	09112 Agro	acte
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ر د د			. m	79397	101	AC115385	ACI	15385 Ratt	Rattus no
31			n d	1917		AF039574	AF	002245 Cri	misch
			(A)	5253		AF112855	AF	112855 Mus	muscu
233			ni n	39430		AE007063	AEO	07063 Myco	Mycobacte
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						ALIGNMENTS			
RESULT 1	179								
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ACCESSION VERSION	NOI	AX2	AX281579 AX281579	GI:1	:1660883				
KEYWORDS	SQ	٠.))))	•			
SOURCE	URCE ORGANISM	human Homo Eukar	sapi yota	ens ; Metazoa;	oa;	Chordata; Cran		; Euteleostomi	comi;
REFERE	NO.	Mam 1	malia;	ut	ja;	Primates; Catarrhir	rrhini; Hominidae	е; Ношо.	
AUTHORS	IORS	And	Andersson, I	.14	thma	Luthman, H. and Marklund	und, S.		enbun 1+
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/organism="Homo sapiens"
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472. 1380
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Sequence 29 from Patent WO0120003.
AX099776 2109 bp
Sequence 3 from Patent WO0120003.
AX099776
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                                                      AX099776.1 GI:13538810
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61; Conservative
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                                                                                                     Homo sapiens
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GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQV
VGLYSRFDVJHLAAQQTVNHLDMSVGFBLRQRTLCLEGVLSCQPHESLGEVIDRIARB
QVHRLVILVDETQHLLGVYSLSDILQALVLSPAGIDALGA"
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LVANGVRAAPLWDSKKQSFVGMLT1TDFILVLHRYYRSPLVQIYEIEQHKIETWREIY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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Sequence 5 from Patent W00177305.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0120003-A 29 22-MAR-2001
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Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
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Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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ALVLSPAGIDALGA"
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Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
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KNRTHRIEDYLDPVSGNVHHILTHREILKELHFENERSLLERSPETARTIODGLGIGFFRDL
AVVLETAPILTALDIFVDRRVSALPVVNECGQVVGIXSRFDVIHLAAQOTYNHLDMSV
GEALRQRTICLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
                                                                                                                                                /translation-"msflegenssympspavtsserirgkrrakalrwtrgksyebg
Eppedgeorerrprassycleartryrtplachbackgrpramchlebctasaad
Sstddyelarerpareamechellerrprach(Lispaapfrick)
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gatlland,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
and Andersson,L.
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
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100.0%; Pred. No. 3.4e-10;
Live 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
                                                                                      /protein_id="CAC35801.1"
/db_xref="G1:13538837"
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/note="AMPKG3"
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Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                        Contact: Sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: Sequence_submissions@genome.wi.mit.edu
Conter project Information
Center project name: 17458
Center clone name: 504_G_11

Sequencing vector: M13; M7/815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135376 bases at least Q40
Consensus quality: 145503 bases at least Q20
Insert size: 161000, aqarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; sum-of-contigs
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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51285: contig of 4820 bp in length
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 8, 2001 this sequence version replaced gi:13431203.
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4 (bases 1 to 206854)
Waterston, R.H.
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Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens BAC clone RP11-459I19 from 2, complete sequence.
AC009974
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Harris, A. and Cotton, M.
The sequence of Homo sapiens BAC clone RP11-459I19
Upublished (2001)
3 (bases 1 to 206854)
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Sulston, J.E. and Waterston, R.
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Waterston, R.H.
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Direct Submission
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Center: Washington University Genome Sequencing Center Center code: WUGSC

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The RPCI-II human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:18 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                                 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Amunresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.
                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 208854 of RP11-459119.
                                                                                                                                                                                                                                         clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE047599 (NID:98364652) tz39c01.y1"
                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted:
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'note="match to EST AL567345 (NID:g12920610)"
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/note="similar to Homo sapiens EST BI114348
(NID:g14565249)"
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence, see http://genome.wustl.edu/gsc
                                                                                                      Center project name: H_NH0459119
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/db_xref="taxon:9606"
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/note="match to EST
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LIVANGYRAARAMSKROSTGWLTTIDPILVLAHRYRSPLVOIYEFEDGHKIETWREIY
LOGCERPLYSISPHOSLFEAVYTLIKHRIHRLPVLDPSGNYLHILTHKRLLKFLHIP
GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRNSALENVUNEGGY
VGLYSREDVTHLAAQOTYHHLDMSVGEALRKRTLCLEGGYLGCOPHESLGEVIDRIARB
QVHRLVLVDFTQHLLGVYSLSDILGAAVLSPAGIDPSGPEKI"
674 C 017 9 498 L
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SSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEATFPKTTPLAQA
DPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2290)
                            967. .1091
/note-"match to EST AA043371 (NID:g1521226) zk53e10.rl"
967. .1090
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AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
  962. .1084
/note="match to EST AI656812 (NID:g4740791) tt54b06.x1"
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                                                                                                                                                                                                                                                                                           1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 ONN, UNITED KINGDOM
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                                                                                                           /note="gimilar to Homo sapiens EST BI114348 (NID:g14565249)" 967. .1085
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                                                                                                                                                                                                    Query Match 100.0%; Score 61; DB 9; L
Best Local Similarity 100.0%; Pred. No. 4.1e-10;
Matches 61; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Carling, D.
Direct Submission
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                                                                 'note" match to EST A1670836 (NID:94850567) wa04g10.x1"
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281. .344
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281. .344
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/note="match to EST BI059713 (NID:g14467240)"
594. .763
                                                                                                                                                        /note="match to EST BG470047 (NID:g13402322)"
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                       to EST BE908408 (NID:g10402954)"
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/note="Similar to Homo sapiens EST BI114348
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/note="match to EST AA043371
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3. .37
/note="match
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and Andersson, L. A mutation in PRKAG3 associated with excess glycogen content in pig
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GPPGFREGPGSRPVAESTGGEAFPERAPLAAAPLAEVDNPPFTEDILPSDCAASAS
GPPGFREGPGSRPVAESTGGEAFPERAPCPSPEULPRIGMODELGREGAVYM
FROMGEHTCVDAMATGSKLVIFDPMLEIKKAFPELVARGVRAAPLMOSKKOSFVGMLTI
TDFILVLHRYTRSPLVQIYEIEBHKIETWRAFTLQGCFKFLVSISPNDSKGOSFVGMLTI
TDFILVLHRYTRSPLVQIYEIEBHKIETWRAFTLGFLLAFSFLVRIGOTGGGFFRDL
AVVEFAPILTALDIFVDRAVSALPVVNSTGGYPKHLLOMNY
GEALRQRFLLCLEGYLSCOPHETLGEVIDRIVREQVHRLVLVDFTQHLLGVVSEISDILQ
                                                                                                                                                                                                                                                  Z. (bases 1 to 1873)
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A.,
Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden
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                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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/protein_id="AAF73988.1"
/db_xref="GI:8215684"
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Pred. No. 7.2e-06;
0; Mismatches 8; Indels 0
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Science 288 (5469), 1248-1251 (2000)
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from Patent W00120003.
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/db_xref="taxon:9823"
/chromosome="15"
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Local Similarity 86.9%;
les 53; Conservative
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Best Local Si
Matches 53,
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mRNA, complete cds.
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ISPNDSLEEAVYALIKNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLRRPSFL
YRTIQDLGIGTFRDLAVLETAPILTALDIFVDRRYSALPVNETGGVYGLTSRRDVI
HLAAQQIYNHLDWYSLSDILQFYLCEGVLSCQPHFTLGEVIDRIYREQVHRLVLVDF
TQHLLGVVSLSDILAALULDAALULBAALDAALGA"

583 c 529 g 375 t
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/db_xref="G1:13538809"
/translation="MHFWQEHTCYDAWATSSKLVIFDTMLEIKKAFFALVANGVRAAP
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Mammalia, Eutheria, Cetartiodactyla, Suina, Guidae, Sus.
1 (bases 1 to 1867)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            same, and uses thereof
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT MATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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              Score 57.8; DB 9; Length 2290;
Pred. No. 4.1e-09;
0; Mismatches 2; Indels 0.
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                94.8%;
96.7%;
            Query Match 94.8
Best Local Similarity 96.7
Matches 59; Conservative
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Sus scrofa
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/db_xref="G1:21261107"
/tb_xref="d1:21261107"
/translation="MSFLEGGESRSWPSRAVTTSSERSHGDGGNKASRWTRQEDVEEG
GPFGGPREGFREGFPFRATPLAQAAPLAEVDNPPTERDILESDCAASAS
DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPFLGWDDELGKPGAQVYM
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 1 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
                                                                             Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof Patent: WO 0120003-A 27 22-MAR-2001; INSTITUT NATIONAL DE A RECHERCHE AGRONOMIQUE (INRA) (FR); Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE) Location/Qualifiers
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            1 (bases 1 to 1873)
Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Pred. No. 7.2e-06;
0; Mismatches 8; Indels 0
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KNRTHRLPYLDPVGGAVLHILFHKRLIKFLHFGTLLPRFSFLYRTJQDLGIGTFRDL
AVVLEFTAPILTALDIFVDRRYSALPVNETGQVVGLYSRFDVIHLAAQQYYNHLDMNV
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220860-A 3 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
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Pred. No. 7.2e-06;
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220854.A 5 14 MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 7 14 *MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location, Qualifiers
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Sequence 5 from Patent WO0220850.
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/db_xref="taxon:9823"
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Pred. No. 7.2e-06;
0; Mismatches 8
                                               /protein_id="CAD32628,1"
/db_xref="G1:21261113"
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86.9%;
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6198.732 Million cell updates/sec
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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61
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	PRKAG3 intron 2 -	PRKAG3 CDNA. HOMO	Human AMPK gamma s	Human AMPK gamma s	Piq AMPK gamma sub	Pig AMPK gamma sub	Pig wild-type PRKA	Pig PRKAG3 polymor	Pig PRKAG3 polymor
SUMMARIES			ID		AAH43685	AAD03296	AAD03320	AAD03295	AAD03319	AAD36456	AAD36457	AAD36458
			DB	22	22	22	22	22	22	24	24	24
			re Match Length DB I	686	1647	2109	2115	1867	1873	1873	1873	1873
	æ	Query	Match	100.0	100.0	100.0	100.0	79.0	79.0	79.0	79.0	79.0
			Score	61	61	61	61	48.2	48.2	48.2	48.2	48.2
		Result	No.	1	7	e	4	S	9	7	80	6

/*tag- d /number= "Exon 4" 946..989 /*tag= e /number= "Intron 4"

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C	112	າທ	41.6	ш		AAV30458	Rhizohium species
Ü	18	വ	41.6	u)		AAV30459	Rhizobium species
O	19	25	41.0				Pseudomonas aerugi
	20	24.8	40.7				Human polynucleof1
	121	24.8	40.7				Human polynucleoti
	770	24.0	40.7				UNA encoding novel
	24	24.4	40.4				numan lung speciil
	25	24.4	40.0				Phytase dene. Asp
	56	24.4	40.0				A. terreus phytase
	27	24.4	40.0				Drosophila melanog
(80 60	24.4	40.0				Drosophila melanog
o (ر د د د	2.4.2	20.7				DNA encoding novel
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O	32	24.2	39.7				DNA encoding novel
υ	33	24.2	39.7				Human peptidase NA
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υ .	41	24.2	39.7			AA258307	n peptida
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AAH	AAH43682						
₽\$	AAH43682		standard;	DNA;	989	BP.	
AC A	AAH43682	3682;					
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3	PRKAG3	33 intron	on 2	- introp	4		
X XX	Human	AMI	activ	ated pro	tein	kinase gamma 3 subupit:	DRKAG3. variant.
K.	metabo	lic	disease; di	e; diabetes;	tes;	obesity; substitution; d	
SO	Homo	sapiens	18.				
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F				/number=		"Intron 3"	
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/note= "Causes P71A"
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            variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCGTTCATGCAGGA 60
                                                                                                                                                                  New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                   encoding the human AMP-activated protein kinase gamma 3 subunit (PRRAG3) DMA. Or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a glora c at nucleotide 320, resulting in the amino acid substitution P71A, in exon 4 variation may be a substitution of a substitution of a T for a c at nucleotide 550; and in exon 10 variation may be a substitution of a resulting in the amino acid substitution of a T for a C at nucleotide 50; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 61; DB 22; Length 989; 100.0%; Pred. No. 1.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
/note= "5' portion of intron 4"
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                            Marklund S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH43685 standard; cDNA; 1647 BP.
                                                                                                                                                                                                                       Example 1; Fig 2; 25pp; English.
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/label= "C230G"
                                                             06-APR-2001; 2001WO-SE00765.
                                                                                 07-APR-2000; 2000US-195665P.
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                                                                                                                            Andersson L, Luthman H,
                                                                                                                                                                                                                                                                                                                                                                                                                      61; Conservative
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                                                                                                                                               WPI; 2001-657170/75.
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                     WO200177305-A2
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This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining to a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, cresulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, cresulting in the amino acid substitution R340M. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on constitution 1 of the open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gamma subunit; adenosine monophosphate-activated kinase; AMPR;
PRRAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
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100.0%; Pred. No. 1.7e-12;
tive 0; Mismatches 0;
                                         /note= "Silent variation"
1037
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/label= "C1037T"
/note= "Causes R340W"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 5; 25pp; English.
/*tag= c
/label= "T559C"
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Best Local Similarity 100.
Matches 61; Conservative
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9

Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA,

(first entry)

13-JUN-2001

AAD03320;

AAD03320 standard; cDNA; 2115 BP.

RESULT 4 AAD03320

489 G 489

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The present sequence is a cDNA encoding human adenosine monophosphate (AMP) damma subunit muscle-specific isoform, prkRAG3. Mutation in PrkRAG3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders associated with muscle metabolism cardiovascular diseases, to modulate AMPK cuchity, and for restoring a normal AMPK function. PRKAG3 sequence activity, and for restoring an normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Dreferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3 are useful for detecting adsyluction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rogel-Gaillard C;
genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
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Le Roy P, Chardon P;
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/product= "Human Prkag3 protein"
1390..2109
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 2; 71pp; English.
                                                                                                                                                                                                                                                                                                                        11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                         10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
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472..1389
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                                                       Homo sapiens
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5'UTR
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The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                        Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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J, Le Roy P, Chardon P;
                                                                                                                                                                   cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                               /product- "Human complete Prkag3 protein"
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(ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 65-68; 71pp; English.
                                                                                                                                                                                                                                        Location/Qualifiers
1..1395
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18-MAY-2000; 2000EP-0401388.
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1 GGGCTGGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA

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Gaps

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100.0%; Score 61; DB 22; Length 2109; 100.0%; Pred. No. 1.8e-12; ive 0; Mismatches 0; Indels 0.

61; Conservative

Similarity

Query Match

Best Local

Matches

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Best Local (
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                                                                 1 GGGCTGGGATGACGAAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                             PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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Chardon P;
                                         Gaps
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                                                                                                                                                                                                                    gamma subunit; adenosine monophosphate-activated kinase; AMPK;
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                          Length 2115;
                                                                                                                                                                                                      Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                         Indels
       Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
                                                                                                                                                                                                                                                                                                                                 scrofa PRKAG3 protein"
                       Score 61; DB 22;
Pred. No. 1.8e-12;
0; Mismatches 0;
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J, Le Roy F
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1390..1867
/*tag= c
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                        100.0%;
100.0%;
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18-MAY-2000; 2000EP-0401388.
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472..1389
                                                                                                                                                                                     (first entry)
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                                Similarity 100.
61; Conservative
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                                                                                                                                                                                                                                                        chromosome 15; ss.
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                        Query Match
Best Local 3
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5'UTR
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Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as the constitution of the carbohydrate metabolism disorders associated with muscle metabolism cativity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered antents are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting cuseful for detecting a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
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Pred. No. 7.6e-08;
0; Mismatches 8; Indels 0;
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86.9%;
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(IOWA ) UNIV IOWA STATE RES FOUND INC
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               replace (595, A
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86.9%;
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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Quest Local Similarity 86.>>,
Best Local Similarity 86.>>,
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                                                                                                                                                                                            The present sequence is a cDNA encoding pig adenosine monophosphate (AMPY) activated kinhase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PKRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK and cardiovascular diseases, to modulate AMPK and its function PKRAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                        preferably a carbohydrate metabolism disorder. Primers that can detect preferably a carbohydrate metabolism disorder. Primers that can detect useful for detecting a dysfunction of a sequence encoding PRRAJ are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally attered allele of PRRAJ are reasonic animal and host cell transformed with PRRAJ or a heterotrimeric AMPK consisting of PRRAJ or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAJ is useful for detecting mutations in a Prkaj gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
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                                                                  New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.0%; Score 48.2; DB 22; Length 1873; 86.9%; Pred. No. 7.6e-08;
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                                                                                                                                                          Claim 12; Page 62-64; 71pp; English.
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                   WPI; 2001-244810/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; ds.
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                                                                                                                          myopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
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g δy g

Qγ

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'standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                 /*tag= e
/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype kinase regulatory gamma subunit (FRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is pig wild-type PRKAG3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rothschild MF, Ciobanu DC, Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48.2; DB 24
Pred. No. 7.6e-08;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
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1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                     Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
                                                                                  /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
                                                  "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.0%; Score 48.2; DB 24; Length 1873; 86.9%; Pred. No. 7.6e-08; Live 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                          Rothschild MF, Ciobanu DC, Malek M, Plastow G;
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     Location/Qualifiers
                                                                 replace (154, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD36459 standard; DNA; 1873 BP.
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                             10-SEP-2001; 2001WO-US28283.
                                    /*tag* a
/product= '
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                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAE22986.
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                                                                  variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                                  Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                              /*tag- a
/product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
replace (89, C)
                                                                                             /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMP activated protein kinase regulatory gamma subunit, PRKAG3 gene, screening; meat quality, single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 24; Length 1873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                       Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
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86.9%; Pred. No. 7.6e-08;
tive 0; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 89-91; 109pp; English.
                                                                                                                                                                                                                                                                                       (IOWA ) UNIV IOWA STATE RES FOUND INC.
Location/Qualifiers
1..1395
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                                                                                                                                                                                                                       08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                                                                                                                     Rothschild MF, Clobanu DC,
                                                                                                                                                                                         10-SEP-2001; 2001WO-US28283.
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Best Local Similarity 86.99,
Best Local Similarity 86.99,
Conservative
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                                                                                                                                                           14-MAR-2002
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                                                               variation
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AAD36458
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The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., plays to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is plg PRKAG3 polymorphic variant DNA (PRKAG3-200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                      "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
                                                                                                                                                                                                                                                                                                                                                                                                                 Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                    /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48.2; DB 24; Length 1873;
Pred. No. 7.6e-08;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    Rothschild MF, Ciobanu DC, Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 102-104; 109pp; English.
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     Location/Qualifiers
1..1395
                                                                    replace (599, A)
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86.9%;
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                                                    /product=
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Best Local Similarity 86.9
Matches 53; Conservative
                                       /*tag=
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                                                                      variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCCTTCATGCAGGA 60
                                   /*tag= a /*tag= a /*tag= prkAG3 polymorphic variant (PRKAG3-199)" /*product= "Pig PRKAG3-199)" /*tag= b /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                 Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                    /standard_name= "Single nucleotide polymorphism (SNP)"
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Pred. No. 7.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 98-100; 109pp; English.
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Location/Qualifiers
1..1395
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86.9%;
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                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                   WO200220850-A2
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                                                                    variation
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9

Gaps

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8; Indels

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cDNA sequence encoding a Ste20-related protein kinase called SMAK.
                                                  20-DEC-2000 (first entry)
              AAA64328;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                               New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                            Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of Chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              evaluation, genetic testing and prognosis of a metabolic disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48.2; DB 22; Length 2022;
Pred. No. 7.7e-08;
0; Mismatches 8; Indels 0;
                                                               "Sus scrofa Prkag3 splice variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                         (INRG ) INRA INST NAT RECH AGRONOMIQUE.
              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.08;
                                                                                                                                                                      11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                      10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                  /product=
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Matches 53; Conservative
                                1..1545
                                                  /*tag=
                                                                                                                                                                                                                                                                           ANDERSSON L.
LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                            2001-244810/25.
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                                                                                                                                                                                                                                                                                                                                            Andersson L, L
Iannuccelli N,
                                                                                                                                                                                                                                                                                                         (KALM/) KALM E.
                                                                                                   WO200120003-A2
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The present sequence encodes a murine Ste20-related protein kinase designated SMAK. SMAR is a caspase activated protein kinase. SMAR activates 2 signalling pathways that are involved in mediating apoptosis. It also mediates actin stress fiber dissolution through caspase-3-cleavage and functions to activate the stress activated protein kinases (cjun-amino terminal kinase (JMK) signalling pathway). SWAK proteins and polynucleotides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate SMAK expression. The SMAK polypeptides may be used as antigens in the production of antibodies, and in assays to identify modulators (agonists and antagonists) of SMAK expression and activity. The SMAK protein is associated with apoptosis and may play a role in preventing neoplasia development, lymphoproliferative conditions, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding a Ste20-related protein kinase designated SMAK, useful for the prevention, diagnosis and treatment of neoplasia development, lymphoproliferative conditions, inflammation, ischemia or
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Mouse; Ste20-related protein kinase; SWAK; caspase-3-cleavage; caspase activated protein kinase; apoptosis; neoplasia development; actin stress fiber dissolution; lymphoproliferative condition; inflammation; ischemia; stroke; autolmmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 ATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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tive 0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                                       /*tag- a
/transl_except= (pos: 4..5, aa: Ser)
/transl_except= (pos: 1373..1376, aa: Xaa)
/product= "SMAK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Xaa is the termination codon"
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56..3674
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ID AA199683 standard; DNA; 4403765 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0120784.
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nes 36; Conserv
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AAA64328 standard; cDNA; 5259 BP.

AAA64328 ID AAA6

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variation; epidemiology; patient treatment; epidemic monitoring; ds
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                                                                                                                                                                                       Fleischmann RD,
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                                                      US6294328-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AN199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                              Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC
                                                                                         Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds.
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                                                                Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
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                                                                                                                                                                                                                                                                                           Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25.8;
Pred. No. 33;
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                                                                                                                                Mycobacterium tuberculosis.
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                                     (first entry)
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Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      1551 and H37Rv differ
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            AAI99683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen.
Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 151 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37RV differ -
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                                                                                                                                                                                                                                                                                                                                                                                            Fraser CM,
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Mycobacterium tuberculosis.
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les 39; Conservative
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BHI40228 ZAMBBD000
BHI40268 VAMBBD000
BHI40663 ZAMBBD000
BHI906421 ug/6bl1.y
BG918873 ug/6bl1.y
BG918873 ug/6bl1.y
BRC51383 TRESF2Z54
ALZ40746 TETRACCOURT
W6455 aZG3603.r1
BH6468546 AGENCOURT
W6459 ZAG3603.r1
BH646856 (01 r4.BH3-BL51609) RH45605.5
BI537568 416137 MA
ARAB8804 UT.M-BH3-BL51609) RH45605.5
BI537568 416137 MA
ARAB8804 UT.M-BH3-BL51609 RH25605.2
BH773519 CMZ-TT003
BF135856 601782168
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BF13680346 EST504391
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BF255789 209720 MA
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
'G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 402 762 436
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
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291826 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF890374.1 GI:12281760
EST.
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PO Box 166, Clay Center, NE 68933-0166, USA
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        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Minimum DB seq Maximum DB seq

Database

Perfect score:

Sequence:

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Scoring table:

Searched:

EST 25-APR-2001

bovine cDNA

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Score

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JOURNAL
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KEYWORDS
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Sequence evaluation of four pooled-tissue normalized bovine cDNA
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v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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Mammalia; Eutheria, Cetartiodactyla; Ruminantia; Pecora, Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                /note-"Vector: pcMv SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimas muscle."
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467815 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BI775360
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No Box 16c, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4390
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                                                                                                                                                                                                     /db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 57 row: H column: 11
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                   /organism="Bos taurus"
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/clone_lib="MARC 2BOV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 685)
Sarakawa T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Oklod, T., Saito, R., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M., and Hayashizaki, Y.
RIKBN Mouse ESTs (Arakawa, T., et al. 2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encyclopedia: real-time sequence clustering for construction of a nonredundant cons library. Genome Res. . 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P.. Shibata,Y., Hayatsu,W., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB630381 EST 26-OCT-2001 BB630381 RIKEN full-length enriched, 6 days neonate skin Mus musculus cDNA clone A030014A04 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fel: 81-45-503-9226
Fex: 81-45-503-9216
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/note-"Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGCIGGGAIGACGAACIGCGGAAACCCGGCGCCCAGAICIACAIGCGCIICAIGCAGGAG
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Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                      Score 45.6; DB 13; Length 548;
Pred. No. 3.4e-05;
0; Mismatches 9; Indels 0
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85.0%;
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Gaps ö

Indels

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This sequence is a single read and was generated as part of a large scale cione-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorapha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon
1 (bases 1 to 1010)
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Tetraodon nigroviridis DNA sequence
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Rost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Welssenbach, J.

Charaterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
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/clone_lib="delocope sequence ID : COAGI63AD09LPl~end : T?"
/note="Genoscope sequence ID : COAGI63AD09LPl~end : T?"
263 c 305 g 160 t 3 others
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                                                                                                                                                                                                                                                        DB 17; Length 910;
genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
/clone="005N22"
                                                                                 /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="163G17"
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Pred. No. 49;
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1. .1010
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Submitted (12-APR-2000)
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                           /note="$ite_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Encyclences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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                                                           /clone="A030014A04" /clone_lib="RIKEN full-length enriched, 6 days neonate
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/lab_host="DH10B"
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                   /organism="Mus musculus"
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                                       /db_xref="taxon:10090"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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1 others

us-09-826-581-5_copy_529_589.rst

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Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93 Library for gene discovery and sequence-ready map construction Unpublished (1999)
Other GSSs: RPCI93-ECORI-4113.TV
Contact: Najib M. El-Sayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS 08-JUL-1999
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                                                Orgriss latipes
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygi; Neopterygi; Feleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Bloniformes; Adrianichthyldae; Oryzinae; Oryzias.
I (bases 1 to 581)
Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
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RPC193-ECORI-4113.TJ RPC193-ECORI Trypanosoma brucei genomic clone RPC193-ECORI-4113, DNA sequence.
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Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences search
page: http://www.tigr.org/tdb/mdb/tbdb/.
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
                                                                                                                                                                                                                         Unpublished (2001)
Contact: Tadasus Ahn.i
Contact: Tadasus Ahn.i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fat: 81-559-81-6856
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235 c 119 q 91 + ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MF01SSA076B04"
/clone_llb="WR01SSA_0DN"
/sex="mixture of female and male"
/tissue_type="whole embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryzias latipes"
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43.9%; Score 26.8; Di
Best Local Similarity 73.9%; Pred. No. 71;
Matches 34; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. 581
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AQ641446.1 GI:5118156
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Trypanosoma brucei
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Fax: 301 838 0208
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                              BG394974 11-MAR-2001 602457369F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4579696 5',
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                                                                                           /note="Organ: eye; Vector: poTBJ; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcorIX/XhoI sites using the following 5' adaptor: GCCACGAGGG. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                  1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 95)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arayed by: The 1.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLMA1297 row: j column: 17
High quality sequence stop: 717.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                         21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
65.6%; Pred. No. 50; tive 0; Mismatches
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:4579696"
/clone_lib="NIH_MGC_16"
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67.98;
Best Local Similarity 65.6
Matches 40; Conservative
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BJ005207
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Best Local Similarity
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI606158 349 bp mRNA linear EST 21-APR-1999 vol5c02.xl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1049954 3', mRNA sequence.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 349)
Marra,M., Hillier,L., Rucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person, B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer adapter of sequence [5' GAGAGAGAGATTCTCCACCCCCCCC 3']. CDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                      encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GCTGGGATGACGAACTGCGGAAACCCGGCGCCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="B020024106"
/clone_lib="RIKEN full-length enriched, 2 cells egg"
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                   Computer-based methods for the mouse full-length cDNA
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ive 0; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="egg"
/dev_stage="2 cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .248
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Matches 38; Conservative
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                                                                                                                                                                                                                                                                                         e mouse tissues.
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                                                                                                                                                                                                                                          Bohui Zhao in Pieter de Jong's laboratory (Roswell Brix
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
Drucei TREU927/4 GUTat 10.1 agarose embedded DNA was
partially digested with a combination of Eco RI and Eco RI
methylase (RPC193-EcoRI segment) or Dpn II (RPC193-DpnII
segment). High molecular weight fragments were ligated in
pBACe3.6 vector digested with Eco RI or Bam HI,
respectively. The average insert size is 141 Kb. Total
coverage (both segments): > 90 X the haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 248)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Iloh, K., Kawal, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Sakau, C., Sakai, K., Shawaxama, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Taqawa, A., Takahashi, F., Takaku, Akahiraka, Y., Turaru, Y., Yasunishi, A., Wartahiki, A., Yasunishi, A., Wanamatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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URt.http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Haytsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                          /clone="RPC193-EcoR1-4113"
/clone="RPC193-EcoR1-4113"
/clone="The-"RPC193-EcoR1"
/clone="The-Tree of the Computer of the Computer of the Computer of the Computer of the Computer of the Computer of the Computer of the Comp
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
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                                     /organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 c
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Best Local Similarity 65.0
Matches 39; Conservative
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Zea mays.
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AW024446
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                                                                                                                                                                                                                                                                                                                                                   3'); double-stranded cDNA was ligated to ECC RI adaptors [AATTCGGATCCTTG], digasted with Not I and cloned into the Not I and ECC RI sites of the modified pT713 vector. Library constructed by Bob Barstead. The CZC12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins.
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ZMMBBb0001L18f Maize B73 Zea mays genomic clone ZMMBBb0001L18f, DNA
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1 (pases 1 to 580)

Tomkins, J. P., Main, D., Golcoechea, J. L., Frisch, D. A. and Wing, R. A. A Deep-Coverage BAC Library for Maize
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                          /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI: Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                  This clone was previously sequenced on the 5' end only, this new
IMAGE Consortium (info@image.llnl.gov) for further information. MGI:581530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
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                                                                                                                                                                                         /clone="IMAGE:1049954"
/clone_lib="Parstead mouse myotubes MPLRB5"
/cell_line="C2C12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.6%; Score 26; DB 9; Length 349
65.5%; Pred. No. 1.2e+02;
ative 0; Mismatches 20; Indels
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100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                          data is from the 3' end
High quality sequence stop: 326.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 71
High quality sequence stop: 510.
Location/Qualifiers
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/clone_lib="Maize B73"
                                                                                                                                                                               /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 864 656 7288
Fax: 864 656 4293
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ZMMBBD0002L18f Maize B73 Zea mays genomic clone ZMMBBb0002L18f, DNA
/tissue_type="Young leaves"
//ab host="E. col!"
//ab host="Yector: pcUGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation, ordering clones
and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genome.clemson.edu/projects/stc/maize/2MABBb " 222 c 150 g 151 t
                                                                                                                          http://www.genome.clemson.edu/projects/stc/maize/ZMAMBBb "
221 c 138 g 146 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 593)
Tomkins, J.P., Malin, D., Golcoechea, J.L., Frisch, D.A. and Wing, R.A.
A Deep-Coverage BAC Library for Maize
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                   1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAG 58
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                                                                                                                                                                                                                                Length 580;
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Pred. No. 1.3e+02;
0; Mismatches 20;
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Pred. No. 1.3e+02;
0; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/lab_host="E. coli"
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
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/clone="ZMMBBb0002L18f"
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Location/Qualifiers
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/strain="B73"
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Best Local Similarity 65.5%;
Matches 38; Conservative
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Matches 38; Conservative
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/note="Vector: pr773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded con with a Co RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 738)
Unpublished (1997)
Context: Robert Strausberg, Ph.D.
Context: Robert Strausberg,
Enail: cgapber@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE_Consortium (info@image.llnl.gov) for further information.
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 ATGACGAACTGCGGAAACCCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAG
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/clone_lib="NRI_CARP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10899 row: p column: 20
                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_mammary_gland_NMLMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.3%; Score 25.8; DB 10;
Best Local Similarity 67.9%; Pred. No. 1.6e+02;
Matches 36; Conservative 0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                         /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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                                                                                                                            MGI:953633
Seq primer: -40RP from Gibco
High quality sequence stop: 472.
                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:1548285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: WWW-bio.llnl.gov/bbrp/image/image.html
Insert Length: 878 Std Error: 0.00
Seq primer: -400PF from Gibco
High quality sequence stop: 394.
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AW024446 648 bp mRNA linear EST 09-MAR-2000 wu76d09.xl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2525969 3' similar to TR:043176 043176 PEPTIDASE HOMOLOG ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Another Torgan: Kidney; Vector: pT773D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 64) http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Emali: cgapbz-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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AW024446.1 GI:5877976
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Unpublished (1997)
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MICOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN ANALYSIS IN MYCOBACTERIUM
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US-09-027-337-9

US-09-644-600-9

US-09-395-6748-5

US-08-943-731-5

US-08-943-731-5

US-08-774-0258-3

US-09-244-093-3

US-09-244-093-4

US-09-244-093-4

US-09-244-093-4

US-09-244-093-4

US-09-044-131-34

US-08-044-131-34

US-09-044-718-13

US-09-044-718-13

US-09-044-718-13

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US-08-285-586-14

US-08-283-696-14

US-08-283-696-14
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Pred. No. 7.4;
0; Mismatches
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US-09-103-840A-2/C
| Sequence 2, Application US/09103840A
| Patent No. 6294328
| GENERAL INFORMATION:
| APPLICANT: FLEISCHANN, ROBERT D.
| APPLICANT: FLEISCHANN, ROBERT D.
| APPLICANT: WHITE, OWEN R.
| APPLICANT: WHITE, OWEN R.
| TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN |
| TITLE OF INVENTION: TUBERCHOSTS
| TITLE OF INVENTION: TUBERCHOSTS
| TITLE OF INVENTION: UNBER: US/09/103,840A
| CURRENT FILING DATE: 1998-06-24
| CURRENT FILING DATE: 1998-06-24
| SEQ ID NOS: 2
| SEQ ID NOS: 2
| SEQ ID NOS: 2
| SEQ ID NOS: 2
| SEQ ID NOS: 2
| SEQ ID NOS: 2
| SEQ ID NOS: 2
| SEQ ID NOS: 3
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ORGANISM: Mycobacterium tuberculosis
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US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
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63.9%;
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OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
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Matches 39; Conservative
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4027.262 Million cell updates/sec
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Sequence 1, A
Sequence 1, A
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Sequence 1
Sequence 3
                                                                                                                                                                        June 13, 2003, 02:39:09; Search time 4.64516 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-103-840A-1
US-09-5148-914-3
US-09-518-914-3
US-09-518-914-3
US-08-804-128-1
US-08-993-359-23
US-08-993-358-1
US-08-362-670B-27
US-08-362-670B-27
US-08-362-670B-27
US-08-362-670B-27
US-08-362-670B-27
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US-08-449-699A-4
US-08-449-699A-4
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US-08-377-292-2
US-07-679-451-1
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61
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Score

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Result No. Gaps

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Pred. No. 5.2;
0; Mismatches 11; Indels
         Best Local Similarity 73.8%; Pred. No. 5.2;
Matches 31; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                   822 ACCAGCTGCGAGATCTGGGCGCCCAGTTCTACGAGCGCTACA 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              822 ACCAGCIGCGAGAICIGGGCGCCCAGIICIACGAGCGCIACA 863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
OCMPOTHER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
join(374..420, 469..1819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New Jersey COUNTRY: United States of America ZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                               E: Hoffmann-La Roche Inc.
340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-ARR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-518-914-1
; Sequence 1, Application US/09518914
; Patent No. 6413731
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhlani, Parul P.
; APPLICANT: Adham, Nika
                                                                                                                                                                                                            US-08-744-231-1; Sequence 1, Application US/08744231; Patent No. 6358722; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.0%;
Best Local Similarity 73.8%;
Matches 31; Conservative C
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; LOCATION:
US-08-744-231-1
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                  1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                         Query Match 42.3%; Score 25.8; DB 4; Length 4411529; Best Local Similarity 63.9%; Pred. No. 7.4; Matches 39; Conservative 0; Mismatches 22; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.0%; Score 24.4; DB 4; Length 2327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTON: POLYPEPTIDES WITH PHYTASE ACTIVITY
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07110
COMPUTER READABLE FORM:
WEDLIN TYPE: Ploppy disk
WEDLIN TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VEF. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(374..420, 469..1819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Hoffmann-La Roche Inc. STREET: 340 Kingsland Street
                                                                                                                                                                                    ; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/744,231
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08868435 Patent No. 6291221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (201) 235-4205
TELEPAK: (201) 235-2363
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2327 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                        LENGTH: 4411529
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US-08-868-435-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-868-435-1
                                                                                                                                                               TYPE: DNA
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DB 2; Length 44377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 23.2; DB
; Pred. No. 26;
0; Mismatches
                                      COMFUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
SOFTWRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: FEBRUARY 21, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/08804198; Patent No. 5945320; GENERAL INFORMATION:
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.0%;
70.5%;
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 70.59
Matches 31; Conservative
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36155..41830
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14046..20036
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20110..31284
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31329..36071
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350..14002
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                                                                                                                                                                 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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; LOCATION:
US-08-804-227C-7
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GENERAL INFORMATION:
APPLICANT: Borowsky, Beth E.
APPLICANT: Ogozalek, Kristine L.
APPLICANT: Ogozalek, Kristine L.
APPLICANT: Hakhan, Parul P.
APPLICANT: Adham, Nika
TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
FILE REFERENCE: 59138-AJPW
CURRENT APPLICATION NUMBER: US/09/518,914
CURRENT APPLICATION NUMBER: US 09/303,593
EARLIER APPLICATION NUMBER: US 09/303,593
EARLIER FILING DATE: 1999-05-03
NUMBER FOR SEQ ID NOS: 44
SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.4%; Score 23.4; DB 4; Length 1508; Best Local Similarity 67.3%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.4%; Score 23.4; DB 4; Length 1541; 67.3%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                               0; Mismatches 16; Indels
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APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                 FILE REFERENCE: 59138-A/JPW
CURRENT APPLICATION NUMBER: US/09/518,914
CURRENT FILING DATE: 2000-03-03
EARLIER APPLICATION NUMBER: US 09/303,593
EARLIER FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 1508
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Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: LILLY CORPORATE CENTER CITY: INDIANAPOLIS
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US-09-518-914-3
; Sequence 3, Application US/09518914
; Patent No. 6413731
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Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                               33; Conservative
                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-09-518-914-1
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ORGANISM: Homo sapiens
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ZIP: 46285
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                                                                                                                                                                                                        TYPE: DNA
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ADDRESSEE: No. 60602980 No. 6060298disk of No. 6060298th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
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COMPUTER: ITEM Compactible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,358A
FILING DATE: 12-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR PAPLICATION WINDER: 1481/96
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: 05-29/97
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 35-127
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35-127
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APPLICANT: Fuglsang, Claus
APPLICANT: Onmann, Anders
APPLICANT: Operann, Anders
APPLICANT: Ostergaard, Peter
TITLE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      35,127
ER: 5101.200-US
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                                                FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A
REGISTRATION NUMBER: 35,127
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                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1320 base pairs TYPE: nucleic acid STRANDEDNESS: single
   12-DEC-1997
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APPLICANT: Lassen, Soren
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MEDIUM TYPE: Diskett
FILING DATE: 12-DEC APPLICATION NUMBER:
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SOFTWARE: RAALSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,654
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APPLICANT: LASSEN, SOFEN
APPLICANT: Bech, Lisbeth
APPLICANT: Puglsang, Claus
APPLICANT: Offnann, Anders
APPLICANT: Ostergaard, Peter
ITLE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/804,198
                           ETLING
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: 99113
TELEPOMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
; INFORMATION FOR SEQ ID NO: 1:
SEQUIENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
; TYPE: nucleic acid
"TYPE: nucleic acid
"TYPE: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,358
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Patent No. 6054306
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14046..20036
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36155..41830
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Best Local Similarity 70.55
Matches 31; Conservative
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31329..36071
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LOCATION: 350..14002
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MEDIUM TYPE: Diskett
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FEATURE:
NAME/KEY:
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LOCATION:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
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135 GGCTGGGATGAGGGGCGGCCGACGACGCCGCGCAACATTCTGCGCCCCA 83
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tive 0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:

ZIP: 02140
COMPUTER: BOALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIN FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,670B
FILING DATE: December 22, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFESTENCE/DOCKET NUMBER: 5202-D
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
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TELEPOMMUNICATION FOR $20
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CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
CLONE: peptide
                                                                                                                            APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wozney, John
APPLICANT: Wolfman, Neil
APPLICANT: Wolfman, Neil
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESSONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
   Sequence 27, Application US/08362670B Patent No. 5658882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/08333576C Patent No. 6027919 GENERAL INFORMATION:
                                                                                                 Celeste, Anthony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1233 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.09
Best Local Similarity 64.29
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..1233
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LOCATION:
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; LOCATION:
US-08-362-670B-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                    Score 22.8; DB 3; Length 1320;
Pred. No. 18;
0; Mismatches 17; Indels 0
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Pred. No. 18;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ostergaard, Peter R.
TITLE OF INVENTION: Phytase Polypeptides
FILE REPERENCE: 5382.500-02.
FILE REPERENCE: 5382.500-02.
FILE REPERENCE: 5382.500-02.
FILE REPERENCE: 5382.500-02.
CURRENT PILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 1480/96
EARLIER PILING DATE: 1996-12-20
EARLIER FILING DATE: 1996-12-20
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 0529/97
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-12-01
EARLIER FILING DATE: 1997-12-01
EARLIER FILING DATE: 1997-12-01
EARLIER FILING DATE: 1997-12-01
EARLIER FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 32
SOUTHARRE: FLASTSEQ for Windows Version 3:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08993359A Patent No. 6039942
                                                         INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                           37.4%;
66.0%;
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Best Local Similarity 66.0%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ohmann, Anders
APPLICANT: Breinholt, Jens
APPLICANT: Fuglsang, Claus C.
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.09
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Peniophora lycii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCATION: (123)...(1439)

NAME/KEY: sig_peptide

CCATION: (123)...(212)

NAME/KEY: mat_peptide

CCATION: (213)...(1439)

US-08-993-359-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lassen, Soren F.
APPLICANT: Bech, Lisbeth
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                         ; MOLECULE TYPE: CDNA
US-08-989-358A-1
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US-08-362-670B-27/c
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LENGTH: 1593
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US-08-993-359-23
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IBM PC compatible
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LOCATION:
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US-08-808-324-27
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.0%; Score 22.6; DB 3; Length 1233; Best Local Similarity 64.2%; Pred. No. 21; Matches 34; Conservative 0; Mismatches 19; Indels 0,
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INMEDIATE SOURCE:
CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
CLONE: peptide
                                                                                                             COMPUTER: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/333,576C
FILING DATE: No. 6027919ember 2, 1994
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: GREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: GENETICS INSTITUTE, INC
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/08808324 Patent No. 6284872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZEL, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/POCKET NUMBER: 5202-
TELEFONNE: 617 489-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Celeste, Anthony J. APPLICANT: Wozney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UDENCH: 1233 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: mat_peptide LOCATION: 847..1233
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STATE: Massachusetts
COUNTRY: USA
                                                                              CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS
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LOCATION: 1..1233
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STRANDEDNESS:
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US-08-333-576C-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GENETICS INSTITUTE, INC.
PRELICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding BMP2 propeptide/BMP-12 mature peptide
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-N0Y-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US94-14030A-27/c

Sequence 27, Application PC/TUS9414030A

; GENERAL INFORMATION:
                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
                                                                                                                                                                                                               5202-D
                                                                                  FILING DATE: Herewith CLASSIFICATION: 514
ATORNEYAGENT INRORMATION:
NAME: LAZAR, STEWON R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202
TELECHOME: 617 498 8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.0%;
64.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 37.08
Best Local Similarity 64.28
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              847..1233
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Sequence 6224, Ap Sequence 6227, Ap Sequence 67, Appl Sequence 2303, Ap Sequence 602, App

Sequence 934, Apple Sequence 1, Appli Sequence 27, Appli Sequence 4, Appli Sequence 1, Appli Sequence 3, Appli Sequence 476, Apple Sequence 476, Apple Sequence 2113, Apple Sequence 2113, Appli Sequence 330, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3118, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2166, Appli Sequence 21872, Appli Sequence 2600, Appli Sequence 79, Seguence:

Run on:

Searched:

Database

Sequence 31548, A Sequence 3, Appli

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Sequence 2. Application US/09826581

Fatent No. US20020142310A1

Fatent No. US20020142310A1

FAPLICANT: Andersson, Leif

APPLICANT: Luthman, L. Helger

APPLICANT: Marklund, Stefan

FILE REFERENCE: 11145-007001

CURRENT APPLICATION NUMBER: US/09/826,581

FRIOR PRING PAPLICATION NUMBER: US/09/826,581

FRIOR APPLICATION NUMBER: US/09/826,581

NUMBER OF SEQ ID NOS: 14

NUMBER OF SEQ ID NOS: 14

SOFTWARE FRASESEQ for Windows Version 4.0

LENGTH: 989
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US-09-738-626-934
US-09-738-626-934
US-09-738-626-1
US-09-945-182-27
US-08-957-425-4
US-10-073-961-476
US-10-073-961-476
US-09-952-360-1
US-09-952-360-1
US-09-952-360-1
US-09-952-360-1
US-09-995-360-1
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US-09-294-093B-79
US-09-918-995-31548
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Patent No. US20020142310A1
GENERAL INFORMATION:
APPLICANT: Anderson, Leif
APPLICANT: Luthman, L. Holger
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   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-2
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Matches 61; Conserv
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Sequence 1, Appli
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Sequence 12740, A
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Sequence 3, Appli
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                                                nucleic search, using sw model
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Result

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APPLICANT: Macina, Roberto A.
APPLICANT: Mair, Manoj
APPLICANT: Mair, Manoj
APPLICANT: Nair, Manoj
APPLICANT: Chen, Selyu
TILE ON INVERTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0214
CURRENT APPLICATION NUMBER: US/09/909,567B
FILMS APPLICATION NUMBER: 60/219,834
PRIOR FILING DATE: 2000-07-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.0%; Score 25; DB 10; Length 1473; 64.9%; Pred. No. 2.7; tive 0; Mismatches 20; Indels
                           APPLICANT: Trawitch John D.
APPLICANT: Trawitch John D.
APPLICANT: Annamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Tofaction of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
FRIOR APPLICATION NUMERR: 60/191,078
FRIOR APPLICATION NUMERR: 60/201
FRIOR APPLICATION NUMERS: 60/201
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-23
FRIOR APPLICATION NUMBER: 60/253,525
FRIOR APPLICATION NUMBER: 60/253,525
FRIOR FILING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/253,525
FRIOR FILING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/253,525
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2001-12-22
FRIOR FILING DATE: 2001-10-21
FRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
SEQ ID NO 114917
             Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 64.99
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(1473)
US-09-815-242-8004
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US-09-909-567B-11
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APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE RESERBERNE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT APPLICATION NUMBER: US 60/195,665
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR APPLICATION NUMBER: US 60/195,665
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5.
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APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARPOOGE
CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
PRIOR PELICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
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Pred. No. 3.1;
0; Mismatches 21;
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; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09939964; Publication No. US20030054522A1; GENERAL INFORMATION:
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Best Local Similarity 64.4%;
Matches 38; Conservative
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APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 100.0
Matches 61; Conservative
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Rhizobium
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APPLICANT: Pan, Juniang
APPLICANT: Pan, Juniang
APPLICANT: Soler-Ferran, Dulce
TITLE OF INVENTION: Method for Identifying Agents Which
TITLE OF INVENTION: Method for Identifying Agents Which
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
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TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
CURRENT APPLICATION NUMBER: US/09/931,381A
PRIOR PELILING DATE: 2001-08-15
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1244
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                                                                                                                                                         2 GGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 39.3%; Score 24; DB 10; Length 1244; Best Local Similarity 68.8%; Pred. No. 6.6; Matches 33; Conservative 0; Mismatches 15; Indels (
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILTE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILTE OF INVENTION: NUCLEIC ACIDS
CURRENT FILING DATE: 2001-01-17
Prior application darenewed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SEQ ID NO 166
LENGTH: 600
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                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09931381A, Patent No. US20020137107A1
GENERAL INFORMATION:
APPLICANT: Butcher, Eugene C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 166, Application US/09764864; Patent No. US20020132753A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kunkel, Eric J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-166
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) LOCATION: (5)...(1093)
US-09-931-381A-17
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ORGANISM: Homo sapiens
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US-09-764-864-166
US-09-898-751A-1
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                                                                                                                                                                                                                                                     TITLE OF INVENTION: Method for Identifying Agents Which
TITLE OF INVENTION: Modulate Chemokine "MEC"-Induced Functions of CCR3 and/or
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
CURRENT APPLICATION NUMBER: US/09/931,381A
PRIOR APPLICATION NUMBER: US. 09/638,914
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Hudak, Susan A.

APPLICANT: Homey, Bernhard

APPLICANT: Morales, Janine M.

APPLICANT: Morales, Janine M.

APPLICANT: McBley Lesite M.

APPLICANT: McBroy, Lesite M.

APPLICANT: DX0812M Albert

APPLICANT: DX0812M Albert

TITLE OF INVENTION: CHEMOKINE AND RECEPTOR USES; COMPOSITIONS; METHODS

FILE REFERENCE: DX0882XM

CURRENT APPLICATION NUMBER: US/09/898,751A

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: US60/115,570

PRIOR APPLICATION NUMBER: US60/113,858

PRIOR FILING DATE: 1999-05-27

PRIOR FILING DATE: 1999-12-24

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PATCHT NOS: 16

SOFTWARE: PATCHT NOS: 16

SSOFTWARE: PATCHT NOS: 16

SSOFTWARE: PATCHT NOS: 16

TENNOM: 100.1
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Pred. No. 6.5;
0; Mismatches 15; Indels
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                                                                       Sequence 19, Application US/09931381A
Patent No. US20020137107A1
GENERAL INFORMATION:
APPLICANT: Butcher, Eugene C.
APPLICANT: Runkel, Eric J.
APPLICANT: Pan, Juniang
APPLICANT: Soler-Ferran, Dulce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09898751A Patent No. US20020160024A1 GENERAL INFORMATION:
APPLICANT: Oldham, Elizabeth R. APPLICANT: Soto, Hortensia APPLICANT: Liu, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.3%;
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Best Local Similarity 68.89
Matches 33; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-931-381A-19
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LOCATION: (1)..(1086)
OTHER INFORMATION:
                                                 US-09-931-381A-19/c
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US-09-898-751A-1/C
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APPLICANT: BOCOWSKY, Beth E.
APPLICANT: Lakhani, Parul P.
APPLICANT: Lakhani, Parul P.
APPLICANT: Adham, Nika
TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
FILE REPREBENCE: 2013 - 4.0FW
CURRENT APPLICATION NUMBER: US/10/146,835
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US/09/518,914
PRIOR APPLICATION NUMBER: US 09/303,593
PRIOR FILING DATE: 1999-05-03
                                                                                               APPLICANT: BOTOWARY, Beth E.
APPLICANT: Gozzalek, Kristine L.
APPLICANT: Lakhlani, Parul P.
APPLICANT: Lakhlani, Natul P.
APPLICANT: Adhani, Natul P.
TILLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS; FILE REPERENCE: 59138-A/JPW
CURRENT APPLICATION NUMBER: US/09/518,914
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
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FERERAL INFORMATION:
APPLICANT: Mendrick, Donna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10146835; Publication No. US20030073167A1; GENERAL INFORMATION:
                          Sequence 1, Application US/10146835 Publication No. US20030073167A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1508
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 1541
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; ORGANISM: Homo sapiens
US-10-146-835-1
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US-09-917-800A-1694
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US-10-146-835-3
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                                                                                                                                                                                                                         APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Randar, Kin
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DEOSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
THER REPERENCE: 31138
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT APPLICATION DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51, Application US/09934868
Patent No. US20020137190a1
FEBERAL INFORMATION:
APPLICANT: Koffas, Mattheos
APPLICANT: CAGAS, Mattheos
APPLICANT: Schezle, Andreas J
APPLICANT: OGOM, James M
APPLICANT: OCOM, James M
APPLICANT: OCOM, James M
APPLICANT: ON TOWNER IN SCHEZLE, AND SENTING METHANOTROPHIC BACTERIAL STRAIN
FILE PREPRENCE: CLIS96 US NA
CURRENT PELING DATE: 2001-09-29, 934, 868
CURRENT PILING DATE: 2001-09-20, PRIOR FILING DATE: 2001-09-01
FRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 81
SOFTWARRE: Microsoft Office 97
SEQ ID NOS: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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GCCGAGCGCCCTACCACTGCGCCGAGTGCGGCAAGCGCTTCACGCAGAAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 GATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGTTCATGCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 38.7%; Score 23.6; DB 9; Length 573; Best Local Similarity 64.8%; Pred. No. 8.8; Matches 35; Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 10
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
                                                                                                                         ; Sequence 84, Application US/10108605; Patent No. US20020160934A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Drosophila melanogaster US-10-108-605-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 38.7%;
Best Local Similarity 64.8%;
Matches 35; Conservative
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                                                                                                                                                                                                   APPLICANT: Broadus, Julie
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                                                                          RESULT 10
US-10-108-605-84
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LENGTH: 573
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APPLICANT: Ramseler, Thomas M.
TITLE OF INVENTION: Directed Genetic Engineering of Xanthomonas campestris FILE REFERENCE: 38-1011582418
CURRENT APPLICATION NUMBER: US/09/927,827
CURRENT PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/279,493
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_022220
US-09-917-800A-1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCA 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.0%; Score 23.2; DB 9; Length 3627; Best Local Similarity 65.4%; Pred. No. 15; Matches 34; Conservative 0; Mismatches 18; Indels 0
                                                                           APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
                                                                                                                                                                                                       CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-11-02
PRIOR PLICATION NUMBER: US 60/290,645
PRIOR PLILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-19
PRIOR PLING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SEQ ID NO 1694
FURNARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09927827
Publication No. US20030036176A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Xanthomonas campestris US-09-927-827-4
Porter, Mark
Johnson, Kory
Castle, Arthur
Elashoff, Michael
Gene Logic, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Rattus norvegicus
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US-09-927-827-4/C
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LENGTH: 3627
                            APPLICANT: APPLICANT:
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Search completed: June 13, 2003, 09:00:41 Job time: 21.2903 secs

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June 13, 2003, 01:49:14; Search time 192.613 Seconds (without alignments) 9216.782 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-826-581-5_COPY_1007_1067
61
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Maximum Match 100%
Listing first 45 summaries
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em_htg_inv:*
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em_htg_pln:*
em_htg_rod:*
em_htg_mam:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score Match Length DB ID 100.0 1647 6 AX281582 61 100.0 2115 6 AX099807 61 100.0 2115 9 AZ214519 61 100.0 2115 9 AZ214519 61 100.0 2115 9 AZ214519 61 100.0 2115 9 AZ214519 61 100.0 2115 9 AZ214519 62 1 100.0 2120 9 BAZ249377 65 2 92.1 1873 6 AX399813 65 2 92.1 1873 6 AX398313 65 2 92.1 1873 6 AX398313 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 65 2 92.1 1873 6 AX398331 67 5 195189 2 AC112601 67 5 195189 2 AC122702 67 6 195189 2 AC122807 68 45 9 195325 2 AC112601 68 45 9 195325 2 AC112601 68 45 9 195325 2 AC112601 68 45 9 195325 2 AC101452 68 45 9 195325 2 AC101452 68 45 9 195325 2 AC101452 68 45 9 195325 2 AC101452 68 45 9 195325 2 AC101452 68 45 9 195325 2 AC101452 68 45 9 195325 2 AC101452 68 45 9 195325 2 AC101452 68 45 9 195325 2 AC101452 68 45 9 195325 2 AC101452 68 45 9 195325 2 AC101630 68 45 9 195325 2 AC101630 68 45 9 195325 2 AC101630 68 45 9 195325 2 AC101630 68 45 9 195325 2 AC10533 68 45 9 15474 2 AC10843 68		Description	1 0	087 087 087	AX099776 Sequence	AX099802 Sequence	AF214519 Homo sapi	AJ249977 Homo sapi	AX099//4 Sequence	AF214520 Sus scrot	AX398331 Sequence	AX398333 Sequence	AX398335 Sequence	AX398337 Sequence	AX398339 Sequence	AX099804 Sequence	AAZ81380 Sequence	ACONTAIN BOND SAPI	AF214521 Sus scrof	AC128070 Rattus no	AC129703 Rattus no	ACIZ/10/ Rattus no	AC129702 Rattus no	AF334948 Canis fam	AC112601 Rattus no	AC112066 Rattus no	ACU96427 Rattus no	AC087332 Mus Muscu	AC019360 Homo sapi	AC063943 Homo sapi	297199 Homo sapien	AC129236 Homo sapi	ALIZOGIO HOMO SAPI	AL845470 Mus muscu	ACI01452 Mus muscu	ACU23022 Homo sapi	AL078605 Human DNA	AC025266 Homo sapi	AC004691 Homo sapi	ACIUS/43 Oryza sat	AC018818 Homo sapi			DNA linear PAT 02-NOV-2001				; Vertebrat	ni; Hominidae;	und,s. d protein kinase gamma 3 subunit	
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2115 bp mRNA linear PRI 03-JUN-2000 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3) mRNA, complete cds.
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GEALRORTLCLEGVLSCQPHESLGEVIDRIAREQVHRILVLVDETQHLLGVVSLSDILQ
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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VGIX SRFDVIHLAAQQYYNHLDMSVGBALRQRTLCLEGVLSCQPHESLGEVIDRIARE
QVHRLVLVDETQHLLGVVSLSDILQALVLSPRGIDALGA*
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/evidence=experimental
/eroduct="%Anb_activated protein kinase gamma 3 subunit"
/protein_id="CAB65117.1"
/db_xref="GI:6688201"
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Varlants of the gamma chain of ampk, dna sequences encoding the
                                                                                           (bases 1 to 2290)
Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of Amp-activated protein kinase gamma-subunit biocorms and their role in Amp binding
Biochem. J. 346 Pt 3, 659-669 (2000)
                                                                                                                                                                                                                                                                                                                          Submitted (12-0CT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 ONN, UNITED KINGDOM
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/function="AMP-activated protein kinase regulatory
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/db_xref="taxon:9606"
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Carling, D.
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EPPGGGEGPRSRPTAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAG
SSTDDVELATEFPATEAWECELEGILEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
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AVVI.ETAPTI.TALDTFVDKRVSAI.PVVNECGQVVGI.YSRFDVTHLAAQQTYNHLDMSV
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                                                                Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2115)

Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,

Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,

Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
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HOMO Sapiens mRNA for AMP-activated protein kinase gamma 3 subunit
(AMPK gamma 3 gene).
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AJ249977.1 GI:6688200
AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
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/protein_id="AAF73987.1"
/db_xref="GI:8215682"
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Pred. No. 9.4e-10;
Mismatches 0; Indels (
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/db_xref="taxon:9606"
/chromosome="2"
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622 c 56
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  AF214519.1 GI:8215681
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Matches 61; Conserv
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GPPGFREGPOSRPVAESTGOEAFPKAPLAQAAPLAEVDNPPTERDILPSDCAASAS
GPPGFREGPOSRPVAESTGOEAFPKAPLAQAAPLAEVDNPPTERDILPSDCAASAS
BSNTDHLDGIEFSAASAGSDELGLVEEKPAPCPSPEVLLFALGMDBELGKPGAQVYM
FPMGBHTCVDAMATSSKLVIFDTMLEIKKAFFALVNAGVRAAPLWDSKKQSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGGFKPLVSISNDSILFEATATA
KNRIHKLPVLDPVSGAVLHILTHKRLLKFLHHFGTLLPRESFLYFTIODLGIGTFRDL
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GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SB); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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                                                                                                                                                    /product="AMP-activated protein kinase gamma subunit"
/protein_id="AAF73988.1"
/db_xref="GI:8215684"
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Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
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/note="unnamed protein product"
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/db_xref="GI:13538835"
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1. .1395
                                                                                              /note="AMPKG3"
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                                                               /gene="PRKAG3"
                                                                                                                              /codon_start=1
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YRT10DIGIGTFRDLAVVLETAPILTALDIFVDRRYSALPVVNETGOVVGLYSRFDVI
HLAAQCTYNHLDMNVGEALRQATLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDB
TQHLLGVVSLSDILDALVLYSAGIDALGA"

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Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
same, and uses thereof
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looff, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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1. 1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56.2; DB 6;
Pred. No. 3.5e-08;
0; Mismatches 3;
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HFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLMDSKKQSFVGMLTI
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GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETGHLLGVVSLSDILQ
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                              Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 3 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 5 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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Pred. No. 3.5e-08;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
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1. 1395
/note="unnamed protein product"
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BSNTDHLDIGIETESASAASGELGILYEEKPRCPSPEPTLLPRIGMDELGKPGAQYYM
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
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Iowa State University Research Foundation, Inc. (US)
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/protein_id="CAD32628.1"
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/db_xref="G1:21261113"
/db_xraiation-"MSFLEQGESRSWPSRAVITSSERSHGDQGNKASRWIRQEDVEEG
GPPGPRESPQSRYARSSYGGDEATFPKATPLAQAAPLAEVDNRPIERDILPSDCAASAS
DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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Novel prkag3 alleles and use of the same as genetic markers reproductive and meat quality traits
Patent: WO 0220850-A 7 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
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                                                                                                                                     Score 56.2; DB 6; Length 1873;
Pred. No. 3.5e-08;
0; Mismatches 3; Indels 0
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AX398337
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                                                                                                                                     Query Match 92.1%;
Best Local Similarity 95.1%;
Matches 58; Conservative
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RESULT 13

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KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIPGTLLPRPSFLYRTIODLGIGTBYDL
AVVLETAPILTALDIFVDRYSALPVVNETGQVVGLYSRFDVIHLAAQQTVNHLDMNV
GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDBTQHLLGVVSLSDILQ
    PAT 27-MAY-2002
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Cetartiodactyla; Suina; Suidae; Sus.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers
reproductive and meat quality traits
Patent: WO 020850-A 9 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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    1. 1395
    /note="unnamed protein product"

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Mammalia; Eutheria; Cetartiodactyla; Sui
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Sequence 31 from Patent W00120003.
AX398339 1873 bp Sequence 9 from Patent W00220850.
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Sus scrofa
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.5e-08;
0; Mismatches 3; Indels 0
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412 a 623 c 593 g
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Best Local Similarity 95.1%;
Matches 58; Conservative
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Search completed: June 13, 2003, 04:39:46 Job time: 194.613 secs

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June 13, 2003, 01:37:39 ; Search time 22.1613 Seconds (without alignments) 6198.732 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human AMP-activate PRKAG3 cDNA. Homo	Human AMPK gamma s Piq AMPK gamma sub	Pig AMPK gamma sub Pig wild-type PRKA	Pig PRKAG3 polymor Pig PRKAG3 polymor
SUMMARIES	ABA08485 AAH43685	AAD03320 AAD03295	AAD03319 AAD36456	AAD36457 AAD36458
 gg	222	555	22	24
% Query Match Length DB	547	2115	1873	1873
% Query Match	100.0	100.0	92.1	92.1
Score	61	61 56.2	56.2 56.2	56.2
Result No.	400	J 4 ₹J	9 /	ထတ

Pig PRRAG3 polymor 7469 Pig PRRAG3 polymor 8321 Sus scrofa PRRAG3 1 polymor 8683 PRRAG3 intron 4 - DNA encoding novel 1194 Human immune/haema Human immune/haema Human immune/haema Human immune/haema 1195 Brosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Nucleotide sequence Nucleotide Successivation recentation of Nucleotide Nu	SIN	ABA08485 standard; cDNA; 547 BP. ABA08485 ABA08485; (11-JAN-2002 (first entry)) Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261. Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261. Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261. Human Cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activit; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumnour; haematopoietic disorder; atternal disorder; asternal artherosclerosis; coronary heart disease; arterial ischemia; atteritis; atterial ischemia; antherosclerosis; coronary heart disease; arterial ischemia; antisathmatory condition; haematory condition; immune disorder; celeopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss. Homo sapiens. WO200157188-A2. WO200157188-A2. E 05-FEB-2001; 2001WO-US03800.
AAD36459 AAD36460 AAH4368321 AAH4368332 AAK81194 AAK81195 AAK81195 AAK81195 AAK81195 AAK81195 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK81196 AAK8110	र्वर्वर वर्ष वर्ष वर्ष	Kinase kinase feration tissue inesis; cancer; in present in presen
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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ss.
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/label= "T559C"
                                                                                                                                                                                                                                                                              07-APR-2000; 2000US-195665P.
                                                                                                                                                                                                                                                             06-APR-2001; 2001WO-SE00765
               21-JAN-2002 (first entry)
                                                                                                        /*tag= a
                                                                                                                                                                                                                                                                                                                            WPI; 2001-657170/75.
P-PSDB; QQB47679.
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                                                                                                                                                                                                                                                                                             (AREX-) AREXIS AB.
                                                                                                                                                                                                                              WO200177305-A2
                                                                        Homo sapiens.
                                                                                                                                                                                                                                              18-0CT-2001.
                               PRKAG3 CDNA
                                                                                                                      variation
                                                                                                                                                       variation
                                                                                                                                                                                       variation
AAH43685;
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Matches
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                                                                                                                                Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 61; DB 22;
100.0%; Pred. No. 1.5e-10;
iive 0; Mismatches 0;
                                                                                                               Claim 1; Page 429; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH43685 standard; cDNA; 1647 BP.
                                         Tang YT, Liu C, Drmanac RT;
03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 61; Conservative
                                                                                               e.g. arthritis and cancer
                                                        WPI; 2001-457740/49.
                        (HYSE-) HYSEQ INC.
                                                                P-PSDB; ABB11241
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This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, iss useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution PJ1A: in exon 4 variation may be a substitution of a T for a C at nucleotide 550, and in exon 0 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340M. There may also be conclected variation in intron 6. The numbering of these convariations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1007 ITCCTGCACATCTTTGGTTCCCTGCTGCTGCCCGGCCCTCCTTCTCTACCGCACTATCCA 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the variant -
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100.0%; Preq. ...
                                                                                                                                                                                                                                  Disclosure; Fig 5; 25pp; English.
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                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAE00223
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                                                                                                                                                                                                                                                                                                            967 G 967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-2001
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                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
                                                                                                                                                                                                                                                           Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New variants of the gamma subunit of verlebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rogel-Gaillard C;
                                                                                                                                                                                                                            Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human Prkag3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
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                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                             AAD03296 standard; DNA; 2109 BP.
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472..1389
/*tag= b
/product- "]
1390..2109
/*tag= c
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18-MAY-2000; 2000EP-0401388
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                                             G 1067
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               61 G
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                                            1067
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5'UTR
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                                                                                             RESULT 3
AAD03296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                           100.0%; Score 61; DB 22; Length 2109; 100.0%; Pred. No. 1.8e-10; ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                           Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
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(ANDE/) ANDERSSON L.
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1..1395
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18-MAY-2000; 2000EP-0401388.
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered aliele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a presently compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PKAG3 gene, or encoding PRKAG3 is useful for detecting mutations in a PKAG3 gene, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKKG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15; ss.
                                                                                                                                                                                             in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
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1390..1867
/*tag= c
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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Matches 61; Conservative
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The present sequence is a cDNA encoding pig adenosine monophosphate

(AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform,

PRRAG3: Prkag3 gane is located in the RN locus of chromosome 15.

Mutation in Prkag3 results in an altered regulation of carbohydrate
metabolism, particularly in skeletal muscle. PRRAG3 is useful as
therapeutic for treating carbohydrate metabolism alsorders such as
therapeutic for treating and sorders associated with muscle metabolism

activity, and for restoring a normal AMPK function. PRRAG3 sequence
and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic disorder,
preferably a carabohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRRAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered allele of PRRAG3 or a
heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for
concoding PRRAG3 is useful for detecting mutations in a PrkaG3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
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                                                                                                                                                                                                                                                              New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                   Robic A, Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA
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                                                                                                      Le Roy P, Chardon P;
                                                               Looft C, Kalm E, Milan D,
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1.1395
/*tag= a
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                                                                                                      Gellin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58; Conservative
                                                                                                                                                                  WPI; 2001-244810/25
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                                                                                                  Iannuccelli N,
(KALM/) KALM E.
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                                                                   Andersson L,
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                                                                                                                                                                                                                                                                                                                                                                               myopathy
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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma subunit gene
                                                                                                                                                                                                                                            /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKMG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger likely to The present sequence is pig wild-type PRKAG3 gene.
                                              AMP activated protein kinase regulatory gamma subunit, PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP;
                                                                                                                                                                                             /product- "Pig PRKAG3 wild-type protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rothschild MF, Ciobanu DC, Malek M, Plastow G;
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Pred. No. 6.2e-09;
0; Mismatches 3,
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                                                                                                                                                socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           replace (599, A)
                                                                                                                                                                                                                                                              replace (154, A)
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95.1%;
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18-JUN-2001; 2001US-299111P.
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                  Pig wild-type PRKAG3 gene.
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Best Local Similarity
Matches 58; Conserv
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                                                                                                                Sus scrofa
                                                                                                                                                                                                               variation
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                                                                                   gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRRAG3 Prag3 gene is located in the RN locus of chromosome is without in Prkag3 results in an altered regulation of carbohydrate including carbohydrate metabolism disorders such as metabolism, to treating arbohydrate metabolism disorders such as clabetes, obesity, and disorders associated with muscle metabolism cartivity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3.

Transgenic animal and host cell transformed with PRRAG3 or a chectorinaric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRRAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                           Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
Iannuccelli N, Gellin J, Le Roy P, Chardon P;
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 /product= "Sus scrofa complete Prkag3 protein"
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Pred. No. 6.2e-09;
0; Mismatches 3;
                                                                                                                                                                            ) INRA INST NAT RECH AGRONOMIQUE.
// ANDERSSON L.
// LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 62-64; 71pp; English.
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95.1%;
                                                                                             11-SEP-2000; 2000WO-EP09896.
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18-MAY-2000; 2000EP-0401388.
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es 58; Conserv
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Gaps ;

3; Indels

DB 24; Length 1873;

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AAD36458 standard; DNA; 1873
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                                                           09-AUG-2002
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                                                                                                                                           Sus scrofa.
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RESULT 9
          AAD36458
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                                                                                                                                                                                                                                                                                                                                                                                                                                 and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma subunit gene
                                                                                                                                                                                 /*tag= a
/product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
replace (89, C)
                                                                                                                                                                                                                         /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; plg; gene; variant; ds.
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                                                                              Pig PRKAG3 polymorphic variant DNA (PRKAG3-30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 89-91; 109pp; English.
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                 AAD36457 standard; DNA; 1873 BP.
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95.1%;
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08-JAN-2001, 2001US-260239P.
18-JUN-2001, 2001US-299111P.
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                                                           (first entry)
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Best Local Similarity
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                                                        09-AUG-2002
                                                                                                                                                                                                                                                                14-MAR-2002
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                                                                                                                                          Sus scrofa
                                                                                                                                                                                                     variation
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                                      AAD36457;
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RESULT 8
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1 TICCIGCACATCITIGGITCCCTGCTGCCCGGCCCTCCTTCCTTACCGCACTATCCAA 60
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replace (154, A)
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                                                                                                                           AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
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                                                                 Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
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Pred. No. 6.2e-09;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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95.1%;
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(first entry)
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Best Local Similarity 95.1
Matches 58; Conservative
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                                                                                                                                                                                            gene; variant; ds.
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AAD36460 standard; DNA; 1873 BP.
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    RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Plg PRKAG3 polymorphic variant (PRKAG3-199)" replace (595, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                             AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
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Pred. No. 6.2e-09;
0; Mismatches 3; Indels 0;
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                                                                                                                                                                       Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
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1..1395
                                          AAD36459 standard; DNA; 1873 BP.
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Local Similarity 95.1%;
les 58; Conservative 0
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                          gene; variant; ds.
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P-PSDB; AAE22987.
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                                                                                     AAD36459;
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Matches
RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                          "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
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                                                                                                                AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
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llarity 95.1%; Pred. No. 6.2e-09;
Conservative 0; Mismatches 3; Indels 0;
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                                                         Pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
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1..1395
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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(first entry)
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es 58; Conserv
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09-AUG-2002
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Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;

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Query Match
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AAH43683
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                                                                                                                                                                                                                                                                                                                  The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Parkag3 game is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as therapeutic for treating carbohydrate metabolism disorders such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Primers that can detect a generic polymorphic marker linked to a sequence encoding PRKAG3, are
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                                                                                                                                                                                                               PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kalm E, Milan D, Robic A, Rogel-Gaillard C; J, Le Roy P, Chardon P;
                                                                                                                                                                                               gamma subunit; adenosine monophosphate-activated kinase; AMPK;
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                      Sus scrofa PRKAG3 splice variant DNA.
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1..1545
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                                AAD03321 standard; DNA; 2022 BP
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18-MAY-2000; 2000EP-0401388
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Gellin J,
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                                                                                                                                                                                                                                                                              Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
                          Gaps
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Length 2022;
                         Indels
Score 56.2; DB 22;
Pred. No. 6.2e-09;
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/note= "5' portion of intron 10"
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"3' portion of intron 4"
                      0; Mismatches
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/number= "Intron 6"
/737.782
/*tag= f
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number= "Intron 5"
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number= "Intron 8"
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           Best_Local Similarity 95.1
Matches 58; Conservative
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or admittating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating insigning of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations are populated and produce other types of data and products dependent on DNA and cambine conding sequences. AAS641964 represent novel human call against coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2820 TGCTGCACCTCACCGGTTACGATCTGCCGATGCACTCCTCTTTCTGCCGCACTGCCCATG 2761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36006
                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; Length 3238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3238 BP; 926 A; 915 C; 858 G; 539 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 8.6;
                                                                                                                                                                              Claim 1; SEQ ID No 13137; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK81194 standard; DNA; 9979 BP.
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2000US-0198123.
2000US-0205515.
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Best Local Similarity 66.7
Matches 40; Conservative
                         P-PSDB; ABG13146
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16-MAR-2000;
17-MAR-2000;
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                                                                                                                                         biodiversity
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24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CCIGCACATCTTGGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCCAAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide Nation and be a mino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e mapping, gene mapping, gene therapy; forensic; medical imaging; diagnostic; genetic disorder; ss.
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Pred. No. 1e-05;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1722 BP; 321 A; 504 C; 534 G; 363 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #13137.
                                                                                                                                                                                                                            Marklund S;
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2000US-0649167.
                                                                                        06-APR-2001; 2001WO-SE00765.
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WO200177305-A2.
                                                                                                                                                                                                                            Andersson L,
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                                              18-OCT-2001
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Best Local 8
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SW; 2000US-0249214 2000US-0249215 2000US-0249216 2000US-0249218 2000US-0249244 2000US-0249245 2000US-0249265 2000US-0249265 2000US-0249265 2000US-024929 2000US-024929 2000US-024929 2000US-025016 2000US-025016 2000US-025016 2000US-025016 2000US-025016 2000US-02501886 2000US-0251186 Barash SC, Ruben 2000US-0241808 2000US-0241809 2000US-0244617 2000US-0246475 2000US-0246475 2000US-0246477 2000US-0246477 2000US-0246527 2000US-0246525 2000US-0246525 2000US-0246525 2000US-0246526 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0249211. 2000US-0249212. 2000US-0249213. SCI INC 2001US-0259678 HUMAN GENOME WPI; 2001-483426/52. 20-CCT-2000)
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818-NOV-2000)
05-JAN-2001; ÇA, (HUMA-) Rosen

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 36006; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAK82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased

us-09-826-581-5_copy_1007_1067.rng

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expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haemactopictic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK64950 and AAM3169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 45.9%; Score 28; DB 22; Length 9979; Best Local Similarity 66.7%; Pred. No. 10; Matches 40; Conservative 0; Mismatches 20; Indels (
                                                                                                                                                                                                                                                                                                                                               Sequence 9979 BP; 2496 A; 2022 C; 2532 G; 2929 T; 0 other;
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A1063338 GH03085.5 BG479057 602256134 BG290491 603288351 BE275257 601122081 BG291149 602287180 BG048516 952021601 BG174779 602336043

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pass sequencing. Bases called and alt_trimmed with phred NO4.e. Vector identified by cross_match with the -minscore 18
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
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AW478129
AA030200
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                  16154066 seqs, 8097743376 residues
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BF470814 UI-M-BH3-AI746867 ul08d11.y AIS09176 mi02d09.y BE030622 128854 MA BB948793 UI-M-BH3-AL661556 AL661556

BI134085 UI-M-BH3-BB618484 BB618484

AI726042 BNLGHil40

EST 30-JUL-2001

Smith, T.P.L., Casas, E.

and -minmatch 12 options. PCR PRimers FORWARD: AGGAAACAGCTATGACCAT

26.2 29.4 27.6 27.6 27.4

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Score

Result Š.

H03359 ZA06909.r1 B1735773 603357036 B152692 601292488 BE307400 601098995 BG974543 602844770 B1155021 602902543 B1664379 602889943 BC136865 601783752 BC288506 602383561 BC71558 AGENCOURT BF58158 60213379 BF78164 60213379 BF78164 60213379 BF78164 60213379 BF78164 60213379 BF78164 60213379 BF78164 60213379 BF78164 60213379 BF78164 60213379 BF78164 60213379 BF78164 60211379 BF78164 60211379 BF78164 60211379 BF78164 60211379 BF78164 60211379 BF78164 BF781670 BF78167 BF7

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/organism="Mus musculus"
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/clone="RPCI-23-271P21"
/clone_lib="RPCI-23"
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/db_xref="taxon:9506"
/db_xref="taxon:9506"
/clone_lib="wilk_GE:573918"
/clone_lib="wilk_GE:573918"
/tissue_type="duodenal adenocarcinoma, cell line"
/tab_bost="bhi00 (phage-resistant)
/tab_bost="bhi00 (phage-resistant)
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: Not!; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: Library in NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM556730 1173 bp mRNA linear EST 20-FEB-2002
AGENCOURT_6540753 NIH_MGC_88 Homo sapiens CDNA clone IMAGE:5737918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIN-WGC http://mgc.nih.gov/.

NIN-WGC http://mgc.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurament: ArCc

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Rlate: LLAM12748 row: m column: 23

High quality sequence stop: 473:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1173)
                                                                                                                                                                                                                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sall; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
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Best Local Similarity 95.1%; Pred. No. 4.3e-06;
Matches 58; Conservative 0; Mismatches 3
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/clone_lib="MARC_2PIG"
/tissue_type="pooled"
/lab_host="DHIOB"
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 119 row: I column: 11
Seq primer: ATTTAGGTGACACTATAG.
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/Actarionale*
//actarionale*
//abchost**Temmale*
//abchost**DH10B*
//abchost**Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Femmale C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electroccompetent cells (BRL Life Technologies).

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Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-271P21.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, plasse contact pleter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 271 row: P column: 21
Seq primer: T7
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
   Gaps
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                                                                                            5 IGCACATCITIGGIICCCIGCIGCCCCGGCCCICCIICCTCIACCGCACIAICCA 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 17;
Pred. No. 3.1e+02;
0; Mismatches 15,
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Email: oliver@helix.nih.gov,
http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC): see http://www.nisc.nih.gov).
Seq primer: MISRPI reverse primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/strain="y[*] w[67c1]/y"
/db_xref="taxon:7227"
/clone="bay3807"
/clone="brosophila melanogaster adult testis library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCNB36 row: g column: 03
High quality sequence start: 7
High quality sequence stop: 645.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 4.9e+02;
0; Mismatches 16
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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44.9%;
Best Local Similarity 69.8%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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JOURNAL
COMMENT
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AUTHORS
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   BF528264 1-DEC-2000 mRNA linear EST 11-DEC-2000 602043043F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180619
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                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 626)
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NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm Bl-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NoT_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 TGCTTGGCCATCTCTAGCATGCTGTCCGCCCCTCCATGCTGTCCCGCAGCC 112
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM9492 row: f column: 12
High quality sequence start: 130
High quality sequence start: 130
High quality sequence store: 605.
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                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster testis expressed sequence tags
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.2%; Score 27.6; DB 12; Length 626; 67.2%; Pred. No. 4.3e+02; tive 0; Mismatches 19; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:4180619"
/clone_lib="NCI_CGAP_Brn67"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .626
/organism≃"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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                                                               5', mRNA sequence.
BF528264
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BE978092/c
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Length 619; Indels

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bukaryota; Badopterrygota; Diosophiladae; Brachycera; Muscomorpha; Ephydroidea; Drosophiladae; C. Chew,M., Dorsett,V., Farfan, J., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Miranda,A., Misra,S., Mungall,C.J., Nunco,J., Parcleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., EDGP/HHMI AT Drosophila EST Project
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GH03085.5prime GH Drosophila melanogaster head pOT2 Drosophila
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//db.bost="Plates Ar.10-AT.120: DH5-alpha. Plates
Ar.121-AT.319: DH5-alpha TonA"
Ar.121-AT.319: DH5-alpha TonA"
Site_2: Xhol; The mRNR for the testis library was made
Site_2: Xhol; The mRNR for the testis library was made
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTFV: Plasmid CDNA library."
                                                                                                                                                                                                                                                                                                                               BF488250
AT2475.Sprime AT Drosophila melanogaster adult testes POTB7
Drosophila melanogaster cons. Similar to CG4714:
FBan0004714 located on: 2R 49F15-50A1;: 04/09/2001, mRNA sequence.
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hit genomic AE003819: arm:2R [8082036,8314191]
hit genomic AE003819: arm:2R [8082036,8314191]
Pate: AT.234 row: G column: 3
High quality sequence stop: 674.
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/db_xref="taxon:7227"
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Fax: 510 486 6798
34; Conservative
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/db_xter_caxue.suc.

/clone_lib="NIH_MGC_l06"

/clone_lib="NIH_MGC_l06"

/tissue_type="natural killer cells, cell line"

/lab_host-"DH10B (phage-resistant)"

/note="Organ: blood; Vector: poTB7; Site_1: XhoI; Site_2:

ECORI; CDNA made by oligo-dT priming. Directionally cloned

into EcoRI;XhoI sites using the following 5' adaptor:

GCCAGCAG(G). Liberry constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NTH MAD Tibrary.
               /du_xia: _daxdi;900.
/clone_lib="NIH_MGC_21"
/tlssue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G): Size-selected >500pp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).*
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://maqe.llnl.gov
Plate: LLCMI689 row: i column: 02
High quality sequence stop: 704.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Best Local Similarity 75.6%; Pred. No. 5e+02;
Matches 34; Conservative 0; Mismatches 11; Indels 0.
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/db_xref="taxon:9606"
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183 c 224
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MNH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                           The fease of to 754)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
On Jul 23, 1998 this sequence version replaced gi:3339282.
Contact: Stapleton, M.
melanogaster cDNA clone GH03085 5 similar to CG4714: FBan0004714 located on: 2R 49F15-50A1;: 04/10/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003819: arm:2R [8082036,8314191]
hit genomic AE003819: arm:2R [8082036,8314191]
estimated-cyto:49F2-50A3: 04/10/2001
Plate: GH.30 row: H column: 1
High quality sequence stop: 754
                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="GH03085"
/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                          Ephydroidea; Drosophilidae; Drosophila.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                     AI063338.2 GI:13759449
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Matches 37; Conservative
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BG479057
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                                                                                                                  fruit fly.
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/db_xrefa="taxongooffor"
/clone=_lib="NIH_MGC_21"
/tissue_lip=="NIH_MGC_21"
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/tissue_type=="choriocarcinoma"
/lab_host="DH10B (phage=resistant)"
/note="Corgan: placenta; vector: poTB7; Site_1: XhoI;
Site_2: EooRI; cona date by oligo-dr priming.
Directionally cloned into EooRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size=selected >S00bp
for average insert size 1.8kb. Library constructed by
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Supersoript II NT (Life Technologies)."
80 a 203 c 228 g 145 t lothers
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/tissue_type="transitional cell papilloma, cell line"
/tab_host='-billow (phage-resistant)"
/note="organ: bladder: Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally, oilgo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 913)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genemics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10409 row: f column: 13
High quality Sequence stop: 701.
Location/Qualifiers
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Cloud through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: IJCM1430 row: c column: 09
High quality sequence stop: 757.
Location/Qualiflers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 5.1e+02;
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/organism="Homo sapiens"
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Tissue Procurement: ATCC
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BG290491
BG290491.1 GI:13047386
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75.6%;
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BG291149.1 GI:13048809
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Contact: Walbot V
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/lab_host="Dmillo" (phage-resistant)"
/noLe="Organ: skin, Vector: poTB7; Site_l: Xho!; Site_2:
ECORI: cDNA made by oligo-dT priming. Directionally
cloned into RockI/Xho! Sites using the following 5/
adaptor: GCCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                         0;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 921)
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Libra distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: image.llnl.gov Plate: LLCM135 row: a column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 5.2e+02;
0; Mismatches 11; Indels 0
                                                                                                                                                                1 TYPECTGCACATETTTGGTTCCCTGCTGCCCCGGCCCTCCTTCCTC 45
                                                                                                                                           Indels
Note: this is a NIH_MGC Library."
1 254 c 287 g 146 t
                                                                    Score 27.4; DB 12;
Pred. No. 5.2e+02;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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/organism-"Homo sapiens"
/db_xref-"taxon:9606"
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High quality sequence stop: 742.
Location/Qualifiers
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75.68;
                                                                    Query Match
Best Local Similarity 75.6%;
Matches 34; Conservative
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Matches 34; Conservative
                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                 226 a
                                                                                                                                                                                                                                                                                                                                                                                     human.
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BC291149/c
                                                                                                                                                                                                                                   RESULT 12
BE275257/c
               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                       DEFINITION
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="transitional cell papilloma, cell line"
/lab.host="DHIOB (phage-resistant)"
/note="organ: bladder; Vector: pcWv-SPORT6; Site_1: Not!;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 926)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ048516
952031G01.y2 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc.
DNA Labrary Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
floud through the I.M.A.G.E. Consortium/Linn at:
http://lmage.lnl.gov
Plate: LLAM10406 row: p column: 19
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Pred. No. 5.2e+02;
0; Mismatches 11; Indels 0;
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SS California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: walbot@stanford.edu
Plate: 952021 row: G column: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:4516098"
/clone_lib="NIH_MGC_93"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 648.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:19822492
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Best Local Similarity 75.6%;
Matches 34; Conservative
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/note="Vector: pUC19; Site_1: ECORI; Site_2: ECORI; The library was prepared by George Rudenko using poly (A) selector RNA and Universal Riboclone cDNA Synthesis System (Promega). CDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into ECORI-digested pUC19 vector. Blue/white selection on
                                               /organism="zea mays"
/cultiva="zwas (Black Mexican Sweet)"
/db_xref="taxon.457"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG174779 887 bp mRNA linear EST 06-FEB-2001 602336043F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4459019 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinaes 1 to 887)

NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausbory, Ph.D.
Email: Gapba: Temail.nih.gov

Cissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10258 row: f column: 12
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/dev_stage="mixed logarithmic and stationary growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carbenicillin-containing plates was used to recover positive clones."
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/clone_lib="kQI_CGAP_Maml"
/clssue_typpe="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism~"Mus musculus"
/strain="FVB/N"
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Location/Qualifiers
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Location/Qualifiers
1. .569
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/lab_host-"DH10B"
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BG174779/c
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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KEYWORDS
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FEATURES
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Search completed: June 13, 2003, 05:58:32 Job time : 155.839 secs Sequence 2, Appli Sequence 1, Appli Sequence 10, Appl Sequence 11, Appl

Sequence 1, Appli Sequence 10, Appl Sequence 11, Appl Sequence 164, App Sequence 4, Appli

Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 10, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 7, Appli

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Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
BK-2 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER TO STATE: US

ZIP: 07065-0907:

ZIP: 07065-0907:

COMPUTER READABLE FORM:

COMPUTER: The PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/148,708

FILING DATE: 08-No. 6407207-1993

CLASSIFICATION: <UNKNOWN>

PRIOR APPLICATION NUMBER: 07/860,709

FILING DATE: CUKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: Caruso, Charles M

NAME: Caruso, Charles M

REGISTRATION NUMBER: 30161
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                                                                                                                                                                                                                                   US-09-576-160B-11
US-09-199-637A-164
US-08-200-016-4
              US-08-369-796-3
US-08-852-091-3
US-08-820-544-3
US-08-956-652-3
US-08-956-869-3
US-08-956-869-3
US-09-364-970-10
US-09-364-970-10
US-09-364-970-10
US-09-087-465-1
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US-09-103-840A-1
US-09-576-160B-10
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                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 18713 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: SINGLE

MOLECULE TYPE: CDNA tO MRNA

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-148-708-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (908) 594-4830
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08148708 Patent No. 6407207 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 387 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 7
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4411529
960 4
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Best Local Similarity
US-08-148-708-7
 Sequence 7, Appli
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Sequence 3, Appli
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Patent No. 5171671
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Sequence 7, Al
Sequence 1, Al
Sequence 1, Al
Sequence 1, Al
Sequence 1, Al
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  5.1.6
Compugen Ltd.
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US-08-095-728B-3
PCT-US92-02320A-3
US-08-592-383-1
5171671-1
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US-07-866-979-3
US-08-466-9706-3
US-08-706-281A-3
US-09-201-746-3
US-09-592-383-7
US-09-347-878-25
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US-08-759-848-7
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US-08-148-708-6
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                  version 5
- 2003 C
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                                                                             nucleic search, using sw model
                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 1.0
                Gencore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                           Title:
Perfect score:
                                                                                nucleic
                                                                                                                                                                                                          Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.6%; Score 26; DB 4; Length 1179; 65.5%; Pred. No. 4.4; tive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Borkowski, Joseph A.
APPLICANT: Strader, Catherine D.
APPLICANT: Strader, Catherine D.
APPLICANT: Hess, John W.
APPLICANT: Chan, Howard Y.
APPLICANT: Trumbaner, Myrna E.
TITLE OF INVENTION: BRADIKININ B2 RECEPTOR MODIFIED TITLE OF INVENTION: BRADIKININ B2 RECEPTOR MODIFIED TITLE OF INVENTION: NON-HUMAN ANIMALS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
STREET: 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                   COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,708
FILING DATE: 08-NG. 6407207-1993
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/860,709
FILING DATE: <UNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: CATUSO, Charles M
REGISTRATION NUMBER: 30161
REFERENCE/DOCKET NUMBER: 18713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPICATE TOPICATE TOPICATE TABLE ; MOLECULE TYPE: DNA (genomic) ; SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-08-148-708-3
                                          NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.,
STREET: P.O. Box 2000
CITY: Rahway
                            BK-2 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (908) 594-4830
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1179 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08759848 Patent No. 5750826 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 65.59
hes 38; Conservative
                                                                                                                                                                                 COUNTRY: US
ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rahway
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Matches
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                                                                  0; Gaps
    0; Gaps
                                                                                                                                                                                                                                                                                         Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
BK-2 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: FLOROPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,708
FILING DATE: 08-No. 6407207-1993
CLASSIFCATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.6%; Score 26; DB 4; Length 909; Best Local Similarity 65.5%; Pred. No. 4.2; Matches 38; Conservative 0; Mismatches 20; Indels
  20; Indels
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION UNBER: 07/860,709
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Caruso, Charles M
REGISTRATION NUMBER: 30161
REFERENCE/DOCKET NUMBER: 18713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-148-708-9
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hess, John W
Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (908) 594-4830
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08148708 Patent No. 6407207 GENERAL INFORMATION:
                                                                                                                                                                                                 : Sequence 9, Application US/08148708; Patent No. 6407207
; GENERAL INFORMATION: APPLICANT: Hess, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NJ
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US-08-148-708-9
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Matches
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TYPE: nucleic acid
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                                                                                                                                                 Query Match
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Best Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 42.6%; Score 26; DB 1; Length 1378; Best Local Similarity 65.5%; Pred. No. 4.5; Matches 38; Conservative 0; Mismatches 20; Indels
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ZIP: 07055-0907

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: TBM PC compatible

COMPUTER: TBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/148,708

FILING DATE: 08-NO. 6407207-1993

CLASSIFCATION: CURNOWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 18713
                                                   CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281,393
FILING DATE: 27-JUL-1994
ATTORNEY/ACENT INFORMATION:
NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSER: MACK & CO., Inc.
STREET: P.O. BOX 2000
CITY: Rahway
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Caruso, Charles M
REGISTRATION NUMBER: 30161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4830
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 1378 base pairs
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 1923.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEPAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1378 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08148708; Patent No. 640720; GENERAL INFORMATION: APPLICANT: Hess, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NJ
                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-148-708-6
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                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application PC/TUS9509383
SENERAL INFORMATION:
APPLICANT: Borkowski, Joseph A.
APPLICANT: Strader, Catherine D.
APPLICANT: Hess, John W.
APPLICANT: Trumbauer, Myrna E.
ITILE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09383
; TOPOLOGY: Linear; MOLECULE TYPE: CDNA tO MRNA; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-148-708-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281,393
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: John W. Wallen III
STREET: 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 195,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic) PCT-US95-09383-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1378 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rahway
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
Les 38; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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TITLE OF INVENTION: Methods and Reagents for Discovering and TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagon: TITLE OF INVENTION: TO Modulate Feeding Behavior in Animals CORRESPONDENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 CGTGCTCATCTGTGGCTCCATGGTGTCCAGTCTCTGCTTCCTGGCATCATT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.7%; Score 24.8; DB 2; Length 1260; 67.3%; Pred. No. 11;
tive 0; Mismatches 17; Indels 0
                                                                                                                                        COMPUTER INTELLIBY COMMITTEE FLORPY GISK
COMPUTER: 1BM PC COMPATIBLE
COMPUTER: 1BM PC COMPATIBLE
COMPUTER: 1BM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/466,906B
FILING DATE: O6-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: No. 5849871nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154-H
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFONE: 312-913-0001
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STREET: 300 South Wacker Drive
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Kesterton, Robert A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA to MRNA
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APPLICANT: Fan, Wei
APPLICANT: Boston, Bruce
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Chen, Wenbiao
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Best Local Similarity 67.33
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                           COMPUTER READABLE FORM:
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960..1260
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GENERAL INFORMATION:
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; LOCATION:
US-08-466-906B-3
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NAME/KEY:
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FEATURE:
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APPLICANT:
APPLICANT:
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Patent No. 5849871
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
TITLE OF INVENTION: Mountjoy, Ress
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: 
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Pred. No. 11;
0; Mismatches 17; Indels 0
                       Sequence 3, Application US/07866979
Relact No. 5532347
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor TITLE OF INVENTION: and USES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBBER: US/07/866,979
FILING DATE: 19920410
CLASSIFICATION: 435
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NAME: No. 553247nan. Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154
TELECOMMULCATION INFORMATION:
TELEPHONE 312-715-100
TELEPHONE: 312-715-100
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Best Local Similarity 67.3%;
Matches 35; Conservative (
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TELEEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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15..959
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                                                                                                                                                                                                                                                                                                                                                STREET: 10 South
CITY: Chicago
STATE: Illinois
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; LOCATION: 960..1
US-07-866-979-3
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LOCATION:
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LOCATION:
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US-07-866-979-3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
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APPLICATION NUMBER: US/09/097,231
FILLIGA DATE: 12-Jun-1998
CLASSIFTCATION: <unional content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the
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CITY: Chicago
STATE: Illinois
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TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
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SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
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Chen, Wenblao
                                                                     INFORMATION FOR SEQ ID NO: 3:
                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 35; Conservative
            312-913-0002
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; LOCATION:
US-09-201-746-3
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FEATURE:
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tive 0; Mismatches 17; Indels C
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Patent No. 626821
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Mountly, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
TITLE OF INVENTION: and Uses
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,746
FILING DATE: 01.DEC-1998
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STRET: 300 South Wacker Drive CITY: Chicago
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETCHILIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,281A
                                                                                           JMBER: US/08/706, 281A 04-SEP-1996
                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY FAGENT INFORMATION:
NAME: No. 6100046nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886
TELECOMMUNICATION INFORMATION:
TELEFAK: 312-913-0001
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ATTORNEY/AGENT INRORANTION:
NO. 6266221nan, Kevin E
REGISTRATION NUMBER: 35,303
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 67.3
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           960..1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15..959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..14
                                                                                                                       FILING DATE: 04 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-706-281A-3
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US-09-201-746-3
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Gaps
                                                                                            LOW, Malcolm J
TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
                                                                        ô
40.7%; Score 24.8; DB 4; Length 1260; 67.3%; Pred. No. 11; Indels 0; Mismatches 17; Indels 0
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Sequence 3, Application US/08592383
Patent No. 5830760
GENERAL INFORMATION:
APPLICANT: TASI, S. and S.J. Collins
TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Reconsers of NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: YALD, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1131)...(2399)
COTHER INFORMATION: Escherichia coli nucleic acid encoding
CTHER INFORMATION: Escherichia coli nucleic acid encoding
CTHER INFORMATION: folypolyglutamate synthetase-dihydrofolate
OTHER INFORMATION: synthetase
PUBLICATION INFORMATION:
DATABABSE ACCESSION NUMBER: M32445/GenBank
US-09-347-878-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 2561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Christensen, O'Connor, Johnson and Kindness STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct) INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.7%; Score 24.2; 62.3%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-7190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: WORD fOF WINDOWS 5.01-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
                Sequence 25, Application US/09347878C Patent No. 6376210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08/099,242
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 62.39
Matches 38; Conservative
                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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ZIP: 98101
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US-09-347-878-25/C
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
                                                                                                                                                                                                                                            SEQ ID NO 25
LENGTH: 2561
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Patent No. 5830760

GENERAL INFORMATION:

"TILE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Recept
NUMBER OF SEQUENCES: 10

"CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: page 11, RAR-alpha N-terminal region; positions 103 to 363 of SEQ.
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0
                                                                                                                                                                                               Query Match 40.7%; Score 24.8; DB 4; Length 1260; Best Local Similarity 67.3%; Pred. No. 11; Matches 35; Conservative 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.7%; Score 24.2; DB 2; Length 261; 66.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31.332
REFERENCE/DOCKET NUMBER: FHCR-1-7190
RELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct)
SRQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: WORD for Windows 5.01-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                             LOCATION: 960..1260
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08/099,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/099,
FILING DATE: JULY 28, 1993
ATTORNEY/AGENT INFORMATION:
                                          15..959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 261 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Conservative
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Best Local Similarity
                                                                                       NAME/KEY:
                  NAME/KEY:
                                          LOCATION:
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CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98101
  FEATURE:
                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-592-383-7
                                                                                                                                                       US-09-097-231-3
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Gaps

18;

us-09-826-581-5_copy_1007_1067.rni

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6 GCACATCTTTGGTTCCCTGCTGCCCGGCCCTCCTTCCTCTACCGCACTATCC 58
        Best Local Similarity 66.0%; Pred. No. 20;
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                 Search completed: June 13, 2003, 06:01:18
Job time: 9.64516 secs
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                                                           TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: Page 4,RAR-alpha403 dominant negative; deleted of 1311-1596 of SEQ
                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: DMITROVSKY, ETHAN
APPLICANT: WARRELL JR, RAYMOND P
APPLICANT: WARRELL STANKEY
APPLICANT: FRANKEL, STANKEY
TITLE OF INVENTION: WETHODS FOR THE DETECTION AND
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL.)
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             6 GCACATCTTTGGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCC 58
                                                                                                                                                                                                                       DB 2; Length 2658;
                                                                                                                                                                                                                                                               18; Indels
                                                                                                                                                                                                            Query Match 39.7%; Score 24.2; Di
Best Local Similarity 66.0%; Pred. No. 19;
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-7UL-1993
CLASSIFICATION: 435
PRIOR APPLICATION 0435
PRIOR APPLICATION DATE: 22-MAR-1991
ATTORNEY AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 38694-A TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400 TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08095728B Patent No. 5843642
LENGTH: 2658 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2928 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: CDS
; LOCATION: 103..1488
; OTHER INFORMATION:
US-08-095-728B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: hRAR ALPHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-095-728B-3
                                                                                                                                                                      US-08-592-383-3
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
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39.7%; Score 24.2; DB 2; Length 2928;

Query Match

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June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds (without alignments) 4579.068 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpna/NSO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/NSO7_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/NSO8_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1029858 seqs, 724030393 residues
                                                                                                                                                                                                                                               US-09-826-581-5_COPY_1007_1067
61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence 5, Appli Sequence 159, Appli Sequence 7, Appli Sequence 5, Appli Sequence 129, Appli Sequence 11, Appli Sequence 59, Appl Sequence 6987, Appl Sequence 6987, Appl Sequence 19, Appli Sequence 3, Appli Sequence 3, Appli Sequence 34, Appli Sequence 21, Appli	
SUMMARIES ID	10 US-09-826-581-5 10 US-09-826-581-3 10 US-10-255-536-159 10 US-10-045-815-7 10 US-10-045-815-7 10 US-09-975-297-129 10 US-09-979-593-1 10 US-09-979-593-1 10 US-09-978-1891-6987 10 US-09-815-944-21 10 US-09-815-944-19 10 US-09-815-944-19	TT #07 0// /0 00 0
Length DB	1047 1722 1722 1722 1722 1022 1224 1226 1226 1226 1260 1260 1260 1260 1260	1
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Score	26.65 26.65 26.66 26.66 26.66 26.66 26.66 27.44 27.48 28.88 28.88 28.88 28.88 28.88 28.88 28.88 28.88 28.88 28.88 28.88 28.88 28.88	
Result No.	0 000 000000)

RESULT 2 US-00-826-581-3 Sequence 3, Application US/09826581 ; Patent No. US20020142310A1

1067 G 1067

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ppl pl App App	hppl Appl hppl hppl hppl Appl App App App App App App App App	GAMMA 3	0;
e 74, Appl 52, Appl e 421, App e 146, App	Sequence 19, Appi Sequence 16, Appi Sequence 22, Appl Sequence 16, Appi Sequence 24, Appi Sequence 3, Appi Sequence 509, App Sequence 509, App	KINASE G	Gaps
Sequence Sequence Sequence Sequence	Sequence Seq	PROTEIN K.	6 4 7; 0;
8 8 8 8 8 8	8 N N N N N N N N N N N N N N N N N N N	TED PRO	Length 1647 Indels
-74 52 -421 -146	00000000000000000000000000000000000000	ALICNMENTS 181 THE HUMAN AMP-ACTIVATED 195,665 195,665 srsion 4.0	
4-898-7 -865-52 4-853-4 4-898-1	1353 135 135 135 135 135 135 135 135 135	ENTS AN AMP 81	61; DB 10 No. 2.1e-1 natches
US-09-764-898-7 S-10-073-865-52 US-09-764-853-4 US-09-764-898-1	US-10-269-353-19 US-10-269-353-16 US-10-269-353-16 US-10-269-353-22 US-10-269-353-9 US-10-269-353-9 US-10-269-353-9 US-10-269-353-9 US-09-978-353-509 US-09-978-353-509 US-09-978-697-509 US-09-99-837-509 US-09-978-697-509 US-09-978-595-509 US-09-978-595-509 US-09-978-568A-509 US-09-978-568A-509 US-09-978-568A-509 US-09-978-568A-509 US-09-978-568A-509 US-09-918-568A-509 US-09-918-568A-509 US-09-918-568A-509 US-09-918-568A-509 US-09-918-568A-509 US-09-918-568A-509	ALICHMENTS 826581 10 C THE HUMAN A 10 C/09/826,581 14-05 16 C THE HUMAN A 10 C/09/826,581 17 TS Version 4.0	Score 61; D Pred. No. 2. Mismatches
10 US 9 US-10 US 10 US	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 US/0982658 [0A] Leif . Holger Stefan MIRANTS OF 7007001 DMBER: US/05 2001-04-05 2001-04-07 14 Windows Ven 15	.08; .08; 0;
1309 1310 1310 1310	1353 14475 14475 1538 1538 1538 1538 1538 1538 1538 153	ation US/0982 N: N: N: N: N: N: N: N: N: N: N: N: N: N	vat
0000	444444444444444444 0000000000000000000	581-5 10. US20020142310A1 INFORMATION: UNT: Andersson, Leif NT: Luthman, L. Holger NT: Marklund, stefan NT: Marklund, stefan NT: Marklund, stefan NT: Marklund, stefan NT: Marklund, stefan NT: Marklund, stefan NT: Marklund, stefan NT: Marklund, stefan NT: Marklund, stefan NT: Marklund, stefan NT: Marklund, stefan NT: Marklund, stefan NT: Marklund, stefan NT: TLING DATE: 2001-04-07 OF SEQ ID NOS: 14 NO 5 SEQ ID NOS: 14 NO 5 SEQ ID NOS: 14 NO 5 SEQ ID NOS: 14 NO 5 SEQ ID NOS: 14 NO 5 SEQ ID NOS: 14 NO 5 SEQ ID NOS: 14 NO 5 SEQ ID NOS: 14 NOS: 14 NOS: 16 SEQ ID NOS: 16 SEQ ID NOS: 17 SEQ ID NOS: 17 SEQ ID NOS: 18 SEQ	h Similarity 61; Conser
24.4	00000000000000000000000000000000000000	AL. SULT 1 -09-826-581-5 gequence 5, Application US/09826581 Batent No. US20020142310A1 GENERAL INFORMATION: APPLICANT: Andersson, Leif APPLICANT: Andersson, Leif APPLICANT: Marklund, Stefan TITLE OF INVENTION: VARENTS OF THE TITLE OF INVENTION: VARENTS OF THE TITLE OF INTENTION: VARENTS OF THE TITLE OF TILING DATE: 2010-04-05 PRIOR PILING DATE: 2000-04-07 SUMBER OF SEQ ID NOS: 14 SOFTWARE: PASLEGG for Windows Versi SEQ ID NO 5 LENGTH: 1047 LENGTH: 1047 TYPE: DNA ORGANISM: HOMO SapienS FRATURE: NAME/KEY: CDS LOCATION: (20)(1486)	Match ocal Sin s 61;
222	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-826-581 Sequence 5, Patent No. GENERAL INF APPLICANT: APPLICANT: APPLICANT: TITLE OF ITLE REPER CURRENT AP FRICH AP CORRENT: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LOCATION: US-09-826-581	Query Match Best Local Matches 6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26.6; DB 9; Length 2416;
Pred. No. 2.3;
0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 43.6%; Score 26.6; DB 9; Length 2322; Best Local Similarity 71.4%; Pred. No. 2.3; Matches 35; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10045815
Patent No. US2002016498A1
GENERAL INFORMATION:
APPLICANT: Wadhwa, Renu
APPLICANT: Ohide, Akivo
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REFERENCE: 06501-091001
CURRENT PAPLICATION NUMBER: US/10/045,815
CURRENT FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 1999-04-26
PRIOR FILING DATE: 1999-04-26
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5.
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: JP 11/118806
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 129, Application US/09925297; Patent No. US20020081559A1; GENERAL INFORMATION: APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: 2282_
: OTHER INFORMATION: n = A,T,C or G
US-10-045-815-7
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// LCCATION: 2376

US-10-045-815-5

US-10-045-815-5
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Best Local Similarity 71.4%;
Matches 35; Conservative (
                                                                                                                                                                                                                                                LOCATION: (12)...(1637) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
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FEATURE:
                                                                                                                                                         TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
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                                                                                                                                    LENGTH: 2322
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                                    APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REPERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Septicant: arcatom, Ralph J.

APPLICANT: Greenspan, Ralph J.

TITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to TITLE OF INVENTION: Balance and the Perception of Gravity FILE REFERENCE: P.NI 3864 and the Perception of Gravity

CURRENT PILICATION NUMBER: US/10/255,536

CURRENT FILING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: US/09/669,751

PRIOR FILING DATE: 1999-12-02

NUMBER OF SEQ ID NOS: 261

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 159

LENGTH: S66
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86.4%; Pred. No. 3.1e-07;
tive 0; Mismatches 8; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10045815
Sequence 7, Application US/10045815
Sequence 7, Application US/10045815
GENERAL INFORMATION:
APPLICANT: Wedhwa, Renu
APPLICANT: Ohide, Akiko
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REPRENCE: 06501-091001
CURRENT APPLICATION NUMBER: US/10/045,815
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US/JP00/02731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 159, Application US/1025536; Publication No. US20030087807A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Conservative
                      APPLICANT: Andersson, Leif
                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Drosophila
US-10-255-536-159
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
GENERAL INFORMATION:
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US-10-045-815-7
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Choi, Julie Y
Denton, R. Rex
Kliem, Stefanie E
                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapien
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LOCATION: (4141)
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                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.6%; Score 26; DB 10; Length 1682; Best Local Similarity 64.4%; Pred. No. 3.7; Matches 38; Conservative 0; Mismatches 21; Indels
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION UNBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SEQ ID NO 129
LENGTH: 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.3%; Score 25.8; DB 9; Length 1 67.9%; Pred. No. 4.4; tive 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chew, Anne
APPLICANT: Chew, Julie Y
APPLICANT: Choi, Julie Y
APPLICANT: Choi, Julie Y
APPLICANT: Choi, St. Rex
APPLICANT: Lee, Helen H
APPLICANT: Nendabalan, Krishnan
TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2
CURRENT APPLICATION UNMER: US/09/979,593
CURRENT FILING DATE: 2001-11-4
PRIOR FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: 60/201,946
PRIOR FILING DATE: 2000-05-05
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US-09-979-593-59/c
Sequence 59, Application US/09979593
Publication No. US20030082555A1
GENERAL INFORMATION:
APPLICANT: Genaissance Pharmaceuticals, Inc.;
APPLICANT: Chew, Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Genaissance Pharmaceuticals, Inc. APPLICANT: Chew, Anne
                                                                                                                                                                                                                                                                                                          ; LOCATION: (24)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/09979593; Publication No. US20030082555A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-979-593-1
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LENGTH: 12043
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US-09-979-593-1/C
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            APPLICANT: Nendabalan, Krishnan
TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
FILE REFERENCE: WMH-0425 PCT ICAM2
CURRENT APPLICATION NUMBER: US/09/979,593
CURRENT APPLICATION NUMBER: PCT/USO1/14714
PRIOR APPLICATION NUMBER: PCT/USO1/14714
PRIOR APPLICATION NUMBER: 60/201,946
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PATENTIN VOICE: 31
SEQ ID NO 59
LENGTH: 12043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
LOCATION: (7961)
OTHER INFORMATION: PS11: polymorphic base G or A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (7902)
OTHER INFORMATION: PS10: polymorphic base G or A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) LOCATION: (8037)
; OTHER INFORMATION: PS12: polymorphic base G or A
US-09-979-593-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: (7187)
OTHER INFORMATION: PS8: polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (7875)
OTHER INFORMATION: PS9: polymorphic base G or A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (7155)
OTHER INFORMATION: PS6: polymorphic base G or A
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (3697)
OTHER INFORMATION: PS1: polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (4141)
OTHER INFORMATION: PS3: polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (4221)
OTHER INFORMATION: PS4: polymorphic base T or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (5302)
OTHER INFORMATION: PS5: polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: allele
LOCATION: (4110)
OTHER INFORMATION: PS2: polymorphic base C
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: (7181)
OTHER INFORMATION: PS7: polymorphic base T
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Matches 36; Conservative
Lee, Helen H
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ZIP: 60606
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US-10-288-160-3
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                         Sequence 2280, Application US/09764891
PUblication No. US20030077808A1
GENERAL INFORMATION:
APPLICATION: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
FILE PAPELICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
FILE DE NOS: 10231
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6987, Application US/09764891
PUBLication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOG6
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper: NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.0%; Score 25; DB 9; Length 635; Best Local Similarity 64.9%; Pred. No. 8.2; Matches 37; Conservative 0; Mismatches 20; Indels
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Pred. No. 8.4;
0; Mismatches
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-6987
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Patent No. US20020038467A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
APPLICANT: Matthews, William
APPLICANT: Moore, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 41.0%;
Best Local Similarity 64.9%;
Matches 37; Conservative
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SEQ ID NO 6987
LENGTH: 22585
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-764-891-2280
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ORGANISM: HOMO sapiens
                                                                                                                           US-09-764-891-2280/c
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                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2280
LENGTH: 635
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Using Mammalian Melanocortin Receptor Agonists and Antaç
To Modulate Feeding Behavior in Animals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Methods and Reagents for Discovering and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 40.7%; Score 24.8; DB 10; Length 200; Best Local Similarity 67.3%; Pred. No. 9.5; Matches 35; Conservative 0; Mismatches 17; Indels 0
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STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/10/288,160
TILING DATE: 05-No. US20030105024A1-2002
CLASSIFICATION: CURNOWN>
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FILING DATE: 04.5EP-1996
ATTORNEY/AGENT INFORMATION:
NAME: No. US20030105024Alnan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                     FILE TELEGRICATION NUMBER: US/09/815,944
CURRENT APPLICATION NUMBER: US/09/815,944
CURRENT FILE DATE: 2001-03-22
CURRENT FILING DATE: 2001-03-22
PRIOR PELLOR DATE: 2000-03-22
PRIOR PELLOR TOWNABER: US 60/191,236
PRIOR PELLOR DATE: 2000-03-22
PRIOR PELLOR NUMBER: US 60/215,214
PRIOR APPLICATION NUMBER: US 60/218,075
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 200
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Boston, Bruce A
Kesterton, Robert A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen, Wenbiao
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GENERAL INFORMATION:
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; Batent No. US20020038467a1
; GENERAL INCORMATION:
    APPLICANT: Allen, Keith D.
    APPLICANT: Allen, Keith D.
    APPLICANT: Anthews, William
    APPLICANT: Matthews, William
    APPLICANT: Phillips, Russell
    TITLE OF INVENTION: TRANSCENIC MICE CONTAINING MELANOCYTE
    TITLE OF INVENTION: TRANSCENIC MICE CONTAINING MELANOCYTE
    TITLE OF INVENTION: STIMULATING HORMONE RECEPTOR GENE DISRUPTIONS
    FILE REFERENCE: R-654
    CURRENT APPLICATION NUMBER: US 60/191,236
    PRIOR APPLICATION NUMBER: US 60/191,236
    PRIOR APPLICATION NUMBER: US 60/215,214
    PRIOR PILLING DATE: 2000-06-29
    PRIOR FILING DATE: 2000-06-29
    PRIOR FILING DATE: 2000-07-12
    PRIOR RELICATION NUMBER: US 60/218,075
    PRIOR RELICATION NUMBER: US 60/219,167
    PRIOR PILLICATION NUMBER: US 60/219,167
    PRIOR FILING DATE: 2000-07-12
    PRIOR FILING DATE: 2000-07-13
    PRIOR FILING DATE: 2000-07-13
    PRIOR FILING DATE: 2000-07-13
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67.3%; Pred. No. 9.7;
tive 0; Mismatches 17; Indels 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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US-09-880-107-3428/c
; Sequence 3428, Application US/09880107
; Patent No. US20020142981A1
TELEFAX: 312-913-0002
TELEX: <URNOWN>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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Sequence 92, Application US/10044090
Patent No. US20020137081A1
Patent No. US20020137081A1
Patent No. US20020137081A1
Patent No. US20020137081A1
PILE BERENATION:
PILE REPRENCE: PA-0028 US
CURRENT APPLICANT NUMBER: US/10/044,090
CURRENT APPLICAND NUMBER: US/10/044,090
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SOFTWARE: PERL Program
SEG ID NO 92
LENGTH: 733
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APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scharf, Uwe
APPLICANT: Gene Logic, Inc.
ITILE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US 60/211, 379
PRIOR PAPLICATION NUMBER: US 60/211, 379
PRIOR PILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 3428
LENGTH: 99014
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Genbank Accession No. US20020142981A1 U78027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 416842.32
; NAME/KEY: unsure
; LOCATION: 665, 690, 698
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-92
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Pred. No. 10;
0; Mismatches 17;
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Best Local Similarity 67.3%;
Matches 35; Conservative
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FEATURE:
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ORGANISM: Homo sapiens
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